

Access DB# 100105

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail Box and Bldg. Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CMI 1507 -- 703-306-4498  
jan.delaval@uspto.gov

## STAFF USE ONLY

Searcher Jan

Searcher Phone # 4698

Searcher Location \_\_\_\_\_

Date Searcher Invented 7/30/03

Date Completed 7/30/03

Searcher Prep & Review Time \_\_\_\_\_

Client Prep Time 20

Time to Time 40

## Type of Search

NA Sequence (#) \_\_\_\_\_

AA Sequence (#) ☒

Structure (#) \_\_\_\_\_

Bibliographic \_\_\_\_\_

Litigation \_\_\_\_\_

Fulltext \_\_\_\_\_

Patent Family \_\_\_\_\_

Other \_\_\_\_\_

## Vendors and cost where applicable

STN \_\_\_\_\_

Dialog \_\_\_\_\_

Questel Orbit \_\_\_\_\_

Orbita \_\_\_\_\_

Lexis Nexis \_\_\_\_\_

Sequence Systems ☒

WWW Internet \_\_\_\_\_

Other (specify) \_\_\_\_\_

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# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 100105

TO: Phuong N Huynh  
Location: 8b13 / 9e12  
Wednesday, July 30, 2003  
Art Unit: 1644  
Phone: 308-4844  
Serial Number: 09 / 865198

From: Jan Delaval  
Location: Biotech-Chem Library  
CM1-1E07  
Phone: 308-4498

jan.delaval@uspto.gov

### Search Notes

09/776,232  
April 14.

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CM1 1E07 - 703-308-4498  
jan.delaval@uspto.gov

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100105

**Delaval, Jan**

---

**From:** Huynh, Phuong N.  
**Sent:** Wednesday, July 30, 2003 8:44 AM  
**To:** Delaval, Jan  
**Subject:** RE: RE: 09/865,198

Jan,

I would like to revise my search. Will you please just search peptide of 1-6, and 21-23 against commercial and interference databases? Thanks.

-----Original Message-----

**From:** Delaval, Jan  
**Sent:** Wednesday, July 30, 2003 8:37 AM  
**To:** Huynh, Phuong N.  
**Subject:** RE: RE: 09/865,198

Neon -

The following sequences ARE NOT peptides: 9, 11-14, 24-26.

I will need authorization to process this request. Please obtain approval from one of the following examiners, and request that the approval be sent directly to me:

Martinell, Fredman, Priebe, P Tung, or M Pak.

Please do not submit multiple search requests.

I will wait for approval prior to processing this request.

Thanks.

Jan

-----Original Message-----

**From:** Huynh, Phuong N.  
**Sent:** Wednesday, July 30, 2003 8:26 AM  
**To:** Delaval, Jan  
**Subject:** RE: 09/865,198

Jan,

Please search peptide of SEQ ID NO: 1-6, 9, 24, 11-14, 22-23 and 25-26 against commercial and interference databases.

Thanks,  
Neon  
Art unit 1644  
Mail 9E12  
Tel 308-4844

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CMI 1E07 - 703-308-4498  
jan.delaval@uspto.gov

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# STIC SEARCH RESULTS

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor  
308-4258, CM1-1E01

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk



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GenCore version 5.1.6  
Copyright. (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 2.95681 Seconds  
(without alignments)  
325.245 Million cell updates/sec

Title: US-09-865-198-1  
Perfect score: 59  
Sequence: 1 GFNIKDFYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	94.9	116	2	S15672	Ig heavy chain V r
2	52	88.1	40	2	S33408	Ig heavy chain V r
3	51	86.4	51	2	S36377	Ig heavy chain V r
4	51	86.4	114	4	A47271	nitrophenyl phosph
5	51	86.4	115	2	S03482	Ig heavy chain V-D
6	51	86.4	117	2	S17586	Ig heavy chain V r
7	51	86.4	120	2	S03471	Ig heavy chain V-D
8	51	86.4	120	2	S03484	Ig heavy chain V-D
9	51	86.4	122	2	S06823	Ig heavy chain V r
10	51	86.4	123	2	PH1403	Ig heavy chain V r
11	51	86.4	178	2	S29594	Ig gamma chain (WM
12	51	86.4	221	2	S49220	Ig gamma-1 chain -
13	51	86.4	233	2	JCS322	p53 specific singl
14	51	86.4	268	2	A56446	Ig heavy chain V r
15	50	84.7	97	2	S16028	Ig heavy chain V r
16	50	84.7	108	2	PH1012	Ig heavy chain V r
17	50	84.7	136	2	S04576	Ig heavy chain pre
18	50	84.7	137	2	S52445	Ig heavy chain V r
19	47	79.7	107	2	PH1013	Ig heavy chain V r
20	47	79.7	118	2	S25174	Ig heavy chain V r
21	44	74.6	118	2	G37267	Ig heavy chain V r
22	43	72.9	40	2	S33409	Ig heavy chain V r
23	42	71.2	85	2	B37262	Ig heavy chain V r
24	42	71.2	120	2	PL0018	Ig heavy chain V-D
25	42	71.2	249	2	S41374	single chain Fv an
26	41	69.5	99	2	D37262	Ig heavy chain V r
27	41	69.5	116	2	S24289	Ig gamma chain V r
28	40	67.8	98	2	G47624	Ig heavy chain V-V
29	40	67.8	117	2	E33989	Ig heavy chain V-5

30	39	66.1	93	2	I47624	Ig heavy chain V-V
31	39	66.1	99	2	C37262	Ig heavy chain V r
32	39	66.1	114	2	S22559	Ig heavy chain V r
33	39	66.1	122	1	A1HUTR	Ig heavy chain V-I
34	38	64.4	107	2	A27646	Ig heavy chain V r
35	38	64.4	115	2	PL0246	Ig heavy chain V r
36	38	64.4	123	1	AVMS13	Ig heavy chain V r
37	38	64.4	1738	2	S20614	Ig heavy chain V r
38	37	62.7	77	2	S46465	conserved hypothet
39	37	62.7	98	2	S26909	Ig heavy chain V r
40	37	62.7	110	2	PH1000	Ig heavy chain V r
41	37	62.7	288	2	S29690	Ig heavy chain V r
42	37	62.7	736	2	B82944	Ig heavy chain VDJ
43	36	61.0	99	2	C48223	ribose/galactose A
44	36	61.0	101	2	PU0001	Ig heavy chain V r
45	36	61.0	111	2	D30515	Ig heavy chain V r

ALIGNMENTS

RESULT 1  
S15672  
Ig heavy chain V region - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S15672  
R/Tempst, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, Bio/Technology 9, 266-271, 1991  
A/Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi  
A/Reference number: S15672; MUID:91337412; PMID:1367535  
A/Accession: S15672  
A/Status: preliminary; nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-116 <TEM>  
A/Cross-references: EMBL:X58835; NID:951978; PIDN:CAA41644.1; PID:951979  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 94.9%; Score 56; DB 2; Length 116;  
Best Local Similarity 90.0%; Pred. NO. 0.0025;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GFNIKDFYMH 10  
Db 26 GFNIKDYMH 35

RESULT 2  
S33408  
Ig heavy chain V region - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 17-Jul-1998  
C/Accession: S33408  
R/Kettlborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.  
Eur. J. Immunol. 23, 206-211, 1993  
A/Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes usi  
A/Reference number: S33391; MUID:93122092; PMID:8419173  
A/Accession: S33408  
A/Molecule type: mRNA  
A/Residues: 1-40 <KET>  
A/Cross-references: EMBL:X73017  
A/Experimental source: strain BALB/c  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 88.1%; Score 52; DB 2; Length 40;  
Best Local Similarity 80.0%; Pred. NO. 0.0045;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

|||||:|  
Db 26 GFNIKDYIYH 35

## RESULT 3

S36377

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 23-Jul-1999

C/Accession: S36377; S33392

R/Ansell, K.H.

Submitted to the EMBL Data Library, April 1993

A/Reference number: S36376

A/Accession: S36377

A/Molecule type: mRNA

A/Residues: 1-51 &lt;ANS&gt;

A/Cross-references: EMBL:X73023; NID:g295891; PIDN:CAA51506.1; PID:g9339949

R/Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.

Eur. J. Immunol. 23, 206-211, 1993

A/Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes used

A/Reference number: S33391; MUID:93122092; PMID:8419173

A/Accession: S33392

A/Molecule type: mRNA

A/Residues: 1-40, 'H' &lt;KET&gt;

A/Cross-references: EMBL:X73023

A/Experimental source: strain BALB/c

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

## Query Match

Best Local Similarity 86.4%; Score 51; DB 2; Length 51;  
Pred. No. 0.0089;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

|||||

Db 26 GFNIKDTYMH 35

## RESULT 4

A47271

nitrophenyl phosphonate-specific antibody 48G7 heavy chain VDJ - synthetic (fragment)

C/Species: synthetic

A/Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli

C/Date: 21-Sep-1993 #sequence\_revision 11-Aug-1995 #text\_change 11-Aug-1995

C/Accession: A47271

R/Lesley, S.A.; Patten, P.A.; Schultz, P.G.

Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993

A/Title: A genetic approach to the generation of antibodies with enhanced catalytic activity

A/Reference number: A47271; MUID:93165660; PMID:8094556

A/Accession: A47271

A/Molecule type: DNA; protein

A/Residues: 1-114 &lt;LES&gt;

A/Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBI:P124855)

A/Note: parts of this sequence were determined by protein sequencing

F;22-96/Disulfide bonds: #status predicted

## Query Match

Best Local Similarity 86.4%; Score 51; DB 4; Length 114;  
Pred. No. 0.021;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

|||||

Db 26 GFNIKDTYMH 35

## RESULT 5

S03482

Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

A/Variety: strain BALB/c

C/Date: 26-Feb-1998 #sequence\_revision 26-Feb-1998 #text\_change 21-Jan-2000

C/Accession: S03482; S07453

R/Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.

EMBO J. 2, 867-872, 1983

A/Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT hypervariable regions.

A/Reference number: S03471; MUID:84057768; PMID:6416834

A/Accession: S03482

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 10-115 &lt;ROC1&gt;

A/Cross-references: EMBL:X03219

A/Note: this sequence was determined from the differentiated gene

R/Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, J.G.; Theze, J.; Fougere

J. Immunol. 129, 2554-2558, 1982

A/Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se

A/Reference number: S07453; MUID:83058021; PMID:6815271

A/Accession: S07453

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-43 &lt;ROC2&gt;

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-98/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 86.4%; Score 51; DB 2; Length 115;  
Pred. No. 0.021;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

|||||

Db 26 GFNIKDTYMH 35

## RESULT 6

S17586

Ig heavy chain V region (E8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C/Accession: S17586

R/Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowditch, K.; Getzoff, E.D.

J. Mol. Biol. 221, 455-462, 1991

A/Title: Biochemical implications from the variable gene sequences of an anti-cytochrome

form.

A/Reference number: S17586; MUID:92015240; PMID:1656053

A/Accession: S17586

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-117 &lt;MYLV&gt;

A/Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 86.4%; Score 51; DB 2; Length 117;  
Pred. No. 0.022;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

|||||

Db 26 GFNIKDTYMH 35

## RESULT 7

S03471

Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000

C/Accession: S03471; S07453

R/Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.

EMBO J. 2, 867-872, 1983

A/Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT

hypervariable regions

A/Reference number: S03471; MUID:84057768; PMID:6416834

A/Accession: S03471

A/Molecule type: mRNA

A/Residues: 7-120 &lt;ROC1&gt;



A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983  
A;Note: this sequence was determined from the differentiated gene  
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere  
J. Immunol. 129, 2554-2558, 1982  
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se  
A;Reference number: S07453; MUID:83058021; PMID:6815271  
A;Accession: S07453  
A;Molecule type: protein  
A;Residues: 1-43 <ROCC2>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 51; DB 2; Length 120;  
Best Local Similarity 90.0%; Pred. No. 0.022;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||  
Db 26 GFNIKDTYMH 35

RESULT 8  
S03484

Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
A;Variety: strain BALB/c  
C;Date: 26-Feb-1998 #sequence\_revision 26-Feb-1998 #text\_change 21-Jan-2000  
C;Accession: S03484; S07453  
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.  
EMBO J. 2, 867-872, 1983  
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT  
hypervariable regions.  
A;Reference number: S03471; MUID:84057768; PMID:6416834  
A;Accession: S03484  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 10-120 <ROCC1>  
A;Cross-references: EMBL:X07144  
A;Note: this sequence was determined from the differentiated gene  
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere  
J. Immunol. 129, 2554-2558, 1982  
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se  
A;Reference number: S07453; MUID:83058021; PMID:6815271  
A;Accession: S07453  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-43 <ROCC2>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 51; DB 2; Length 120;  
Best Local Similarity 90.0%; Pred. No. 0.022;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||  
Db 26 GFNIKDTYMH 35

## RESULT 9

Ig heavy chain V region (clone IIC) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000  
C;Accession: S06823  
R;Miller III, A.; Glasel, J.A.  
J. Mol. Biol. 209, 763-778, 1989  
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp  
A;Reference number: S06815; MUID:90064531; PMID:2555519  
A;Accession: S06823  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA

A;Residues: 1-122 <MIL>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 51; DB 2; Length 122;  
Best Local Similarity 90.0%; Pred. No. 0.023;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||  
Db 26 GFNIKDTYMH 35

RESULT 10  
PH1403

Ig heavy chain V region (clone micro m- 46-6, 46-12) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jan-2000  
C;Accession: PH1403  
R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta  
J. Exp. Med. 176, 1209-1214, 1992  
A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in  
ia virus.  
A;Reference number: PH1403; MUID:93018837; PMID:1402663  
A;Accession: PH1403  
A;Molecule type: DNA  
A;Residues: 1-123 <SHI>  
C;Genetics:  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;35-118/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 51; DB 2; Length 123;  
Best Local Similarity 90.0%; Pred. No. 0.023;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||  
Db 46 GFNIKDTYMH 55

## RESULT 11

S29594  
Ig gamma chain (WM65) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C;Accession: S29594  
R;Seymour, R.  
submitted to the EMBL Data Library, February 1991  
A;Reference number: S29594  
A;Accession: S29594  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-178 <SEY>  
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591  
C;Keywords: immunoglobulin

Query Match 86.4%; Score 51; DB 2; Length 178;  
Best Local Similarity 90.0%; Pred. No. 0.034;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||  
Db 39 GFNIKDTYMH 48

## RESULT 12

S49220  
Ig gamma-1 chain - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 21-Jan-2000

C;Accession: S49220

R;KIPP, B.; Becker, W.P.; Schlaak, M.M.

submitted to the EMBL Data Library, September 1994

A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a

A;Reference number: S49220

A;Accession: S49220

A;Molecule type: mRNA

A;Residues: 1-221 <KIP>

A;Cross-references: EMBL:Z37502; NID:g541778; PIDN:CAA85732.1; PID:g541779

A;Experimental source: strain Balb/c

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;1-120/Domain: V region #status predicted <VRG>

F;121-221/Domain: C region #status predicted <CRG>

F;139-203/Domain: immunoglobulin homology <IMM>

#### Query Match

Best Local Similarity 86.4%; Score 51; DB 2; Length 221;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

DB 26 GFNIKDTYMH 35

#### RESULT 13

JC5322

p53 specific single-chain antibody pab421 - human

C;Species: Homo sapiens (man)

C;Date: 15-May-1997 #sequence\_revision 15-May-1997 #text\_change 18-Jul-1997

C;Accession: JC5322

R;Jannot, C.B.; Hynes, N.E.

Biochem. Biophys. Res. Commun. 230, 242-246, 1997

A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.

A;Reference number: JC5322; MUID:97168950; PMID:9016757

A;Accession: JC5322

A;Molecule type: mRNA

A;Residues: 1-233 <JAN>

A;Experimental source: hybridoma cell

C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

#### Query Match

Best Local Similarity 86.4%; Score 51; DB 2; Length 233;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

DB 22 GFNINDYYMH 31

#### RESULT 14

AS6446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C;Species: Mus musculus (house mouse)

C;Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C;Accession: AS6446

R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical

A;Reference number: AS6446; MUID:95229583; PMID:7713873

A;Accession: AS6446

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-268 <TAN>

A;Cross-references: GB:U20617

C;Keywords: heterotetramer; immunoglobulin

#### Query Match

Best Local Similarity 86.4%; Score 51; DB 2; Length 268;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

DB 28 GFNIKDTYMH 37

#### RESULT 15

S16028

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Jun-2000

C;Accession: S16028

R;Tutter, A.; Brodeur, P.; Shlomchik, M.; Riblet, R.

submitted to the EMBL Data Library, September 1990

A;Description: Structure, Map position, and evolution of two newly diverged mouse immune

A;Reference number: S16028

A;Accession: S16028

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-97 <TVT>

A;Cross-references: EMBL:X55934; NID:g55284; PIDN:CAA39399.1; PID:G1334156

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;14-97/Domain: immunoglobulin homology <IMM>

#### Query Match

Best Local Similarity 84.7%; Score 50; DB 2; Length 97;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

DB 25 GFNIKDDYMH 34

Search completed: July 30, 2003, 09:44:03  
Job time : 3.95681 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:35 ; Search time 1.56146 Seconds  
(without alignments)  
301.171 Million cell updates/sec

Title: US-09-865-198-1  
Perfect score: 59  
Sequence: 1 GFNIKDFYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	66.1	122	1	HV3A_HUMAN P01762 homo sapien
2	38	64.4	123	1	HV24_MOUSE P01793 mus musculu
3	38	64.4	1738	1	PPCK_THEAC Q9hiv2 thermoplasm
4	38	64.4	1738	1	YCF1_EPIVI Q00383 epifagus vi
5	36	61.0	122	1	HV20_MOUSE P01789 mus musculu
6	36	61.0	122	1	HV21_MOUSE P01790 mus musculu
7	36	61.0	123	1	HV18_MOUSE P01787 mus musculu
8	36	61.0	123	1	HV19_MOUSE P01788 mus musculu
9	36	61.0	123	1	HV22_MOUSE P01791 mus musculu
10	36	61.0	123	1	HV23_MOUSE P01792 mus musculu
11	36	61.0	144	1	HV26_MOUSE P01795 mus musculu
12	36	61.0	405	1	SPI2_HUMAN Q75830 homo sapien
13	36	61.0	505	1	SPK2_CAEEL P52192 caenorhabdi
14	36	61.0	606	1	PPCK_MYCTU P96393 mycobacteri
15	36	61.0	699	1	CRAR_HUMAN P48740 h complemen
16	36	61.0	704	1	CRAR_MOUSE P98064 mus musculu
17	35.5	60.2	3951	1	VGFI1_IBVB P27920 avian infec
18	35	59.3	98	1	HV57_MOUSE P18528 mus musculu
19	35	59.3	314	1	MIAA_CHLMU Q9p1f7 chlamydia m
20	35	59.3	314	1	MIAA_CHLTR O84771 chlamydia t
21	35	59.3	365	1	ID12_METAC O8tt35 methanosarc
22	35	59.3	605	1	PPCK_MYCSM Q9agj6 mycobacteri
23	35	59.3	759	1	Y363_METUA Q57809 methanococc
24	35	59.3	1162	1	LEPR_MOUSE P48356 mus musculu
25	34	57.6	119	1	HV31_HUMAN P01773 homo sapien
26	34	57.6	228	1	DCHS_KLEOR Q810z4 klebsiella
27	34	57.6	237	1	CD63_RABIT Q28709 coryctolagus
28	34	57.6	282	1	PORI_DROME Q94920 drosophila
29	34	57.6	295	1	SYGA_BACSU P54380 bacillus su
30	34	57.6	307	1	PLD_CORPS P20626 corynebacte
31	34	57.6	340	1	MOAA_STACA Q9zime staphylococ
32	34	57.6	360	1	CCPH_HSVSA Q01016 herpesvirus
33	34	57.6	377	1	DCHS_KLEPL P28578 klebsiella

34	34	57.6	405	1	SPI2_MOUSE Q9jk88 mus musculu
35	34	57.6	454	1	DNAA_BUCAP P29434 buchnera ap
36	34	57.6	535	1	C7C1_MAIZE Q43250 zea mays (m
37	34	57.6	540	1	Z136_HUMAN P52737 homo sapien
38	34	57.6	589	1	PPCK_THEVO P58306 thermoplasm
39	34	57.6	622	1	PPCK_RALSO Q8y3g3 ralstonia s
40	34	57.6	2038	1	FSH_DROME P13709 drosophila
41	34	57.6	2244	1	PYRI_SCHPO Q09794 schizosacch
42	33	55.9	120	1	HV3U_HUMAN P01782 homo sapien
43	33	55.9	138	1	END5_BPT4 P04418 bacterioph
44	33	55.9	156	1	ARGR_ECOLI P15282 escherichia
45	33	55.9	165	1	YB09_MYCPN P75453 mycoplasma

ALIGNMENTS

RESULT 1									
HV3A_HUMAN									
ID	HV3A_HUMAN	STANDARD;	PRT;	122 AA.					
AC	P01762;								
DT	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DT	15-SEP-2003 (Rel. 42, Last annotation update)								
DE	Ig heavy chain V-II region TRO.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE (MYELOMA PROTEIN TRO).								
RX	MEDLINE=76023781; PubMed=809331;								
RA	Kratzlin H., Altevogt P., Ruban E., Kortt A., Staroscik K.,								
RA	Hilschmann N.;								
RT	"The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),								
RT	II. The amino acid sequence of the H-chain, alpha-type, subgroup III;								
RT	structure of the complete IgA-molecule."								
RL	Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).								
CC	-I- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.								
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.								
DR	PIR; A02045; AIHUTR.								
DR	HSSP; P01772; 2FB4.								
DR	GO; GO:0005576; C:extracellular; NAS.								
DR	GO; GO:0003823; F:antigen binding activity; NAS.								
DR	GO; GO:0006955; P:immune response; NAS.								
DR	InterPro; IPR007110; Ig-like.								
DR	InterPro; IPR003006; Ig_MHC.								
DR	InterPro; IPR003596; Ig_v.								
DR	Pfam; PF00047; Ig_1.								
DR	SMART; SM00406; IGV; 1.								
DR	PROSITE; PSS0835; IG_LIKE; 1.								
KW	Immunoglobulin V region; Pyrrolidone carboxylic acid.								
FT	DOMAIN 1 108 IG-LIKE.								
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.								
FT	NON_TER 122 122								
SQ	SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;								
Query Match									
Best Local Similarity		66.1%;		Score 39; DB 1; Length 122;					
Matches 6; Conservativity		2; Mismatches		1; Indels		0; Gaps		0;	
RESULT 2									
HV24_MOUSE									
ID	HV24_MOUSE	STANDARD;	PRT;	123 AA.					
AC	P01793;								
DT	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DT	15-SEP-2003 (Rel. 42, Last annotation update)								

DE Ig heavy chain V region HPCG13.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81197602; PubMed=7231520;  
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;  
RT "Igc antibodies to phosphorylcholine exhibit more diversity than  
RT their Igm counterparts.";  
RL Nature 291:29-34(1981).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS PHOSPHORYLCHOLINE.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; F93256; AVMS13.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 114 IG-LIKE.  
FT NON\_TER 123 123  
SQ SEQUENCE 123 AA; 13808 MW; 6599F256CCEDE50 CRC64;  
  
Query Match 64.4%; Score 38; DB 1; Length 123;  
Best Local Similarity 66.7%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
OY 1 GFNIKDFYM 9  
DB 26 GFTLSDFYM 34  
  
RESULT 3  
PPCK\_THEAC STANDARD; PRT; 588 AA.  
AC O9HLV2;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) (PEP  
DE carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).  
GN PCKG OR TA0123.  
OS Thermoplasma acidophilum.  
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;  
OC Thermoplasmataceae; Thermoplasma.  
OX NCBI\_TaxID=2303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 1728;  
RX MEDLINE=20479972; PubMed=11029001;  
RA Muepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,  
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;  
RT "The genome sequence of the thermophilic scavenger Thermoplasma  
RT acidophilum.";  
RL Nature 407:508-513(2000).  
CC -1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate  
CC + CO(2).  
CC -1- PATHWAY: Rate-limiting gluconeogenic enzyme.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP]  
CC FAMILY.  
-----  
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CC -----  
DR EMBL; AL445063; CAC11270.1; ALT\_INIT.  
DR HAMAP; MF 00452; -; 1.  
DR InterPro; IPR000364; PEP\_carboxykin.  
DR Pfam; PF00821; PEPCK; 1.  
DR ProDom; PD004738; PEPCK\_N; 1.  
DR PROSITE; PS00505; PEPCK\_GTP; FALSE NEG.  
KW Gluconeogenesis; Lyase; Decarboxylase; GTP-binding; Complete proteome.  
FT NP\_BIND 209 216 GTP (POTENTIAL).  
FT ACT\_SITE 260 260 BY SIMILARITY.  
SQ SEQUENCE 588 AA; 67307 MW; 30E963E7E62D78C1 CRC64;  
  
Query Match 64.4%; Score 38; DB 1; Length 588;  
Best Local Similarity 50.0%; Pred. No. 19;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
OY 1 GFNIKDFYMH 10  
DB 458 GYNISDYFRH 467  
  
RESULT 4  
YCF1\_EPIVI STANDARD; PRT; 1738 AA.  
ID YCF1\_EPIVI  
AC Q00383;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical 208 kDa protein ycf1 (ORF 1738).  
GN YCF1.  
OS Epifagus virginiana (Beechdrops).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; Lamiales; Orobanchaceae; Orobanchaceae; Epifagus.  
OX NCBI\_TaxID=4177;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92114084; PubMed=1731088;  
RA Wolfe K.H., Morden C.W., Palmer J.D.;  
RT "Small single-copy region of plastid DNA in the non-photosynthetic  
RT angiosperm Epifagus virginiana contains only two genes. Differences  
RT among dicots, monocots and bryophytes in gene organization at a non-  
RT bioenergetic locus.";  
RL J. Mol. Biol. 223:95-104(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93066301; PubMed=1332054;  
RA Wolfe K.H., Morden C.W., Palmer J.D.;  
RT "Function and evolution of a minimal plastid genome from a  
RT nonphotosynthetic parasitic plant.";  
RT Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652(1992).  
CC -1- FUNCTION: NOT YET KNOWN.  
CC -1- SIMILARITY: BELONGS TO THE YCF1 FAMILY.  
-----  
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CC -----  
DR EMBL; X61368; CAA43644.1; -.  
DR EMBL; M81884; AAA65870.1; -.  
DR PIR; S20614; S20614.  
KW Chloroplast; Hypothetical protein.  
SQ SEQUENCE 1738 AA; 208318 MW; 65C63F63BDC8364B CRC64;  
  
Query Match 64.4%; Score 38; DB 1; Length 1738;  
Best Local Similarity 87.5%; Pred. No. 56;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 1 GENIKDFY 8  
Db 278 GSNIKDFY 285

## RESULT 5

HV20\_MOUSE STANDARD; PRT; 122 AA.  
AC P01789;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region M603.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=80199926; PubMed=6769593;  
RA Early P., Huang H., Davis M., Calame K., Hood L.;  
RT "An immunoglobulin heavy chain variable region gene is generated from  
three segments of DNA: VH, D and JH.";  
RL Cell 19:981-992(1980).  
RN [2]  
RP SEQUENCE OF 1-120.  
RX MEDLINE=75017346; PubMed=4213527;  
RA Rudikoff S., Potter M.;  
RT "Variable region sequence of the heavy chain from a phosphorylcholine  
binding myeloma protein.";  
RL Biochemistry 13:4033-4038(1974).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.  
RX MEDLINE=75065510; PubMed=4530984;  
RA Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,  
RA Davies D.R.;  
RT "The three-dimensional structure of a phosphorylcholine-binding mouse  
immunoglobulin Fab and the nature of the antigen binding site.";  
RL Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
BINDS PHOSPHORYLCHOLINE.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; B90795; AVMS63.  
DR PDB; 1MCP; 15-JUL-92.  
DR PDB; 2MCP; 15-JUL-92.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; 3D-structure.  
FT DOMAIN 1 121  
FT SITE 33 33 H-BOND WITH THE PHOSPHATE GROUP OF PHOS-  
FT H-BOND WITH THE PHOSPHATE GROUP OF PHOS-  
FT SITE 52 52 H-BOND WITH THE PHOSPHATE GROUP OF PHOS-  
FT STRAND 3 7  
FT STRAND 11 12  
FT TURN 14 15  
FT STRAND 17 25  
FT TURN 30 31  
FT STRAND 33 39  
FT TURN 41 42  
FT STRAND 46 50  
FT TURN 54 55  
FT STRAND 61 61  
FT TURN 64 69  
FT STRAND 70 75  
FT TURN 76 79  
FT STRAND 80 86  
FT HELIX 90 92

FT STRAND 94 103  
FT STRAND 107 112  
FT STRAND 116 120  
FT NON TER 122 122  
SQ SEQUENCE 122 AA; 13626 MW; BA2C864438B64F0F CRC64;

Query Match 61.0%; Score 36; DB 1; Length 122;  
Best Local Similarity 66.7%; Pred. No. 9.1;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GENIKDFYM 9  
Db 26 GFTFSDPYM 34

## RESULT 6

HV21\_MOUSE STANDARD; PRT; 122 AA.  
ID HV21\_MOUSE  
AC P01790;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region M511.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81054880; PubMed=6776528;  
RA Robinson E.A., Appella E.;  
RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain  
(MOPC 511).";  
RL Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
BINDS PHOSPHORYLCHOLINE.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR HSSP; P01789; 1MCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 114  
FT NON TER 122 122 IG-LIKE.  
SQ SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;

Query Match 61.0%; Score 36; DB 1; Length 122;  
Best Local Similarity 66.7%; Pred. No. 9.1;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GENIKDFYM 9  
Db 26 GFTFSDPYM 34

## RESULT 7

HV18\_MOUSE STANDARD; PRT; 123 AA.  
ID HV18\_MOUSE  
AC P01787;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE (TEPC 15).  
RX MEDLINE=76222762; PubMed=819932;

RA Rudikoff S., Potter M.;  
RT "size differences among immunoglobulin heavy chains from  
RT phosphorylcholine-binding proteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).  
RN [2]  
RP SEQUENCE FROM N.A. (H107).  
RX MEDLINE=80199926; PubMed=6769593;  
RA Early P., Huang H., Davis M., Calame K., Hood L.;  
RT "An immunoglobulin heavy chain variable region gene is generated from  
RT three segments of DNA: VH, D and JH.";  
RL Cell 19:981-992(1980).  
RN [3]  
RP SEQUENCE (S107).  
RX MEDLINE=76110488; PubMed=813561;  
RA Rudikoff S., Barstad P., Potter M., Hood L.;  
RL Unpublished results, cited by:  
RL Hood L., Campbell J.H., Elgin S.C.R.;  
RL Annu. Rev. Genet. 9:305-353(1975).  
RN [4]  
RP SEQUENCE (HPCM1; HPCM2 AND HPCM3).  
RX MEDLINE=81197602; PubMed=7231520;  
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;  
RT "IgG antibodies to phosphorylcholine exhibit more diversity than  
RT their IgM counterparts.";  
RL Nature 291:29-34(1981).  
CC -1- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.  
CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND  
CC HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A93804; AVMS7S.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 114 IG-LIKE.  
FT NON TER 123  
SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;  
Query Match 61.0%; Score 36; DB 1; Length 123;  
Best Local Similarity 66.7%; Pred. No. 9.2;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GFNIKDFYM 9  
DB 26 GFTFSDPYM 34  
RESULT 8  
HV19\_MOUSE STANDARD; PRT; 123 AA.  
AC P01788;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region H8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RA Barstad P.;  
RL Thesis (1975), California Institute of Technology / Pasadena, U.S.A.  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS PHOSPHORYLCHOLINE.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 114 IG-LIKE.  
FT NON TER 123  
SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 114 IG-LIKE.  
FT NON TER 123  
SQ SEQUENCE 123 AA; 13805 MW; 9D581401912F7000 CRC64;  
Query Match 61.0%; Score 36; DB 1; Length 123;  
Best Local Similarity 66.7%; Pred. No. 9.2;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GFNIKDFYM 9  
DB 26 GFTFSDPYM 34

RESULT 9  
HV22\_MOUSE STANDARD; PRT; 123 AA.  
AC P01751;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region HPCM6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81197602; PubMed=7231520;  
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;  
RT "IgG antibodies to phosphorylcholine exhibit more diversity than  
RT their IgM counterparts.";  
RL Nature 291:29-34(1981).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS PHOSPHORYLCHOLINE.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; D93256; AVMSH6.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 114 IG-LIKE.  
FT NON TER 123  
SQ SEQUENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;  
Query Match 61.0%; Score 36; DB 1; Length 123;  
Best Local Similarity 66.7%; Pred. No. 9.2;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GFNIKDFYM 9  
DB 26 GFTFSDPYM 34  
RESULT 10  
HV23\_MOUSE STANDARD; PRT; 123 AA.  
AC P01792;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region HPCG8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
   their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; E93256; AVMSH8.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 114 IG-LIKE.
FT NON TER 123
SQ SEQUENCE 123 AA; 13879 MW; 4559D3106CAF7D8D CRC64;
```

```
Query Match 61.0%; Score 36; DB 1; Length 123;
Best Local Similarity 66.7%; Pred. No. 9.2;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 GFNIKDFYM 9
Db 26 GFTFSDFYM 34
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RESULT 11
HV26_MOUSE STANDARD; PRT; 144 AA.
AC P01795;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region M167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93358330; PubMed=6101208;
RA Kim S., Davis M., Sinn E., Patten P., Hood L.;
RT "Antibody diversity: somatic hypermutation of rearranged VH genes.";
RL Cell 27:573-581(1981).
RN [2]
RP SEQUENCE OF 20-142.
RX MEDLINE=76222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
   phosphorylcholine-binding proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS PHOSPHORYLCHOLINE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00516; AAC18867.2; ALT_TERM.
DR PIR; A90818; AVMS67.
DR HSSP; P01789; IMCP.
```

```
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION M167.
FT DOMAIN 20 133 IG-LIKE.
FT CONFLICT 125 125 N -> D (IN REF. 2).
FT NON TER 144 144
SQ SEQUENCE 144 AA; 16219 MW; BECB4A2C956CF769 CRC64;
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Query Match 61.0%; Score 36; DB 1; Length 144;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 GFNIKDFYM 9
Db 45 GFTFSDFYM 53
```

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RESULT 12
SPI2_HUMAN STANDARD; PRT; 405 AA.
ID SPI2_HUMAN
AC O75830;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serpin I2 precursor (Myoepithelium-derived serine protease inhibitor)
DE (Pancpin) (Protease inhibitor 14) (TSA2004).
GN SERPIN2 OR P114 OR MEPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98287625; PubMed=9624529;
RA Ozaki K., Nagata M., Suzuki M., Fujiwara T., Miyoshi Y., Ishikawa O.,
RA Ohgashi H., Imaka S., Takahashi E., Nakamura Y.;
RT "Isolation and characterization of a novel human pancreas-specific
   gene, pancpin, that is down-regulated in pancreatic cancer cells.";
RL Genes Chromosomes Cancer 22:179-185(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99199247; PubMed=10097100;
RA Xiao G., Liu Y.E., Gentz R., Sang Q.A., Ni J., Goldberg I.D.,
RA Shi Y.E.;
RT "Suppression of breast cancer growth and metastasis by a serpin
   myoepithelium-derived serine proteinase inhibitor expressed in the
   mammary myoepithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3700-3705(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- TISSUE SPECIFICITY: Expressed in pancreas and adipose tissues.  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AB006423; BAA33766.1; -.  
 DR EMBL; AF130470; AAD34723.1; -.  
 DR EMBL; BC027859; AAH27859.1; -.  
 DR HSSP; P05120; 1BY7.  
 DR Genew; HGNC:8945; SERPINI2.  
 DR MIM; 605587; -.  
 DR GO; GO:0004868; F:serpin; TAS.  
 DR GO; GO:0008181; F:tumor suppressor; TAS.  
 DR GO; GO:0006928; P:cell motility; TAS.  
 DR InterPro; IPR000215; Serpin.  
 DR Pfam; PF00079; serpin; 1.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSITE; PS00284; SERPIN; 1.  
 KW Serpin; Serine protease inhibitor; Glycoprotein; Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 405 SERPIN 12.  
 FT ACT\_SITE 357 358 REACTIVE\_BOND (BY SIMILARITY).  
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 405 AA; 46145 MW; 5BA18C60E4FDE9A4 CRC64;  
 QY 1 GFNIKDFYMH 10  
 Db 116 GFTVKEQYLH 125  
 Query Match 61.0%; Score 36; DB 1; Length 405;  
 Best Local Similarity 50.0%; Pred. No. 30;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 RESULT 13  
 IRK4 CAEEL STANDARD; PRT; 505 AA.  
 AC P52152;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inward rectifier potassium channel Irk-4.  
 GN IRK-4 OR R03E9.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Wilcox L.;  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INWARD RECTIFIER K+ CHANNELS ARE CHARACTERIZED BY A  
 CC GREATER TENDANCY TO ALLOW POTASSIUM TO FLOW INTO THE CELL RATHER  
 CC THAN OUT OF IT.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE INWARD RECTIFIER-TYPE K+ CHANNEL  
 CC FAMILY.  
 CC -----

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 CC -----  
 DR EMBL; U40947; AAC48070.1; -.  
 DR PIR; T28859; T28859.  
 DR WormPep; R03E9.4; CE04787.  
 DR InterPro; IPR001838; K+channel\_IR.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR Pfam; PF01007; IRK; 1.  
 DR PRINTS; PRO1320; KIRCHANNEL.  
 DR ProDom; PD001103; K+channel\_IR; 2.  
 KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;  
 KW Potassium transport.  
 FT DOMAIN 1 114 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 115 135 POTENTIAL.  
 FT DOMAIN 136 190 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 191 211 POTENTIAL.  
 FT DOMAIN 212 505 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 505 AA; 57419 MW; C1DF6FDB2B280434 CRC64;  
 QY 3 NIKDFYMH 10  
 Db 400 NIKDYCH 407.  
 Query Match 61.0%; Score 36; DB 1; Length 505;  
 Best Local Similarity 62.5%; Pred. No. 38;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 14  
 PECK MYCTU STANDARD; PRT; 606 AA.  
 ID PECK MYCTU  
 AC P96393;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) (PEP  
 DE carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).  
 GN PCKG OR PCKA OR PCKI OR RV0211 OR MT0221 OR MTCY08D5.06.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sultston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RA "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RT



RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate  
CC + CO(2).  
CC -1- PATHWAY: Rate-limiting gluconeogenic enzyme.  
CC -1- SUBUNIT: Monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP]  
CC FAMILY.  
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CC -----  
DR EMBL; Z92669; CAB07006.1; -.  
DR EMBL; AE006931; AAK4442.1; -.  
DR PIR; A70960; A70960.  
DR TIGR; MT0221; -.  
DR Tuberculist; RV0211; -.  
DR HAMAP; MF\_00452; -. 1.  
DR InterPro; IPR000364; PEP\_carboxykin.  
DR Pfam; PF00821; PEPCK; 1.  
DR ProDom; PD004738; PEPCK\_N; 1.  
DR PROSITE; PS00505; PEPCK\_GTP; 1.  
KM Gluconeogenesis; Lyase; Decarboxylase; GTP-binding; Complete proteome.  
FT NP BIND 222 229 GTP (POTENTIAL).  
FT ACT\_SITE 273 273 BY SIMILARITY.  
SQ SEQUENCE 606 AA; 67253 MW; AEE29412B6BCAE3 CRC64;  
  
QY Query Match 61.0%; Score 36; DB 1; Length 606;  
Best Local Similarity 40.0%; Pred. No. 45;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
  
Db 1 GFNIKDFYMH 10  
471 GYNVGDYFQH 480  
  
RESULT 15  
CRAR\_HUMAN STANDARD; PRT; 699 AA.  
ID CRAR\_HUMAN  
AC P48740; O95570; Q9UF09;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Complement-activating component of Ra-reactive factor precursor  
DE (EC 3.4.21.-) (Ra-reactive factor serine protease p100) (RaRF)  
DE (Mannan-binding lectin serine protease 1) (Mannose-binding protein  
DE associated serine protease) (MASP-1).  
OS MASP1 OR CRARF OR CRARF1 OR PRSS5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=94059062; PubMed=8240317;  
RA Takada F., Takayama Y., Hatsuse H., Kawakami M.;  
RT "A new member of the C1s family of complement proteins found in a  
RT bactericidal factor, Ra-reactive factor, in human serum.";  
RL Biochem. Biophys. Res. Commun. 196:1003-1009(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=94289349; PubMed=8018603;  
RA Sato T., Endo Y., Matsushita M., Fujita T.;  
RT "Molecular characterization of a novel serine protease involved in  
RT activation of the complement system by mannose-binding protein.";  
RL Int. Immunol. 6:665-669(1994).

RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=97079701; PubMed=8921412;  
RA Endo Y., Sato T., Matsushita M., Fujita T.;  
RT "Exon structure of the gene encoding the human mannose-binding  
RT protein-associated serine protease light chain: comparison with  
RT complement C1r and C1s genes.";  
RL Int. Immunol. 8:1355-1358(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99402590; PubMed=10475605;  
RA Takayama Y., Takada F., Nowatari M., Kawakami M., Matsu-ura N.;  
RT "Gene structure of the p100 serine-protease component of the human Ra-  
RT reactive factor.";  
RL Mol. Immunol. 36:505-514(1999).  
CC -1- FUNCTION: COMPONENT OF THE BACTERICIDAL RA-REACTIVE FACTOR RARF  
CC WHICH SPECIFICALLY BINDS TO RA AND R2 POLYSACCHARIDES EXPRESSED BY  
CC CERTAIN ENTEROBACTERIA. IT TRIGGERS THE ACTIVATION OF COMPLEMENT  
CC CASCADE BY ACTIVATING THE C4 AND C2 COMPONENTS. IT ACTIVATES THE  
CC C4 COMPONENT BY CLEAVING THE ALPHA-CHAIN OF C4.  
CC -1- SUBUNIT: RARF CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT  
CC (CRARF) AND A POLYSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT.  
CC CRARF IS AN HETERODIMER OF A HEAVY (P70) AND A LIGHT CHAIN (P29)  
CC LINKED BY A DISULFIDE BOND.  
CC -1- DOMAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR TO C1R AND C1S.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: Contains 2 Sushi (SCR) domains.  
CC -1- SIMILARITY: Contains 2 CUB domains.  
CC -1- SIMILARITY: Contains 1 EGF-like domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; D17525; BAA04477.1; -.  
DR EMBL; D28593; BAA05928.1; -.  
DR EMBL; D61695; BAA34864.1; -.  
DR EMBL; AB010822; BAA34864.1; JOINED.  
DR EMBL; AB010813; BAA34864.1; JOINED.  
DR EMBL; AB010814; BAA34864.1; JOINED.  
DR EMBL; AB010815; BAA34864.1; JOINED.  
DR EMBL; AB010816; BAA34864.1; JOINED.  
DR EMBL; AB010817; BAA34864.1; JOINED.  
DR EMBL; AB010818; BAA34864.1; JOINED.  
DR EMBL; AB010819; BAA34864.1; JOINED.  
DR EMBL; AB010820; BAA34864.1; JOINED.  
DR EMBL; AB010821; BAA34864.1; JOINED.  
DR EMBL; D61690; BAA34864.1; JOINED.  
DR EMBL; D61691; BAA34864.1; JOINED.  
DR EMBL; D61692; BAA34864.1; JOINED.  
DR EMBL; D61693; BAA34864.1; JOINED.  
DR EMBL; D61694; BAA34864.1; JOINED.  
DR EMBL; AB007617; BAA89206.1; -.  
DR EMBL; AB007602; BAA89206.1; JOINED.  
DR EMBL; AB007603; BAA89206.1; JOINED.  
DR EMBL; AB007604; BAA89206.1; JOINED.  
DR EMBL; AB007605; BAA89206.1; JOINED.  
DR EMBL; AB007606; BAA89206.1; JOINED.  
DR EMBL; AB007607; BAA89206.1; JOINED.  
DR EMBL; AB007608; BAA89206.1; JOINED.  
DR EMBL; AB007609; BAA89206.1; JOINED.  
DR EMBL; AB007610; BAA89206.1; JOINED.  
DR EMBL; AB007611; BAA89206.1; JOINED.  
DR EMBL; AB007612; BAA89206.1; JOINED.  
DR EMBL; AB007613; BAA89206.1; JOINED.  
DR EMBL; AB007614; BAA89206.1; JOINED.  
DR EMBL; AB007615; BAA89206.1; JOINED.  
DR EMBL; AB007616; BAA89206.1; JOINED.

DR PIR; I54763; I54763.  
DR HSSP; P00736; IAPQ.  
DR MEROPS; S01.198; -.  
DR Genew; HGNC:6901; MASP1.  
DR MIM; 600521; -.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000859; CUB\_domain.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00084; sushi; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Complement pathway; Serine protease; Protease;  
KW Glycoprotein; Sushi; Repeat; Signal; EGF-like domain; Hydroxylation.  
FT SIGNAL 1 19  
FT CHAIN 20 699  
FT FT  
FT CHAIN 20 448  
FT CHAIN 449 699  
FT DOMAIN 20 138  
FT DOMAIN 139 182  
FT DOMAIN 185 297  
FT DOMAIN 300 363  
FT DOMAIN 366 433  
FT DOMAIN 449 699  
FT ACT\_SITE 490 490  
FT ACT\_SITE 552 552  
FT ACT\_SITE 646 646  
FT MOD\_RES 159 159  
FT DISULFID 73 91  
FT DISULFID 143 157  
FT DISULFID 153 166  
FT DISULFID 168 181  
FT DISULFID 185 212  
FT DISULFID 242 260  
FT DISULFID 301 349  
FT DISULFID 329 362  
FT DISULFID 367 414  
FT DISULFID 397 432  
FT DISULFID 436 572  
FT DISULFID 614 631  
FT DISULFID 642 672  
FT CARBOHYD 49 49  
FT CARBOHYD 178 178  
FT CARBOHYD 385 385  
FT CARBOHYD 407 407  
FT CONFLICT 235 235  
FT CONFLICT 285 285  
FT CONFLICT 499 499  
FT CONFLICT 499 499  
FT CONFLICT 527 527  
FT CONFLICT 543 543  
FT CONFLICT 552 552  
FT CONFLICT 643 643  
SQ SEQUENCE 699 AA; 79258 MW; ADD9697AE6AB01B5 CRC64;

Query Match 61.0%; Score 36; DB 1; Length 699;  
Best Local Similarity 60.0%; Pred. No. 52;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GFNIKDFYMH 10  
Db 55 GFRIKLYFMH 64

Search completed: July 30, 2003, 09:44:58  
Job time : 3.56146 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 7.74086 Seconds  
(without alignments)  
333.364 Million cell updates/sec

Title: US-09-865-198-1  
Perfect score: 59  
Sequence: 1 GFNIKDFYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	79.7	109	11 Q9JL85	Q9JL85 mus musculu
2	43	72.9	468	11 Q99L31	Q99L31 mus musculu
3	43	72.9	603	5 Q8IUD7	Q8IUD7 plasmodium
4	41	69.5	156	16 Q8ESF8	Q8ESF8 oceanobacil
5	38	64.4	948	16 Q8E225	Q8E225 leptospira
6	37	62.7	431	2 Q9F7S7	Q9F7S7 uncultured
7	37	62.7	497	10 Q8RYQ7	Q8RYQ7 oryza sativ
8	37	62.7	534	3 O13321	O13321 metathizium
9	37	62.7	542	2 Q8GA98	Q8GA98 synecococc
10	37	62.7	736	16 Q9PRD1	Q9PRD1 ureaplasma
11	37	62.7	5922	5 Q8IIN2	Q8IIN2 plasmodium
12	36.5	61.9	327	16 Q8D2M7	Q8D2M7 wigglewort
13	36	61.0	150	17 Q979C1	Q979C1 thermoplasm
14	36	61.0	185	8 Q9MIX6	Q9MIX6 uroleucon r
15	36	61.0	186	8 Q9MIX5	Q9MIX5 uroleucon s
16	36	61.0	186	8 Q9MIX4	Q9MIX4 uroleucon r

17	36	61.0	222	17 Q97XU3	Q97XU3 sulfolobus
18	36	61.0	225	16 Q34769	Q34769 bacillus su
19	36	61.0	309	2 Q9X432	Q9X432 streptococc
20	36	61.0	309	16 Q8E6C7	Q8E6C7 streptococc
21	36	61.0	309	16 Q8E0Q9	Q8E0Q9 streptococc
22	36	61.0	369	16 Q8NP54	Q8NP54 corynebacte
23	36	61.0	372	5 Q8MT70	Q8MT70 drosophila
24	36	61.0	385	16 Q8FPC3	Q8FPC3 corynebacte
25	36	61.0	488	4 Q8IUV8	Q8IUV8 homo sapien
26	36	61.0	521	12 Q84358	Q84358 mastomys na
27	36	61.0	570	10 Q9LYQ1	Q9LYQ1 arabidopsis
28	36	61.0	600	10 Q8RY84	Q8RY84 arabidopsis
29	36	61.0	646	5 Q97132	Q97132 drosophila
30	36	61.0	719	13 Q9PVY2	Q9PVY2 triakis scy
31	36	61.0	728	4 Q96RS4	Q96RS4 homo sapien
32	36	61.0	733	11 Q920S0	Q920S0 mus musculu
33	36	61.0	733	11 Q8CD27	Q8CD27 mus musculu
34	36	61.0	791	5 Q22142	Q22142 caenorhabdi
35	36	61.0	2763	5 Q813X5	Q813X5 plasmodium
36	35.5	60.2	6629	12 Q91QT2	Q91QT2 avian infec
37	35	59.3	156	8 Q20623	Q20623 physarum po
38	35	59.3	170	8 Q20625	Q20625 physarum po
39	35	59.3	252	4 Q9H9F2	Q9H9F2 homo sapien
40	35	59.3	279	4 Q9BOG8	Q9BOG8 homo sapien
41	35	59.3	316	5 Q8ITI10	Q8ITI10 plasmodium
42	35	59.3	319	10 Q8VWY2	Q8VWY2 spinacia ol
43	35	59.3	365	16 Q8R695	Q8R695 fusobacteri
44	35	59.3	389	8 Q9MJ75	Q9MJ75 physarum po
45	35	59.3	399	2 Q9F0P1	Q9F0P1 klebsiella

ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	109 AA.
ID Q9JL85			
AC Q9JL85;			
DT 01-OCT-2000 (TREMBLrel. 15, Created)			
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE Anti-myosin immunoglobulin heavy chain variable region (Fragment).			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP .SEQUENCE FROM N.A.			
RC STRAIN=BALB/c;			
RX MEDLINE=20448942; PubMed=10992488;			
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;			
RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin."			
RT Infect. Immun. 68:5803-5808(2000).			
RL EMBL; AF206021; AAF69319.1; -			
DR HSSP; P01810; 2FBJ.			
DR InterPro; IPR007110; IG_1like.			
DR InterPro; IPR003006; IG_MHC.			
DR InterPro; IPR003596; IG_v.			
DR Pfam; PF00047; 1g; 1.			
DR SMART; SM00406; IGV; 1.			
DR PROSITE; PSS0835; IG_LIKE; 1.			
FT NON_TER	1		
FT NON_TER	1		
FT NON_TER	1		
SO SEQUENCE	109 AA;	11944 MW;	DFE615FE6CED4EDE CRC64;
Query Match	79.7%;	Score 47;	DB 11; Length 109;
Best Local Similarity	80.0%;	Pred. No. 0.66;	
Matches	8; Conservative	1; Mismatches	1; Indels 0; Gaps 0;
QY	1 GFNIKDFYMH 10		

Db 18 GFNIEDTYMH 27

## RESULT 2

O99L31 PRELIMINARY; PRT; 468 AA.  
AC O99L31;  
DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)  
DE Similar to RIKEN CDNA 181060009 gene.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC003878; AAH03878.1; -.  
DR HSSP; P01842; 7FAB.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 72.9%; Score 43; DB 11; Length 468;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GFNIKDFYMH 10  
Db 45 GFNIKDSLHM 54

## RESULT 3

O81JD7 PRELIMINARY; PRT; 603 AA.  
AC O81JD7;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)  
DE Hypothetical protein.  
GN PF10\_0261.  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3D7;  
RX MEDLINE=22255705; PubMed=12368864;  
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,  
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,  
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,  
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,  
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,  
RA Martin D.M.A., Faltz A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,  
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,  
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,  
RA Fraser C.M., Barrett B.;  
RT "Genome sequence of the human malaria parasite Plasmodium  
RT falciparum.";  
RL Nature 419:498-511(2002).  
DR EMBL; AB014833; AAN35458.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 603 AA; 71631 MW; 2D178B275234A75C CRC64;

Query Match 72.9%; Score 43; DB 5; Length 603;

Best Local Similarity 66.7%; Pred. No. 19;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 FNIKDFYMH 10  
Db 15 YNIKDFFLH 23

## RESULT 4

O8ESF8 PRELIMINARY; PRT; 156 AA.  
AC O8ESF8;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)  
DE Hypothetical protein.  
GN OB0681.  
OS Oceanobacillus iheyensis.  
OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.  
OX NCBI\_TaxID=182710;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;  
RX MEDLINE=22220767; PubMed=12235376;  
RA Takami H., Takaki Y., Uchiyama I.;  
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya  
RT Ridge and its unexpected adaptive capabilities to extreme  
RT environments.";  
RL Nucleic Acids Res. 30:3927-3935(2002).  
DR EMBL; AP004595; BAC12637.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 156 AA; 17548 MW; 4B784980F816C301 CRC64;

Query Match 69.5%; Score 41; DB 16; Length 156;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFNIKDFY 8  
Db 60 GFNVEDFY 67

## RESULT 5

O8EZ25 PRELIMINARY; PRT; 948 AA.  
AC O8EZ25;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)  
DE ATP-dependent RNA helicase.  
GN LA4036.  
OS Leptospira interrogans.  
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.  
OX NCBI\_TaxID=173;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;  
RA Ren S.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE011558; AAN51234.1; -.  
KW Helicase; Complete proteome.  
SQ SEQUENCE 948 AA; 110694 MW; F5B209FDABD3612C CRC64;

Query Match 64.4%; Score 38; DB 16; Length 948;  
Best Local Similarity 55.6%; Pred. No. 23e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 FNIKDFYMH 10  
Db 669 FNLQDYYSH 677

## RESULT 6

```
Q9F7S7
ID Q9F7S7 PRELIMINARY; PRT; 431 AA.
AC Q9F7S7;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Predicted Xaa-Pro aminopeptidase.
OS uncultured proteobacterium EBAC31A08.
OC Bacteria; Proteobacteria; environmental samples.
OX NCBI_TaxID=133804;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20446260; PubMed=10988064;
RA Beja O., Aravind L., Koonin E.V., Suzuki M.T., Hadd A., Nguyen L.P.,
RA Jovanovich S.B., Gates C.M., Feldman R.A., Spudich J.L., Spudich E.N.,
RA Delong E.F.;
RT "Bacterial rhodopsin: evidence for a new type of phototrophy in the
RT Sea.";
RL Science 289:1902-1906(2000).
DR EMBL; AF279106; AAG10442.1; -.
DR HSSP; P15034; 1A16.
DR MEROPS; M24.004; -.
DR InterPro; IPR000994; Peptidase_M24.
DR Pfam; PF00557; Peptidase_M24; 1.
KW Aminopeptidase.
SQ SEQUENCE 431 AA; 48222 MW; 9E4B05F210AAB902 CRC64;

Query Match          62.7%; Score 37; DB 2; Length 431;
Best Local Similarity 100.0%; Pred.No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KDFYMH 10
Db 340 KDFYMH 345

RESULT 7
Q8RYQ7 PRELIMINARY; PRT; 497 AA.
ID Q8RYQ7;
AC Q8RYQ7;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Putative cytochrome p450.
GN OSJNB0051H17.12.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
RT clone:OSJNB0051H17.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AP004232; BAB90702.1; -.
DR Gramene; Q8RYQ7; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; p450; 1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 497 AA; 56136 MW; E18FB1E625DBC672 CRC64;

Query Match          62.7%; Score 37; DB 10; Length 497;
Best Local Similarity 62.5%; Pred.No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFY 8
Db 221 GFNIKDFY 228
```

```
RESULT 8
O13321 PRELIMINARY; PRT; 534 AA.
ID O13321;
AC O13321;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Proline rich protein 5Med.
OS Metarhizium anisopliae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae; Metarhizium.
OX NCBI_TaxID=5530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ARSEF2575;
RA Joshi L., St Leger R.J., Roberts D.W.;
RT "Identification and isolation of differentially expressed cDNAs in
RT Metarhizium anisopliae.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF012440; AAB69315.1; -.
SQ SEQUENCE 534 AA; 55702 MW; C1442431B7E15043 CRC64;

Query Match          62.7%; Score 37; DB 3; Length 534;
Best Local Similarity 60.0%; Pred.No. 2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10
Db 336 GFNIKDFYMH 345

RESULT 9
O8GA98 PRELIMINARY; PRT; 542 AA.
ID O8GA98;
AC O8GA98;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE 2-isopropylmalate synthase (EC 4.1.3.12).
GN LEU1.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE OF 1-268 FROM N.A.
RX MEDLINE=20026086; PubMed=10556522;
RA Miller B., Heuser T., Zimmer W.;
RT "A Synechococcus leopoliensis SAUG 1402-1 operon harboring the 1-
RT deoxyxylulose 5-phosphate synthase gene and two additional open
RT reading frames is functionally involved in the dimethylallyl
RT diphosphate synthesis.";
RL FEBS Lett. 460:485-490(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Holtman C.K., Sandoval P., Chen Y., Socias T., Mohler B.J.,
RA McMurtry S., Gonzalez A., Salinas I., Golden S.S., Youderian P.;
RT "Synechococcus elongatus PCC 7942 cosmid 3E9.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; X04616; CAD55648.1; -.
KW Lyase.
SQ SEQUENCE 542 AA; 59000 MW; C6157FCA110A77C CRC64;

Query Match          62.7%; Score 37; DB 2; Length 542;
Best Local Similarity 55.6%; Pred.No. 2e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 FNIKDFYMH 10
Db 408 FDLKDFHVVH 416

RESULT 10
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Q9PRD1
ID Q9PRD1 PRELIMINARY; PRT; 736 AA.
AC Q9PRD1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Ribose/galactose ABC transporter (N-term domain).
GN RBSC-1 OR UN014.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum."
RL Nature 407:757-762(2000).
DR EMBL; AE002101; AAF30419.1; -.
DR InterPro; IPR001851; Bac_inmem_transp.
DR Pfam; PF02653; BPD_transp_2; 1.
KW Complete proteome.
SQ SEQUENCE 736 AA; 84636 MW; 33872F58F29B6EB3 CRC64;

Query Match 62.7%; Score 37; DB 16; Length 736;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYM 9
Db 48 GYNIRDFFI 56

RESULT 11
O8IIN2 PRELIMINARY; PRT; 5922 AA.
ID Q8IIN2;
AC Q8IIN2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
GN PF11_0528.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Patil A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014837; AAN35722.1; -.
KW Hypothetical protein.
SQ SEQUENCE 5922 AA; 710211 MW; 2066B6DBA444B225 CRC64;

Query Match 62.7%; Score 37; DB 5; Length 5922;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KQFYMH 10
Db 11111111
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Db 4977 KDFYMH 4982

RESULT 12
Q8D2M7 PRELIMINARY; PRT; 327 AA.
ID Q8D2M7;
AC Q8D2M7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE YRBH protein.
GN YRBH.
OS Wigglesworthia brevipalpis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Wigglesworthia.
OX NCBI_TaxID=164609;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22297718; PubMed=12219091;
RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
RA Aksoy S.;
RT "Genome sequence of the endocellular obligate symbiont of tsetse
RT flies, Wigglesworthia glossinidia."
RL Nat. Genet. 32:402-407(2002).
DR EMBL; AB063522; BAC24473.1; -.
KW Complete proteome.
SQ SEQUENCE 327 AA; 36142 MW; C07B34A843E032C2 CRC64;

Query Match 61.9%; Score 36.5; DB 16; Length 327;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 GFNIKDF-YMH 10
Db 183 GFNIKDFSLH 193

RESULT 13
Q979C1 PRELIMINARY; PRT; 150 AA.
ID Q979C1;
AC Q979C1;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE N-terminal acetyltransferase complex subunit.
GN TV1240 OR TVG1279984.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium."
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000995; BAB60382.1; -.
DR InterPro; IPR000182; GCN5acetyltransf.
DR Pfam; PF00583; Acetyltransf. 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 150 AA; 17571 MW; 3D295C42084CE4DB CRC64;

Query Match 61.0%; Score 36; DB 17; Length 150;
Best Local Similarity 60.0%; Pred. No. 85;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10
Db 121 GFNIKEFTVN 130
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RESULT 14
Q9MIX6
ID Q9MIX6 PRELIMINARY; PRT; 185 AA.
AC Q9MIX6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE NADH dehydrogenase subunit 1 (EC 1.6.5.3) (NADH-ubiquinone
DE oxidoreductase chain 1) (Fragment).
GN NDI.
OS Uroleucon rudbeckiae.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Aphididae; Macrosiphini; Uroleucon.
OX NCBI_TaxId=87319;
RN [1]
RP SEQUENCE FROM N.A.
RA Moran N.A., Kaplan M.E., Gelsey M.J., Murphy T.G., Scholes E. III.;
RT "Phylogenetics and evolution of the aphid genus Uroleucon based on
RT mitochondrial and nuclear DNA sequences."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
DR EMBL; AF057048; AAF78830.1; -.
DR InterPro; IPR001694; Resp_NADH_dh1.
DR Pfam; PF00146; NADHdh; 1.
KW NAD; Oxidoreductase; Transmembrane; Ubiquinone; Mitochondrion.
FT NON_TER 1 185
FT NON_TER 1 185
SQ SEQUENCE 185 AA; 22120 MW; 7AFA904CEB78FABC CRC64;

Query Match 61.0%; Score 36; DB 8; Length 185;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FNIKDFYMH 10
||:||||:
Db 123 FNINDFYIY 131

RESULT 15
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ID Q9MIX5 PRELIMINARY; PRT; 186 AA.
AC Q9MIX5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE NADH dehydrogenase subunit 1 (EC 1.6.5.3) (NADH-ubiquinone
DE oxidoreductase chain 1) (Fragment).
GN NDI.
OS Uroleucon solidaginis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Aphididae; Macrosiphini; Uroleucon.
OX NCBI_TaxId=87321;
RN [1]
RP SEQUENCE FROM N.A.
RA Moran N.A., Kaplan M.E., Gelsey M.J., Murphy T.G., Scholes E. III.;
RT "Phylogenetics and evolution of the aphid genus Uroleucon based on
RT mitochondrial and nuclear DNA sequences."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
DR EMBL; AF057052; AAF78831.1; -.
DR InterPro; IPR001694; Resp_NADH_dh1.
DR Pfam; PF00146; NADHdh; 1.
KW NAD; Oxidoreductase; Transmembrane; Ubiquinone; Mitochondrion.
FT NON_TER 1 186
FT NON_TER 1 186
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SQ SEQUENCE 186 AA; 21967 MW; 7344E4DD2DF58D4E CRC64;

Query Match 61.0%; Score 36; DB 8; Length 186;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FNIKDFYMH 10
||:||||:
Db 123 FNINDFYIY 131

Search completed: July 30, 2003, 09:42:29
Job time : 10.852 secs
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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: July 30, 2003, 09:42:53 ; Search time 12.2924 Seconds  
(without alignments)  
96.613 Million cell updates/sec

Title: US-09-865-198-1  
Perfect score: 59  
Sequence: 1 GFNIKDFYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	10	9	US-09-976-787-1 Sequence 1, Appli
2	59	100.0	10	10	US-09-865-198-1 Sequence 1, Appli
3	59	100.0	10	11	US-09-798-689-1 Sequence 1, Appli
4	59	100.0	117	9	US-09-976-787-7 Sequence 7, Appli
5	59	100.0	117	9	US-09-976-787-23 Sequence 23, Appli
6	59	100.0	117	10	US-09-865-198-7 Sequence 7, Appli
7	59	100.0	117	10	US-09-865-198-22 Sequence 22, Appli
8	59	100.0	117	11	US-09-798-689-7 Sequence 7, Appli
9	59	100.0	238	9	US-09-976-787-29 Sequence 29, Appli
10	59	100.0	238	10	US-09-865-198-28 Sequence 28, Appli
11	59	100.0	238	11	US-09-798-689-21 Sequence 21, Appli
12	59	100.0	240	9	US-09-976-787-28 Sequence 28, Appli
13	59	100.0	240	10	US-09-865-198-27 Sequence 27, Appli
14	56	94.9	112	14	US-10-032-482-7 Sequence 7, Appli
15	56	94.9	117	11	US-09-802-083-1 Sequence 1, Appli

	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56	56
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	117	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124	124
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## ALIGNMENTS

RESULT 1  
US-09-976-787-1  
Sequence 1, Application US/09976787  
Patent No. US20020064528A1  
GENERAL INFORMATION:  
APPLICANT: Znu, Zhenping  
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
FILE REFERENCE: 11245/46505  
CURRENT APPLICATION NUMBER: US/09/976, 787  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 09/493, 539  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/117, 726  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 1  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-976-787-1

Query Match 100.0%; Score 59; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e-05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
Db 1 GFNIKDFYMH 10

RESULT 2  
US-09-865-198-1  
Sequence 1, Application US/09865198  
Patent No. US20020103345A1  
GENERAL INFORMATION:  
APPLICANT: Znu, Zhenping

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; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-1
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Query Match      100.0%; Score 59; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       1 GFNIKDFYMH 10
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## RESULT 3

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US-09-798-689-1
; Sequence 1, Application US/09798689
; Publication No. US20030103973A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; TITLE OF INVENTION: Combined with Radiation and Chemotherapy
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-1
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Query Match      100.0%; Score 59; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 GFNIKDFYMH 10
        |||||
Db       1 GFNIKDFYMH 10
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## RESULT 4

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US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
```

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; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7
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Query Match      100.0%; Score 59; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 GFNIKDFYMH 10
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Db       26 GFNIKDFYMH 35
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## RESULT 5

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US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23
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Query Match      100.0%; Score 59; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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OY      1 GFNIKDFYMH 10
        |||||
Db       26 GFNIKDFYMH 35
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## RESULT 6

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US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
```

; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-7

Query Match 100.0%; Score 59; DB 10; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||  
Db 26 GFNIKDFYMH 35

## RESULT 7

US-09-865-198-22  
; Sequence 22, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; PRIOR FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 22  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-22

Query Match 100.0%; Score 59; DB 10; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||  
Db 26 GFNIKDFYMH 35

## RESULT 8

US-09-798-689-7  
; Sequence 7, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CTP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/326,552  
; PRIOR FILING DATE: 1994-10-20  
; PRIOR APPLICATION NUMBER: 08/196,041  
; PRIOR FILING DATE: 1994-02-10  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mouse

US-09-798-689-7

Query Match 100.0%; Score 59; DB 11; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||  
Db 26 GFNIKDFYMH 35

## RESULT 9

US-09-976-787-29  
; Sequence 29, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 29  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-29

Query Match 100.0%; Score 59; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||  
Db 26 GFNIKDFYMH 35

## RESULT 10

US-09-865-198-28  
; Sequence 28, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 28  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-28

Query Match 100.0%; Score 59; DB 10; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||  
Db 26 GFNIKDFYMH 35

## RESULT 11

US-09-798-689-21  
; Sequence 21, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; TITLE OF INVENTION: Combined with Radiation and Chemotherapy  
; FILE REFERENCE: Sequence listings 1-41 for 381-25 CIP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/326,552  
; PRIOR FILING DATE: 1994-10-20  
; PRIOR APPLICATION NUMBER: 08/196,041  
; PRIOR FILING DATE: 1994-02-10  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-798-689-21

Query Match 100.0%; Score 59; DB 11; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

Db 26 GFNIKDFYMH 35

## RESULT 12

US-09-976-787-28  
; Sequence 28, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 28  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-28

Query Match 100.0%; Score 59; DB 9; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

Db 26 GFNIKDFYMH 35

## RESULT 13

US-09-865-198-27  
; Sequence 27, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho  
; TITLE OF INVENTION: Production  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 27  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-27

Query Match 100.0%; Score 59; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

Db 26 GFNIKDFYMH 35

## RESULT 14

US-10-032-482-7  
; Sequence 7, Application US/10032482  
; Publication No. US20020197270A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Irun  
; APPLICANT: ROTTER, Varda  
; APPLICANT: Wolkowicz, Roland  
; APPLICANT: RUIZ, Pedro  
; APPLICANT: EREZ-ALON, Neta  
; APPLICANT: HERKEL, Johannes  
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR  
; TITLE OF INVENTION: IMMUNITY  
; FILE REFERENCE: COHEN42  
; CURRENT APPLICATION NUMBER: US/10/032,482  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: US/09/445,602  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: PCT/IL98/00266  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: IL 121041  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-032-482-7

Query Match 94.9%; Score 56; DB 14; Length 112;  
Best Local Similarity 90.0%; Pred. No. 0.0044;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10

Db 23 GFNIKDFYMH 32

## RESULT 15

US-09-802-083-1  
; Sequence 1, Application US/09802083  
; Publication No. US20030119075A1

GENERAL INFORMATION:

APPLICANT: Kirchhofer, Daniel K.  
APPLICANT: Lowe, David G.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Anti-Tissue Factor Antibodies with Enhanced  
TITLE OF INVENTION: Anticoagulant Potency  
FILE REFERENCE: P1736R1  
CURRENT APPLICATION NUMBER: US/09/802,083  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: US 60/189,775  
PRIOR FILING DATE: 2000-03-16  
NUMBER OF SEQ ID NOS: 28  
SEQ ID NO 1  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Mus Musculus  
US-09-802-083-1

Query Match 94.9%; Score 56; DB 11; Length 117;  
Best Local Similarity 90.0%; Pred. No. 0.0046;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
Db 26 GFNIKDYMH 35

Search completed: July 30, 2003, 10:20:28  
Job time : 13.2924 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 3.22259 Seconds  
(without alignments)  
131.295 Million cell updates/sec

Title: US-09-865-198-1  
Perfect score: 59  
Sequence: 1 GENIKDFYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	94.9	117	3	US-08-732-708C-43
2	56	94.9	118	3	US-08-767-128-22
3	56	94.9	124	1	US-08-017-570-4
4	56	94.9	124	1	US-08-017-570-6
5	56	94.9	124	1	US-08-471-426-4
6	56	94.9	124	1	US-08-471-426-6
7	56	94.9	124	4	US-09-672-609-1
8	56	94.9	124	4	US-09-672-609-2
9	56	94.9	124	4	US-09-672-609-3
10	56	94.9	124	4	US-09-672-609-4
11	56	94.9	124	4	US-09-672-609-5
12	56	94.9	124	4	US-09-672-609-6
13	56	94.9	124	4	US-09-672-609-7
14	56	94.9	124	4	US-09-672-609-8
15	56	94.9	124	4	US-09-672-609-9
16	56	94.9	124	4	US-09-672-609-10
17	56	94.9	124	4	US-09-672-609-11
18	56	94.9	124	4	US-09-672-609-12
19	56	94.9	124	4	US-09-025-403A-1
20	56	94.9	124	4	US-09-025-403A-2
21	56	94.9	124	4	US-09-025-403A-3
22	56	94.9	124	4	US-09-025-403A-4
23	56	94.9	124	4	US-09-025-403A-5
24	56	94.9	124	4	US-09-025-403A-6
25	56	94.9	124	4	US-09-025-403A-7
26	56	94.9	124	4	US-09-025-403A-8
27	56	94.9	124	4	US-09-025-403A-9

28	56	94.9	124	4	US-09-025-403A-10	Sequence 10, Appl
29	56	94.9	124	4	US-09-025-403A-11	Sequence 11, Appl
30	56	94.9	124	4	US-09-025-403A-12	Sequence 12, Appl
31	56	94.9	124	5	PCT-US94-01709-4	Sequence 4, Appli
32	56	94.9	124	5	PCT-US94-01709-6	Sequence 6, Appli
33	56	94.9	535	4	US-08-983-035A-38	Sequence 38, Appl
34	52	88.1	136	4	US-09-564-329A-11	Sequence 11, Appl
35	51	86.4	118	2	US-08-232-081B-8	Sequence 8, Appli
36	51	86.4	118	2	US-08-232-081B-38	Sequence 38, Appli
37	51	86.4	120	2	US-08-950-660-2	Sequence 2, Appli
38	51	86.4	120	4	US-08-871-488A-15	Sequence 15, Appl
39	51	86.4	120	5	PCT-US93-00030-2	Sequence 19, Appl
40	51	86.4	120	5	PCT-US93-00924-2	Sequence 2, Appli
41	51	86.4	120	5	PCT-US93-00924-2	Sequence 2, Appli
42	51	86.4	121	2	US-08-822-830B-2	Sequence 2, Appli
43	51	86.4	121	2	US-08-822-830B-13	Sequence 13, Appl
44	51	86.4	121	4	US-09-157-452B-2	Sequence 2, Appli
45	51	86.4	121	4	US-09-157-452B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-732-708C-43  
Sequence 43, Application US/08732708C  
Patent No. 6127524  
GENERAL INFORMATION:  
APPLICANT: Casipit, Clayton L.  
APPLICANT: Wong, Hing C.  
APPLICANT: Huang, Bee Y.  
TITLE OF INVENTION: BINDING MOLECULES AND COMPUTER-BASED  
NUMBER OF INVENTION: METHODS OF INCREASING THE BINDING AFFINITY THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Di, Bronstein, Roberts & Cushman, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/732,708C  
FILING DATE: 18-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Buchanan, Robert L.  
REGISTRATION NUMBER: 40,927  
REFERENCE/DOCKET NUMBER: 46491  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX:  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
FEATURE:

LOCATION: 50  
OTHER INFORMATION: Xaa is Trp, Ala, or Tyr  
LOCATION: 99  
OTHER INFORMATION: Xaa is Tyr, Ala or Phe  
LOCATION: 104  
OTHER INFORMATION: Xaa is Tyr or Phe  
US-08-732-708C-43

Query Match 94.9%; Score 56; DB 3; Length 117;  
Best Local Similarity 90.0%; Pred. No. 0.0033;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFNIKDFYMH 10  
|||||:||||  
Db 26 GFNIKDYMH 35

## RESULT 2

US-08-767-128-22  
Sequence 22, Application US/08767128  
Patent No. 611079

GENERAL INFORMATION:  
APPLICANT: WYLIE, DWANE E.  
APPLICANT: LOPEZ, OSVALDO  
APPLICANT: MURRAY, PETER JOSEPH  
APPLICANT: GOEBEL, PETER  
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 6111079west Center, 90 South Seventh St  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/767,128  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE: 04-DEC-1996  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09258  
FILING DATE: 05-JUN-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/541,373  
FILING DATE: 10-OCT-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/462,798  
FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.

REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.49USF1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/371-5278

TELEFAX: 612/332-9081  
TELEX:

INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-767-128-22

Query Match 94.9%; Score 56; DB 3; Length 118;  
Best Local Similarity 90.0%; Pred. No. 0.0033;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFNIKDFYMH 10  
|||||:||||  
Db 26 GFNIKDYMH 35

## RESULT 3

US-08-017-570-4  
Sequence 4, Application US/08017570  
Patent No. 5472693

GENERAL INFORMATION:  
APPLICANT: GOURLIE, BRIAN B  
APPLICANT: RIXON, MARK W  
APPLICANT: MEZES, PETER S  
APPLICANT: KAPLAN, DONALD A  
APPLICANT: SCHIOM, JEFFREY  
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC  
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Duane C. Ulmer  
STREET: P.O. Box 1967  
CITY: Midland  
STATE: MI  
COUNTRY: US  
ZIP: 48641-1967

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/017,570  
FILING DATE: 19930216

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941  
REFERENCE/DOCKET NUMBER: C-38,777

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-017-570-4

Query Match 94.9%; Score 56; DB 1; Length 124;  
Best Local Similarity 90.0%; Pred. No. 0.0035;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFNIKDFYMH 10  
|||||:||||  
Db 26 GFNIKDYMH 35

## RESULT 4

US-08-017-570-6  
Sequence 6, Application US/08017570  
Patent No. 5472693

GENERAL INFORMATION:  
APPLICANT: GOURLIE, BRIAN B



APPLICANT: RIXON, MARK W  
APPLICANT: MEZES, PETER S  
APPLICANT: KAPLAN, DONALD A  
APPLICANT: SCHLOM, JEFFREY  
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC  
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Duane C. Ulmer  
STREET: P.O. Box 1967  
CITY: Midland  
STATE: MI  
COUNTRY: US  
ZIP: 48641-1967  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/017,570  
FILING DATE: 19930216  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: ULMER, DUANE C  
REGISTRATION NUMBER: 34,941  
REFERENCE/DOCKET NUMBER: C-38,777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 636-8104  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 124 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-017-570-6

Query Match 94.9%; Score 56; DB 1; Length 124;  
Best Local Similarity 90.0%; Pred. No. 0.0035;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
Db 26 GFNIKDYMH 35

RESULT 5  
US-08-471-426-4  
Sequence 4, Application US/08471426  
Patent No. 5808033  
GENERAL INFORMATION:  
APPLICANT: GOURLIE, BRIAN B  
APPLICANT: RIXON, MARK W  
APPLICANT: MEZES, PETER S  
APPLICANT: KAPLAN, DONALD A  
APPLICANT: SCHLOM, JEFFREY  
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC  
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Duane C. Ulmer  
STREET: P.O. Box 1967  
CITY: Midland  
STATE: MI  
COUNTRY: US  
ZIP: 48641-1967  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,426

FILING DATE: 06-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/017,570  
FILING DATE: 16-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: ULMER, DUANE C  
REGISTRATION NUMBER: 34,941  
REFERENCE/DOCKET NUMBER: C-38,777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 636-8104  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 124 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-426-4

Query Match 94.9%; Score 56; DB 1; Length 124;  
Best Local Similarity 90.0%; Pred. No. 0.0035;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
Db 26 GFNIKDYMH 35

RESULT 6  
US-08-471-426-6  
Sequence 6, Application US/08471426  
Patent No. 5808033  
GENERAL INFORMATION:  
APPLICANT: GOURLIE, BRIAN B  
APPLICANT: RIXON, MARK W  
APPLICANT: MEZES, PETER S  
APPLICANT: KAPLAN, DONALD A  
APPLICANT: SCHLOM, JEFFREY  
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC  
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Duane C. Ulmer  
STREET: P.O. Box 1967  
CITY: Midland  
STATE: MI  
COUNTRY: US  
ZIP: 48641-1967  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,426  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/017,570  
FILING DATE: 16-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: ULMER, DUANE C  
REGISTRATION NUMBER: 34,941  
REFERENCE/DOCKET NUMBER: C-38,777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 636-8104  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 124 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-426-6

Query Match 94.9%; Score 56; DB 1; Length 124;  
Best Local Similarity 90.0%; Pred. No. 0.0035;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||||:||||  
Db 26 GFNIKDYMH 35

## RESULT 7

US-09-672-609-1  
; Sequence 1, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.  
; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Word 97 SR-2  
; SEQ ID NO 1  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: Murine Col-1 VH  
; LOCATION: 1..124  
US-09-672-609-1

Query Match 94.9%; Score 56; DB 4; Length 124;  
Best Local Similarity 90.0%; Pred. No. 0.0035;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||||:||||  
Db 26 GFNIKDYMH 35

## RESULT 8

US-09-672-609-2  
; Sequence 2, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.  
; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Word 97 SR-2  
; SEQ ID NO 2  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Human NEMM VH FR template  
; LOCATION: 1..124  
; OTHER INFORMATION: Amino acid sequence of the human framework regions from  
; OTHER INFORMATION: the NEMM antibody heavy chain variable region, with CDR2 and CDR3

; OTHER INFORMATION: amino acid residues depicted by Xaa  
US-09-672-609-2

Query Match 94.9%; Score 56; DB 4; Length 124;  
Best Local Similarity 90.0%; Pred. No. 0.0035;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||||:||||  
Db 26 GFNIKDYMH 35

## RESULT 9

US-09-672-609-3  
; Sequence 3, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.  
; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Word 97 SR-2  
; SEQ ID NO 3  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Humanized COL-1 VH, HuVH  
; LOCATION: 1..124  
; OTHER INFORMATION: Humanized heavy chain variable region containing human  
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,  
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98  
US-09-672-609-3

Query Match 94.9%; Score 56; DB 4; Length 124;  
Best Local Similarity 90.0%; Pred. No. 0.0035;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNIKDFYMH 10  
|||||:||||  
Db 26 GFNIKDYMH 35

## RESULT 10

US-09-672-609-4  
; Sequence 4, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.  
; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Word 97 SR-2  
; SEQ ID NO 4  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

```
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HuVHA
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-672-609-4
```

```
Query Match          94.9%; Score 56; DB 4; Length 124;
Best Local Similarity 90.0%; Pred. No. 0.0035;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 GFNIKDFYMH 10
         |||||:|
Db       26 GFNIKDYMH 35
```

## RESULT 11

```
US-09-672-609-5
; Sequence 5, Application US/09672609
; Patent No. 6333405
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
```

```
; CURRENT APPLICATION NUMBER: US/09/672,609
```

```
; CURRENT FILING DATE: 2000-09-28
```

```
; PRIOR APPLICATION NUMBER: 09/025,403
```

```
; PRIOR FILING DATE: 1998-02-18
```

```
; NUMBER OF SEQ ID NOS: 50
```

```
; SOFTWARE: Microsoft Word 97 SR-2
```

```
; SEQ ID NO 5
```

```
; LENGTH: 124
```

```
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
```

```
; NAME/KEY: Humanized COL-1 VH, HuVHA
```

```
; LOCATION: 1..124
```

```
; OTHER INFORMATION: Humanized heavy chain variable region containing human
```

```
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
```

```
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
```

```
US-09-672-609-5
```

```
Query Match          94.9%; Score 56; DB 4; Length 124;
Best Local Similarity 90.0%; Pred. No. 0.0035;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 GFNIKDFYMH 10
         |||||:|
Db       26 GFNIKDYMH 35
```

## RESULT 12

```
US-09-672-609-6
; Sequence 6, Application US/09672609
; Patent No. 6333405
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Anderson, W.H. Kerr
```

```
; APPLICANT: Tempest, Philip R.
```

```
; APPLICANT: Carr, Frank J.
```

```
; APPLICANT: Harris, William J.
```

```
; APPLICANT: Armour, Kathryn
```

```
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
```

```
; FILE REFERENCE:
```

```
; CURRENT APPLICATION NUMBER: US/09/672,609
```

```
; CURRENT FILING DATE: 2000-09-28
```

```
; PRIOR APPLICATION NUMBER: 09/025,403
```

```
; PRIOR FILING DATE: 1998-02-18
```

```
; NUMBER OF SEQ ID NOS: 50
```

```
; SOFTWARE: Microsoft Word 97 SR-2
```

```
; SEQ ID NO 6
```

```
; LENGTH: 124
```

```
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
```

```
; NAME/KEY: Humanized COL-1 VH, HuVHA
```

```
; LOCATION: 1..124
```

```
; OTHER INFORMATION: Humanized heavy chain variable region containing human
```

```
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
```

```
; OTHER INFORMATION: Ile-29, Lys-30, Ala-79, Asn-97, and Thr-98
```

```
US-09-672-609-6
```

```
Query Match          94.9%; Score 56; DB 4; Length 124;
Best Local Similarity 90.0%; Pred. No. 0.0035;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 GFNIKDFYMH 10
         |||||:|
Db       26 GFNIKDYMH 35
```

## RESULT 13

```
US-09-672-609-7
; Sequence 7, Application US/09672609
; Patent No. 6333405
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Anderson, W.H. Kerr
```

```
; APPLICANT: Tempest, Philip R.
```

```
; APPLICANT: Carr, Frank J.
```

```
; APPLICANT: Harris, William J.
```

```
; APPLICANT: Armour, Kathryn
```

```
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
```

```
; FILE REFERENCE:
```

```
; CURRENT APPLICATION NUMBER: US/09/672,609
```

```
; CURRENT FILING DATE: 2000-09-28
```

```
; PRIOR APPLICATION NUMBER: 09/025,403
```

```
; PRIOR FILING DATE: 1998-02-18
```

```
; NUMBER OF SEQ ID NOS: 50
```

```
; SOFTWARE: Microsoft Word 97 SR-2
```

```
; SEQ ID NO 7
```

```
; LENGTH: 124
```

```
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
```

```
; NAME/KEY: Humanized COL-1 VH, HuVHA
```

```
; LOCATION: 1..124
```

```
; OTHER INFORMATION: Humanized heavy chain variable region containing human
```

```
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
```

```
; OTHER INFORMATION: Ile-29, Lys-30, Tyr-80, Asn-97, and Thr-98
```

```
US-09-672-609-7
```

```
Query Match          94.9%; Score 56; DB 4; Length 124;
Best Local Similarity 90.0%; Pred. No. 0.0035;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 GFNIKDFYMH 10
         |||||:|
Db       26 GFNIKDYMH 35
```

## RESULT 14

```
US-09-672-609-8
; Sequence 8, Application US/09672609
; Patent No. 6333405
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Anderson, W.H. Kerr
```

```
; APPLICANT: Tempest, Philip R.
```

```
; APPLICANT: Carr, Frank J.
```

```
; APPLICANT: Harris, William J.
```

```
; APPLICANT: Armour, Kathryn
```

```
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
```

```
; FILE REFERENCE:
```

;; CURRENT APPLICATION NUMBER: US/09/672,609  
;; CURRENT FILING DATE: 2000-09-28  
;; PRIOR APPLICATION NUMBER: 09/025,403  
;; PRIOR FILING DATE: 1998-02-18  
;; NUMBER OF SEQ ID NOS: 50  
;; SOFTWARE: Microsoft Word 97 SR-2  
;; SEQ ID NO 8  
;; LENGTH: 124  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: Humanized COL-1 VH, HUVHATAY  
;; LOCATION: 1..124  
;; OTHER INFORMATION: Humanized heavy chain variable region containing human  
;; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,  
;; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98  
US-09-672-609-8

Query Match 94.9%; Score 56; DB 4; Length 124;  
Best Local Similarity 90.0%; Pred. No. 0.0035;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GFNIKDFYMH 10  
|||:|  
Db 26 GFNIKDYMH 35

## RESULT 15

US-09-672-609-9  
;; Sequence 9, Application US/09672609  
;; Patent No. 633405  
;; GENERAL INFORMATION:  
;; APPLICANT: Anderson, W.H. Kerr  
;; APPLICANT: Tempest, Philip R.  
;; APPLICANT: Carr, Frank J.  
;; APPLICANT: Harris, William J.  
;; APPLICANT: Armour, Kathryn  
;; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
;; FILE REFERENCE:  
;; CURRENT APPLICATION NUMBER: US/09/672,609  
;; CURRENT FILING DATE: 2000-09-28  
;; PRIOR APPLICATION NUMBER: 09/025,403  
;; PRIOR FILING DATE: 1998-02-18  
;; NUMBER OF SEQ ID NOS: 50  
;; SOFTWARE: Microsoft Word 97 SR-2  
;; SEQ ID NO 9  
;; LENGTH: 124  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: Humanized COL-1 VH, HUVHASTAY  
;; LOCATION: 1..124  
;; OTHER INFORMATION: Humanized heavy chain variable region containing human  
;; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,  
;; OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, Tyr-80, Asn-97, and  
;; OTHER INFORMATION: Thr-98  
US-09-672-609-9

Query Match 94.9%; Score 56; DB 4; Length 124;  
Best Local Similarity 90.0%; Pred. No. 0.0035;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GFNIKDFYMH 10  
|||:|  
Db 26 GFNIKDYMH 35

Search completed: July 30, 2003, 09:38:27  
Job time: 4.22259 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 5.02658 Seconds  
(without alignments)  
325.245 Million cell updates/sec

Title: US-09-865-198-2  
Perfect score: 101  
Sequence: 1 WIDPENGDSGYAPKFOG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	89.1	82	2 A36025	Ig heavy chain V r
2	82	81.2	118	2 S25174	Ig heavy chain V r
3	82	81.2	136	2 S04576	Ig heavy chain pre
4	80	79.2	116	2 S15672	Ig heavy chain V r
5	78	77.2	137	2 S52445	Ig heavy chain V r
6	67	66.3	85	2 E37262	Ig heavy chain V r
7	67	66.3	98	2 S26918	Ig heavy chain V r
8	67	66.3	132	2 S31596	Ig heavy chain V r
9	67	66.3	136	2 S31600	Ig heavy chain V r
10	67	66.3	143	1 E1HUND	Ig heavy chain pre
11	64	63.4	86	2 S54912	Ig heavy chain V r
12	64	63.4	110	2 PH1670	Ig heavy chain V r
13	64	63.4	171	2 S23623	Ig heavy chain V r
14	63	62.4	127	2 S34014	Ig heavy chain V r
15	62	61.4	98	2 S26938	Ig heavy chain V r
16	62	61.4	98	2 S26912	Ig heavy chain V r
17	62	61.4	99	2 D37262	Ig heavy chain V r
18	62	61.4	107	2 PH1013	Ig heavy chain V r
19	62	61.4	108	2 PH1012	Ig heavy chain V r
20	62	61.4	117	2 S31680	Ig heavy chain V r
21	62	61.4	117	2 S18551	Ig heavy chain V r
22	62	61.4	118	2 S36265	Ig heavy chain V r
23	62	61.4	120	2 S03471	Ig heavy chain V-D
24	62	61.4	122	2 S06823	Ig heavy chain V r
25	62	61.4	123	2 D33548	Ig heavy chain V-1
26	62	61.4	123	2 PH1403	Ig heavy chain V r
27	62	61.4	129	2 S46393	Ig heavy chain V r
28	62	61.4	135	2 S49530	anti-Sm antibody V
29	60	59.4	120	2 S03484	Ig heavy chain V-D

30	60	59.4	221	2 S49220	Ig gamma-1 chain -
31	59	58.4	77	2 S46465	Ig heavy chain V r
32	59	58.4	98	2 S26909	Ig heavy chain V r
33	58	57.4	86	2 S29544	Ig heavy chain V r
34	58	57.4	98	2 S26921	Ig heavy chain V r
35	58	57.4	116	2 S24289	Ig gamma chain V r
36	58	57.4	178	2 S29594	Ig gamma chain (WM
37	57	56.4	114	2 PH1667	Ig heavy chain V r
38	57	56.4	118	2 PH1666	Ig heavy chain V r
39	57	56.4	120	2 S31999	Ig heavy chain V r
40	56.5	55.9	98	2 S26911	Ig heavy chain V r
41	56	55.4	115	2 S03482	Ig heavy chain V-D
42	56	55.4	126	2 I44151	Ig heavy chain V r
43	55	54.5	107	2 A27646	Ig heavy chain V r
44	54	53.5	99	2 C37262	Ig heavy chain V r
45	54	53.5	109	2 PH1668	Ig heavy chain V r

## ALIGNMENTS

```
RESULT 1
A36025
Ig heavy chain V region (PR8-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 23-Jul-1999
C:Accession: A36025; E36025
R:Catton, A.J.; Kopyrowski, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 6450-6454, 1990
A:Title: Influenza virus hemagglutinin-specific antibodies isolated from a combinatorial
A:Reference number: A36025; MUID:90349634; PMID:1696733
A:Accession: A36025
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-82 <CAT>
A:Cross-references: GB:M55999; NID:g194955; PIDN:AAA38112.1; PID:g194956
A>Note: PR8-1
A:Accession: E36025
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 19-82 <CA2>
A:Cross-references: GB:M57273; NID:g194963; PIDN:AAA38116.1; PID:g194964
A>Note: clone PR8-21
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      89.1%; Score 90; DB 2; Length 82;
Best Local Similarity 88.2%; Pred. No. 4.6e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 WIDPENGDSGYAPKFOG 17
Db      12 WIDPENGDTETAPKFOG 28

RESULT 2
S25174
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S25174; S33133
R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A:Description: Structure and binding properties of monoclonal antibodies to core histone
A:Reference number: S25174
A:Accession: S25174
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <MON>
A:Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
A:Accession: S33133
A:Status: preliminary
A:Molecule type: mRNA
```



A;Residues: 1-118 <MO2>  
A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 82; DB 2; Length 118;  
Best Local Similarity 82.4%; Pred. No. 1.2e-05;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
Db 50 WIDPENGDTQYASKFOG 66

RESULT 3

S04576  
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000  
C;Accession: S04576  
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th  
Eur. J. Immunol. 17, 91-95, 1987  
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involve  
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 82; DB 2; Length 136;  
Best Local Similarity 82.4%; Pred. No. 1.4e-05;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
Db 69 WIDPENGDTQYASKFOG 85

RESULT 4

S15672  
Ig heavy chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C;Accession: S15672  
R;Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris,  
Bio/Technology 9, 266-271, 1991  
A;Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi  
A;Reference number: S15672; MUID:91337412; PMID:1367535  
A;Accession: S15672  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-116 <TEM>  
A;Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA41644.1; PID:g51979  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 80; DB 2; Length 116;  
Best Local Similarity 82.4%; Pred. No. 2.5e-05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
Db 50 WIDPENGDTQYAPKFOG 66

RESULT 5

S52445  
Ig heavy chain V region precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C;Accession: S52445  
R;Berdoz, J.; Kraehenbuhl, J.P.  
Submitted to the EMBL Data Library, November 1994  
A;Description: Specific amplification by the polymerase chain reaction of rearranged ge  
A;Reference number: S52445  
A;Accession: S52445  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-137 <BER>

A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440  
C;Genetics:

A;Intons: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-115/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 78; DB 2; Length 137;  
Best Local Similarity 76.5%; Pred. No. 6.1e-05;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
Db 69 WIDPENGNTVYDPKFOG 85

RESULT 6

E37262  
Ig heavy chain V region (6H2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 09-May-1997  
C;Accession: E37262  
R;Goshorn, S.C.; Retzel, E.; Jemerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A;Title: Common structural features among monoclonal antibodies binding the same antigen  
A;Reference number: A38601; MUID:9115823; PMID:1703527  
A;Accession: E37262  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-85 <GOS>  
A;Cross-references: GB:M57991  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.3%; Score 67; DB 2; Length 85;  
Best Local Similarity 75.0%; Pred. No. 0.0019;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPENGDSGYAPKFOG 17  
Db 29 IDPANGDTQYDPKFOG 44

RESULT 7

S26918  
Ig heavy chain V region (DP-15) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S26918  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A;Reference number: S26885; MUID:93021117; PMID:1404388

A;Accession: S26918

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-98 <TOM>

A;Cross-references: EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID:g32858

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin



F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 67; DB 2; Length 98;  
Best Local Similarity 58.8%; Pred. No. 0.0023;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
|::|:|::|::|::|::|  
Db 50 WMNPNSGNTGYAOKFOG 66

RESULT 8  
S31596

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31596  
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31596  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-132 <CUI>  
A/Cross-references: EMBL:Z14166; NID:g30996; PIDN:CAA78535.1; PID:g30997  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 67; DB 2; Length 132;  
Best Local Similarity 58.8%; Pred. No. 0.0031;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
|::|:|::|::|::|::|  
Db 69 WMNPNSGNTGYAOKFOG 85

RESULT 9  
S31600

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31600  
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31600  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-136 <CUI>  
A/Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 67; DB 2; Length 136;  
Best Local Similarity 58.8%; Pred. No. 0.0032;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
|::|:|::|::|::|::|  
Db 69 WMNPNSGNTGYAOKFOG 85

RESULT 10  
E1HUND

Ig heavy chain precursor V-I region (Nd) - human (fragments)

C/Species: Homo sapiens (man)  
C/Date: 31-Mar-1981 #sequence\_revision 05-Apr-1983 #text\_change 21-Jan-2000  
C/Accession: A93933; A02026

R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; C  
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982

A/Title: Cloning and sequence determination of the gene for the human immunoglobulin eps

A/Reference number: A93933; MUID:83065234; PMID:6815656

A/Accession: A93933

A/Molecule type: mRNA

A/Residues: 1-143 <KEN>

R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3

A/Reference number: A94418

A/Contents: annotation; partial sequence

A/Note: this epsilon chain was isolated from a myeloma protein

C/Genetics:

A/Gene: GDB:IGHV@

A/Cross-references: GDB:128528; OMIM:147070

A/Map position: 14q32.33-14q32.33

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin; pyroglyutamic acid

F;1-15/Domain: signal sequence #status predicted <SIG>

F;16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>

F;30-113/Domain: immunoglobulin homology <IMM>

F;16/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer

F;37-111/Disulfide bonds: #status experimental

Query Match 66.3%; Score 67; DB 1; Length 143;  
Best Local Similarity 58.8%; Pred. No. 0.0034;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
|::|:|::|::|::|::|  
Db 65 WINPNSGNTGYAPRFOG 81

RESULT 11  
S54912

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 17-Feb-1998 #sequence\_revision 26-Feb-1998 #text\_change 21-Jan-2000  
C/Accession: S54912  
R/Tomlinson, M.; Walter, G.; Cook, X.Y.Z.; Winter, G.  
submitted to the EMBL Data Library, November 1992  
A/Reference number: S54912  
A/Accession: S54912  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-86 <TOM>  
A/Cross-references: EMBL:Z18904; NID:g840779; PIDN:CAA79341.1; PID:g840780  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 64; DB 2; Length 86;  
Best Local Similarity 64.7%; Pred. No. 0.0058;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
|::|:|::|::|::|::|  
Db 38 WINPNSGNTGYAKKFOG 54

RESULT 12  
PH1670

Ig heavy chain V region (clone 2A12) - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C/Accession: PH1670  
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A/Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphyloc  
A/Reference number: PH1642; MUID:93301610; PMID:8315388  
A/Accession: PH1670  
A/Molecule type: mRNA  
A/Residues: 1-110 <HIL>  
A/Experimental source: B cell

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;7-93/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 64; DB 2; Length 110;  
Best Local Similarity 58.8%; Pred. No. 0.0076;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
|::|::|::|::|::|  
DB 42 WMNPNNGTGYAQKFOG 58

## RESULT 13

S23623  
Ig heavy chain V region precursor - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S23623  
R/Olee, T.; Lu, E.-W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;  
J. Exp. Med. 175, 831-842, 1992  
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from  
A;Reference number: S23623; MUID:92156804; PMID:1740665  
A;Accession: S23623  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-171 <OLE>  
A;Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 64; DB 2; Length 171;  
Best Local Similarity 58.8%; Pred. No. 0.012;  
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
|::|::|::|::|::|  
DB 69 WINPNSGGTGYGKFOG 85

## RESULT 14

S34014

Ig heavy chain V region - human

C;Species: Homo sapiens (man)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C;Accession: S34014; S30535  
R/Mariette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
A;Reference number: S34001; MUID:93209281; PMID:7681398  
A;Accession: S34014  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-127 <MAR>  
A;Cross-references: EMBL:Z18321  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 127;  
Best Local Similarity 52.9%; Pred. No. 0.013;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
|::|::|::|::|::|  
DB 50 WMNPSSGNTGYAQKFOG 66

## RESULT 15

S26938

Ig heavy chain V region (DP-75) - human (fragment)  
C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence\_revision 17-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S26938

R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A;Reference number: S26885; MUID:93021117; PMID:1404388

A;Accession: S26938  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-98 <TOM>

A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 61.4%; Score 62; DB 2; Length 98;  
Best Local Similarity 58.8%; Pred. No. 0.014;  
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFOG 17  
|::|::|::|::|::|  
DB 50 WINPNSGGTNYAQKFOG 66

Search completed: July 30, 2003, 09:44:03  
Job time : 5.02658 secs

GenCore version 5.1.6  
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OM protein - protein-search, using sw model

Run on: July 30, 2003, 09:31:35 ; Search time 2.65449 Seconds  
(without alignments)  
301.171 Million cell updates/sec

Title: US-09-865-198-2  
Perfect score: 101  
Sequence: 1 WIDPENGDSGYAPKFG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	66.3	147	1	HVIC_HUMAN P01744 homo sapien
2	51	50.5	117	1	HVIB_HUMAN P01743 homo sapien
3	51	50.5	117	1	HVIG_HUMAN P23083 homo sapien
4	50	49.5	350	1	NVD9_HUMAN Q9bw91 homo sapien
5	46	45.5	117	1	HV12_MOUSE P01756 mus musculu
6	46	45.5	117	1	HV13_MOUSE P01757 mus musculu
7	46	45.5	118	1	HV51_MOUSE P06330 mus musculu
8	46	45.5	245	1	VE4_HPV5B P26550 human papil
9	46	45.5	839	1	GLT5_WHEAT P10388 triticum ae
10	45	44.6	117	1	HV52_MOUSE P06327 mus musculu
11	45	44.6	245	1	VE4_HPV5B P06924 human papil
12	44	43.6	101	1	GLT1_WHEAT P02861 triticum ae
13	44	43.6	474	1	GLN1_FRAAL P46033 frankia aln
14	43	42.6	132	1	ROMA_KLEPN Q48412 klebsiella
15	43	42.6	159	1	17KD_RICPR P16624 rickettsia
16	43	42.6	159	1	17KD_RICPR P22882 rickettsia
17	43	42.6	238	1	YIGB_ECOLI P23306 escherichia
18	43	42.6	524	1	FTWH_MYCTU O06223 mycobacteri
19	43	42.6	838	1	GLT4_WHEAT P08489 triticum ae
20	42	41.6	80	1	17KD_RICCA P29697 rickettsia
21	42	41.6	117	1	HV14_MOUSE P01758 mus musculu
22	42	41.6	120	1	HV03_MOUSE P01747 mus musculu
23	42	41.6	154	1	17KD_RICAM P50927 rickettsia
24	42	41.6	154	1	17KD_RICAU P50928 rickettsia
25	42	41.6	154	1	17KD_RICMO P50929 rickettsia
26	42	41.6	154	1	17KD_RICPA P50930 rickettsia
27	42	41.6	154	1	17KD_RICRH P50931 rickettsia
28	42	41.6	159	1	17KD_RICCN P05372 rickettsia
29	42	41.6	159	1	17KD_RICJA Q52764 rickettsia
30	42	41.6	809	1	CN4D_HUMAN Q08499 homo sapien
31	42	41.6	4543	1	LRP1_CHICK P98157 gallus gall
32	41.5	41.1	505	1	FXO4_HUMAN P98177 homo sapien
33	41.5	41.1	597	1	ETFD_CAEEL Q11190 c probable

34	41.5	41.1	957	1	AMPE_HUMAN Q07075 homo sapien
35	41	40.6	140	1	HV02_MOUSE P01746 mus musculu
36	41	40.6	406	1	PNCB_METMA Q8psj3 methanosarc
37	41	40.6	434	1	ENO_STAAM Q99vk5 staphylococ
38	41	40.6	434	1	ENO_STAAM Q69174 staphylococ
39	41	40.6	434	1	ENO_STRPY P82479 streptococc
40	41	40.6	435	1	ENO_STRPY Q8e6g0 streptococc
41	41	40.6	482	1	CA1B_RAT P20909 rattus norv
42	41	40.6	670	1	CUI3_HUMAN O95447 homo sapien
43	41	40.6	1281	1	IP3S_MOUSE Q92329 mus musculu
44	41	40.6	1804	1	CA1B_MOUSE Q61245 mus musculu
45	41	40.6	1806	1	CA1B_HUMAN P12107 homo sapien

ALIGNMENTS

RESULT 1  
HVIC\_HUMAN STANDARD; PRT; 147 AA.  
AC P01744;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-I region ND precursor (Fragments).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83065234; PubMed=6815656;  
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
RA Bell L.O., Gould H.J.;  
RT "Cloning and sequence determination of the gene for the human  
RT immunoglobulin epsilon chain expressed in a myeloma cell line."  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).  
RN [2]  
RP SEQUENCE OF 20-147.  
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RL (in) Bach M.K. (eds.);  
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
RL Marcel Dekker, New York (1978).  
CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA  
CC PROTEIN.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR HSSP; P01789; IMCP.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.  
FT SIGNAL 1 19  
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.  
FT DOMAIN 20 131 IG-LIKE.  
FT MOD\_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 41 115  
FT CONFLICT 21 21 T -> V (IN REF. 2).  
FT CONFLICT 53 54 IH -> HI (IN REF. 2).  
FT CONFLICT 67 68 VG -> GV (IN REF. 2).  
FT CONFLICT 125 125 MISSING (IN REF. 2).  
FT NON\_TER 147 147  
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 66.3%; Score 67; DB 1; Length 147;  
Best local Similarity 58.8%; Pred. No. 0.0011;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```
QY      1 WIDPENGDSGYAPKFOG 17
        ||:| :| :||:|
Db      69 WINPNSGGTNYAPRFQG 85
```

## RESULT 2

```

HV1B_HUMAN          STANDARD;          PRT;          117 AA.
ID   HV1B_HUMAN      P01743;
AC   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DR   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region HG3 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
[1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83144028; PubMed=6298778;
RA   Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT   "Evolutionary aspects of immunoglobulin heavy chain variable region
RL   (VH) gene subgroups.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
CC   EMBL: J0C240; AAA52988.1; -.
DR   PIR: A02024; HVHUNG.
DR   HSSP: P01772; 2FB4.
DR   GO: GO:0005576; C:extracellular; NAS.
DR   GO: GO:0003823; F:antigen binding activity; NAS.
DR   GO: GO:0006955; P:immune response; NAS.
DR   InterPro: IPR007110; Ig-like.
DR   InterPro: IPR003006; Ig_MHC.
DR   InterPro: IPR003596; Ig_v.
DR   Pfam: PF00047; Ig; 1.
DR   SMART: SM00406; IGV; 1.
DR   PROSITE: PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1          19
FT   CHAIN           20         117      IG HEAVY CHAIN V-I REGION HG3.
FT   DOMAIN          20         >117      IG-LIKE.
FT   NON_TER         117        117
SQ   SEQUENCE        117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match          50.5%; Score 51; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 0.31;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGDSGYAPKFG 17
   |:| |:| |||||
Db 70 INPSGGSTSYAQKFG 85

RESULT 3
HV1G_HUMAN
ID   HV1G_HUMAN      STANDARD;          PRT;          117 AA.
AC   P23083;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOY-1991 (Rel. 20, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region V35 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- CATALYTIC ACTIVITY: ADP-ribose + H(2)O = AMP + D-ribose 5-
phosphate.
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. NUDF SUBFAMILY.
CC -----
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CC -----
DR EMBL; AY026252; AAK07671.1; -.
DR EMBL; BC000542; AAH00542.1; -.
DR Genew; HGNC:8056; NUDT9.
DR MIM; 606022; -.
DR GO; GO:0005622; C:intracellular; NAS.
DR GO; GO:0019144; F:ADP-sugar diphosphatase activity; NAS.
DR GO; GO:0005227; F:calcium activated cation channel activity; NAS.
DR GO; GO:0006812; P:cation transport; NAS.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
DR PROSITE; PS00893; NUDIX; FALSE_NEG.
KW Hydrolase.
FT DOMAIN 215 237 NUDIX BOX.
SQ SEQUENCE 350 AA; 39125 MW; 2EA5B24B8FB3420 CRC64;

Query Match
Best Local Similarity 49.5%; Score 50; DB 1; Length 350;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKF 15
Db 110 WADPQISESNFSPKF 124

RESULT 5
HVI2_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]

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RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match
Best Local Similarity 45.5%; Score 46; DB 1; Length 117;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGDSGYAPKFG 17
Db 51 INPNNGGTSTYNQKFKG 66

RESULT 6
HVI3_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

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Query Match	45.5%;	Score 46;	DB 1;	Length 117;
Best Local Similarity	50.0%;	Pred. No. 1.9;		
Matches	8;	Conservative 3;	Mismatches 5;	Indels 0;
Gaps	0;			
Oy	2 IDPENGDSGYAPKFOG 17			
	:       :       :			
Db	51 INPNNGGTSTYNOKFKG 66			

```

RESULT 7
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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XX	MEDLINE=84182519; PubMed=6201362;
RA	Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT	"A V region determinant (idiotope) expressed at high frequency in B
RL	lymphocytes is encoded by a large set of antibody structural genes.";
DR	EMBO J. 3:517-523(1984).
DR	PIR; A02040; MHMS38.
DR	HSSP; P01789; IMCP.
DR	InterPro; IPR007110; IG_1like.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF00047; IG; 1.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 98 V SEGMENT.
FT	DOMAIN 99 104 D SEGMENT.
FT	DOMAIN 105 118 J SEGMENT.
FT	DISULFID 22 96 BY SIMILARITY.
FT	NON TER 118 118
SQ	SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
Query Match	
Best Local Similarity 45.5%; Score 46; DB 1; Length 118;	
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	

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QY      2 IDPENGDSGYAPKFCG 17
      |:| | | : | | | |
Db      51 INPNNGGTSTYNQKFKG 66

RESULT 8
VE4_HPVB
ID      VE4_HPVB      STANDARD;      PRT;      245 AA.
AC      P26550;
DT      01-AUG-1992 (Rel. 23, Created)
DT      01-AUG-1992 (Rel. 23, Last sequence update)
DT      01-AUG-1992 (Rel. 23, Last annotation update)
DE      Probable E4 protein.
OS      Human papillomavirus type 5b.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Papillomavirus.
OX      NCBI_TaxID=10599;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=91306467; PubMed=1649510;
RA      Yabe Y., Sakai A., Hitsumoto T., Kato H., Ogura H.;
RT      "A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic
RT      segment amplified in a carcinoma: nucleotide sequences and genomic
RT      organizations.";
RL      Virology 183:793-798(1991).

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DR EMBL; D90252; BAA14296.1; -.  
DR PIR; C40480; W4WLB5.  
KW Early protein.  
SQ SEQUENCE 245 AA; 25622 MW; E4944F95B3D353B2 CRC64;

Query Match	45.5%;	Score 46;	DB 1;	length 245;
Best Local Similarity	61.5%;	Pred. No. 4.4;		
Matches	8;	Conservative	1;	Mismatches 4;
				Indels 0;
				Gaps 0;
QY	4	PENGDSGYAPKFQ	16	
Db	155	PNNGHSGHGPKVQ	167	

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RESULT 9
GLTS_WHEAT
ID GLTS_WHEAT STANDARD; PRT; 839 AA.
AC P10388;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glutenin, high molecular weight subunit DX5 precursor.
GN GLU-1D-1D OR GLU-D1-1B.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Cheyenne;
RX MEDLINE=89098419; PubMed=2563152;
RA Anderson O.D., Greene F.C., Yip R.E., Halford N.G., Shewry P.R.,
RA Malpica-Romero J.M.;
RT "Nucleotide sequences of the two high-molecular-weight glutenin genes
RT from the D-genome of a hexaploid bread wheat, Triticum aestivum L. cv
RT Cheyenne."
RL Nucleic Acids Res. 17:461-462(1989).
RN [2]
RN REVISIONS, SEQUENCE FROM N.A.
RP STRAIN=cv. Cheyenne;
RA Anderson O.D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE
CC PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE
CC VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
CC -1- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
CC -1- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
CC GROUP 1 CHROMOSOMES OF WHEAT.
CC -1- MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE
CC NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQPGQ AND
CC GQPGGQGGGYPTS.
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CC -----
CC EMBL; X12928; CAA31395.1; -
CC InterPro; IPR001419; Glutenin.
CC Pfam; PF03157; Glutenin hmw; 1.

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```
DR PRINTS; PR00210; GLUTENIN.
KW Seed storage protein; Repeat; Multigene family; Signal.
FT SIGNAL 1 21
FT CHAIN 22 839
FT DOMAIN 131 801
FT SEQUENCE 839 AA; 89359 MW; 0F14E1106D552643 CRC64;
SQ
Query Match
Best Local Similarity 45.5%; Score 46; DB 1; Length 839;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 WIDPENGDSGYAP 13
Db 158 WEEPEOGQGGYYP 170
RESULT 10
HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unarranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC -----
DR EMBL; M13787; AAA38499.1; -.
DR PIR; A02029; HVMSA1.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;
Query Match
Best Local Similarity 44.6%; Score 45; DB 1; Length 117;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 1 WIDPENGDSGYAPKFG 17
Db 69 WYFGDGSITKNEKFKG 85
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RESULT 11
VE4_HPVO5 STANDARD; PRT; 245 AA.
ID VE4_HPVO5
AC P06924;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Probable E4 protein.
OS Human papillomavirus type 5.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10578;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87207670; PubMed=3033892;
RA Zachow K.R., Ostrow R.S., Faras A.J.;
RT "Nucleotide sequence and genome organization of human papillomavirus
RT type 5.";
RL Virology 158:251-254(1987).
CC -----
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CC -----
DR EMBL; M17463; AAA46987.1; -.
KW Early protein.
SQ SEQUENCE 245 AA; 25758 MW; 8F5ECDFB28D87E80 CRC64;
Query Match
Best Local Similarity 44.6%; Score 45; DB 1; Length 245;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 4 PENGDSGYAPKFG 16
Db 155 PHNGHSGHEPKVQ 167
RESULT 12
GLT1_WHEAT STANDARD; PRT; 101 AA.
ID GLT1_WHEAT
AC P02861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Glutenin, high molecular weight subunit PC256 (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Forde J., Forde B.G., Fry R.P., Kreis M., Shewry P.R., Mifflin B.J.;
RT "Identification of barley and wheat cDNA clones related to the high-
RT M-r polypeptides of wheat gluten.";
RL FEBS Lett. 162:360-366(1983).
CC -1- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE
CC PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE
CC VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
CC -1- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
CC -1- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
CC GROUP 1 CHROMOSOMES OF WHEAT.
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DR EMBL; X00054; CAA24933.1; -.  
DR PIR; A03352; EEW1.  
DR InterPro; IPR001419; Glutenin.  
DR Pfam; PF03157; Glutenin\_hmw; 1.  
DR PRINTS; PR00210; GLUTENIN.  
KM Seed storage protein; Repeat; Multigene family.  
FT NON\_TER 1  
SQ SEQUENCE 101 AA; 10896 MW; EF6D6ADDDFEED993 CRC64;

Query Match 43.6%; Score 44; DB 1; Length 101;  
Best Local Similarity 46.2%; Pred. No. 3.4;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAP 13  
Db 12 WLPQPROGQGGYYP 24

RESULT 13  
Gln1\_FRAAL STANDARD; PRT; 474 AA.  
ID Gln1\_FRAAL  
AC P46033;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Glutamine synthetase I (EC 6.3.1.2) (Glutamate--ammonia ligase I)  
DE (GSI).  
GN GLNA.  
OS Frankia alni.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Frankineae; Frankiaceae; Frankia.  
OX NCBI\_TaxID=1859;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Cpil;  
RX MEDLINE=93273742; PubMed=8099074;  
RA Hosted T.J., Rochefort D.A., Benson D.R.;  
RT "Close linkage of genes encoding glutamine synthetases I and II in  
RT Frankia alni Cpil."  
RL J. Bacteriol. 175:3679-3684(1993).  
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +  
CC L-glutamine.  
CC -!- ENZYME REGULATION: THE ACTIVITY OF THIS ENZYME IS CONTROLLED  
CC BY ADENYLATION. THE FULLY ADENYLATED ENZYME COMPLEX IS INACTIVE  
CC (BY SIMILARITY).  
CC -!- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO  
CC HEXAGONS.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- MISCELLANEOUS: TWO FORMS OF GLUTAMINE SYNTHETASE (GSI AND GSII)  
CC CAN BE FOUND IN THIS NITROGEN FIXING BACTERIA, GSI IS A TYPICAL  
CC PROKARYOTIC GLUTAMINE SYNTHETASE WHEREAS GSII IS SIMILAR TO THE  
CC EUKARYOTIC ENZYME.  
CC -!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.  
CC -----  
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DR EMBL; L10631; -; NOT\_ANNOTATED\_CDS.  
DR HSSP; P06201; 1LGR.  
DR InterPro; IPR001691; Gln\_synth.  
DR InterPro; IPR004809; GlnA.  
DR InterPro; IPR001637; GlnA\_adenyltn.  
DR Pfam; PF00120; gln-synt; 1.  
DR Pfam; PF03951; gln-synt\_N; 1.

DR ProDom; PD001057; Gln\_synt\_C; 1.  
DR TRICPAMS; TIGR00653; GlnA; 1.  
DR PROSITE; PS00180; GLNA\_1; 1.  
DR PROSITE; PS00181; GLNA\_ATP; 1.  
DR PROSITE; PS00182; GLNA\_ADENYLATION; 1.  
KM Nitrogen fixation; Ligase; Multigene family.  
FT BINDING 402 402 AMP (UNDER CONDITIONS OF ABUNDANT  
FT GLUTAMINE) (BY SIMILARITY).  
SQ SEQUENCE 474 AA; 53951 MW; FEIDB19AC1735652 CRC64;

Query Match 43.6%; Score 44; DB 1; Length 474;  
Best Local Similarity 53.8%; Pred. No. 19;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 5 ENGDSGYAPKFG 17  
Db 168 EGNLGYKPRFKG 180

RESULT 14  
ROMA\_KLEPN STANDARD; PRT; 132 AA.  
ID ROMA\_KLEPN  
AC Q48412;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Outer membrane protein roma (Fragment).  
GN ROMA.  
OS Klebsiella pneumoniae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ECL8;  
RX MEDLINE=96032015; PubMed=7551053;  
RA George A.M., Hall R.M., Stokes H.W.;  
RT "Multidrug resistance in Klebsiella pneumoniae: a novel gene, rama,  
RT confers a multidrug resistance phenotype in Escherichia coli."  
RL Microbiology 141:1909-1920(1995).  
CC -!- SIMILARITY: TO M.TUBERCULOSIS RV0906.  
CC -----  
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DR EMBL; U19581; AAA85696.1; -.  
DR PIR; T09626; T09626.  
KM Outer membrane.  
FT NON\_TER 1  
SQ SEQUENCE 132 AA; 14745 MW; BCB216F27F9C853B CRC64;

Query Match 42.6%; Score 43; DB 1; Length 132;  
Best Local Similarity 63.6%; Pred. No. 6.6;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 NGDSGYAPKFG 16  
Db 44 SGDSGYGPHFK 54

RESULT 15  
17KD\_RICPR STANDARD; PRT; 159 AA.  
ID 17KD\_RICPR  
AC P16624;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 17 kDa surface antigen precursor.

GN OMP OR, RP833.  
OS Rickettsia prowazekii.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=782;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Madrid E;  
RX MEDLINE=89359171; PubMed=2768201;  
RA Anderson B.E., Tzianabos T.;  
RT "Comparative sequence analysis of a genus-common rickettsial antigen  
gene.";  
RL J. Bacteriol. 171:5199-5201 (1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Madrid E;  
RX MEDLINE=99039499; PubMed=9823893;  
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,  
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,  
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;  
RT "The genome sequence of Rickettsia prowazekii and the origin of  
mitochondria.";  
RL Nature 396:133-140 (1998).  
CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid  
CC anchor (Probable).  
CC -----  
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CC -----  
DR EMBL; M28482; AAA26378.1; ALT\_SEQ.  
DR EMBL; AJ235273; CAA15258.1; -.  
DR PIR; D33971; D33971.  
DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
KW Outer membrane; lipoprotein; Antigen; Signal; Complete proteome.  
FT SIGNAL 1 19  
FT CHAIN 20 159 17 kDa SURFACE ANTIGEN.  
FT LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).  
SQ SEQUENCE 159 AA; 16672 MW; A33D404B65EEB071 CRC64;  
Query Match 42.6%; Score 43; DB 1; Length 159;  
Best Local Similarity 54.5%; Pred. No. 8.2;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 WIDPENGDSGY 11  
|:|:|:|:  
Db 102 WRNPDNGNGY 112

Search completed: July 30, 2003, 09:44:59  
Job time : 3.65449 secs

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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 13.1595 Seconds  
(without alignments)  
333.364 Million cell updates/sec

Title: US-09-865-198-2  
Perfect score: 101  
Sequence: 1 WIDPENGDSGYAPKFG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	74.3	468	11 Q99L31	Q99L31 mus musculu
2	58	57.4	614	4 Q96GA6	Q96GA6 homo sapien
3	57	56.4	109	11 Q9UL85	Q9J185 mus musculu
4	56.5	55.9	150	4 Q9Y298	Q9Y298 homo sapien
5	56	55.4	497	4 Q8WY24	Q8WY24 homo sapien
6	55	54.5	125	4 Q9UL95	Q9UL95 homo sapien
7	54	53.5	119	4 Q9UL94	Q9UL94 homo sapien
8	54	53.5	481	11 Q8VCV5	Q8VCV5 mus musculu
9	51	50.5	124	4 Q9UL92	Q9UL92 homo sapien
10	51	50.5	480	11 Q8K0Z4	Q8K0Z4 mus musculu
11	50	49.5	300	4 Q8NCB9	Q8NCB9 homo sapien
12	50	49.5	350	4 Q96KB3	Q96KB3 homo sapien
13	50	49.5	350	4 Q8NBN1	Q8NBN1 homo sapien
14	50	49.5	350	11 Q8K1J4	Q8K1J4 mus musculu
15	50	49.5	350	11 Q8BVU5	Q8BVU5 mus musculu
16	50	49.5	500	4 Q9BRV0	Q9BRV0 homo sapien

17	49	48.5	754	10 Q94IL2	Q94IL2 secale cere
18	49	48.5	754	10 Q93WF0	Q93WF0 secale cere
19	49	48.5	754	10 Q94IK9	Q94IK9 secale cere
20	48	47.5	311	16 Q92ME3	Q92ME3 rhizobium m
21	48	47.5	329	5 Q27501	Q27501 caenorhabdi
22	48	47.5	403	16 Q8YIU7	Q8YIU7 ralstonia s
23	48	47.5	484	11 Q99LA6	Q99LA6 mus musculu
24	48	47.5	526	17 Q8TJE3	Q8TJE3 methanosarc
25	47.5	47.0	474	11 Q8R3H6	Q8R3H6 mus musculu
26	47	46.5	102	11 Q9UL79	Q9UL79 mus musculu
27	47	46.5	208	16 Q92FI2	Q92FI2 listeria in
28	47	46.5	209	16 Q8YA89	Q8YA89 listeria mo
29	47	46.5	366	5 Q27528	Q27528 caenorhabdi
30	47	46.5	375	5 Q9XW33	Q9XW33 caenorhabdi
31	47	46.5	509	17 Q9HMH4	Q9hmb4 halobacteri
32	47	46.5	520	11 Q92IT2	Q92IT2 mus musculu
33	47	46.5	643	16 Q8CXI6	Q8CXI6 oceanobacil
34	46	45.5	117	11 Q9QXE9	Q9QXE9 mus musculu
35	46	45.5	117	11 Q9QXF0	Q9QXF0 mus musculu
36	46	45.5	159	4 Q96QSO	Q96QSO homo sapien
37	46	45.5	300	4 Q8NG26	Q8NG26 homo sapien
38	46	45.5	327	5 Q23671	Q23671 caenorhabdi
39	46	45.5	350	4 Q8NG25	Q8NG25 homo sapien
40	46	45.5	363	2 Q93NF9	Q93NF9 archaeobacte
41	46	45.5	390	9 Q9TIR0	Q9TIR0 bacterioph
42	46	45.5	481	11 Q91WT1	Q91WT1 mus musculu
43	46	45.5	626	3 Q991I2	Q991I2 usclilago ma
44	46	45.5	1737	11 Q9JIO4	Q9JIO4 rattus norv
45	45.5	45.0	118	11 Q9ZIC4	Q9ZIC4 mus musculu

ALIGNMENTS

RESULT 1					
ID	Q99L31	PRELIMINARY;	PRT;	468	AA.
AC	Q99L31;				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, last annotation update)				
DE	Similar to RIKEN CDNA 181060009 gene.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Strausberg R.;				
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC003878; AA03878.1; -.				
DR	HSSP; P01842; 7FAB.				
DR	InterPro; IPR007110; Ig_1like.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR003596; IG_v.				
DR	Pfam; PF00047; Ig; 3.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PSS0835; IG_LIKE; 4.				
DR	PROSITE; PS00290; IG_MHC; 1.				
SQ	SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;				
Query Match					
Best Local Similarity		74.3%;	Score 75;	DB 11;	Length 468;
Matches 12;		Conservative	3;	Mismatches	1;
				Indels	0;
				Gaps	0;
OY	1 WIDPENGDSGYAPKFG 16				
	: :				
Db	69 WIDPEDEGTYAPKFG 84				
RESULT 2					
ID	Q96GA6	PRELIMINARY;	PRT;	614	AA.

AC Q96GA6;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strauberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC009851; AA09851.1; -.  
DR InterPro; IPR000005; HTHArac.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 57.4%; Score 58; DB 4; Length 614;  
Best Local Similarity 62.5%; Pred. No. 1.1;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFO 16  
Db 69 WITPFGNTNTYAQKFO 84

RESULT 3

Q9JL85 PRELIMINARY; PRT; 109 AA.  
AC Q9JL85;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Anti-myosin immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of  
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
RT with cardiac myosin."  
RL Infect. Immun. 68:5803-5808 (2000).  
DR EMBL; AF206021; AAF69319.1; -.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 56.4%; Score 57; DB 11; Length 109;  
Best Local Similarity 68.8%; Pred. No. 0.23;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGDSGYAPKFOG 17  
Db 43 IDPATGHSKYDPKFOG 58

RESULT 4

Q9Y298 PRELIMINARY; PRT; 150 AA.  
ID Q9Y298  
AC Q9Y298;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE IGG VH protein precursor (Fragment).  
GN IGG VH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98322155; PubMed=9657749;  
RA Jacquemin M.G., Vander Elst L.P.L.;  
RT "Mechanism and kinetics of factor VIII inactivation: study with an  
RT IGG4 monoclonal antibody derived from a hemophilia A patient with  
RT inhibitor."  
RL Blood 92:496-506 (1998).  
DR EMBL; AJ224083; CAA11829.1; -.  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Signal.  
FT SIGNAL 1  
FT NON\_TER 150  
FT NON\_TER 150  
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 55.9%; Score 56.5; DB 4; Length 150;  
Best Local Similarity 55.0%; Pred. No. 0.39;  
Matches 11; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 WI--DPENGDSGYAPKFOG 17  
Db 66 WVGSPFDSGESIVAREFOG 85

RESULT 5

Q8WY24 PRELIMINARY; PRT; 497 AA.  
ID Q8WY24  
AC Q8WY24;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE SNC66 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;  
RT "Identification and characterization of SNC66, a Ig-like gene which is  
RT down-regulated in colorectal cancer."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF283666; AAL36987.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.



DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 55.4%; Score 56; DB 4; Length 497;  
Best Local Similarity 47.1%; Pred. No. 1.8;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKFOG 17  
|::|:|::|:|  
Db 69 WMINPQTGNTTEFAQKFOG 85

## RESULT 6

O9UL95 PRELIMINARY; PRT; 125 AA.

AC Q9UL95;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035019; AAD56255.1; -.

DR HSSP; P01810; 2FBJ.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

FT NON\_TER 1

FT 125

SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 54.5%; Score 55; DB 4; Length 125;  
Best Local Similarity 52.9%; Pred. No. 0.55;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKFOG 17  
|::|:|::|:|  
Db 50 WINPNSGCTNYAQKVOG 66

## RESULT 7

O9UL94 PRELIMINARY; PRT; 119 AA.

AC Q9UL94;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035020; AAD56256.1; -.

DR HSSP; P01810; 2FBJ.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

FT NON\_TER 1

FT 119

SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 53.5%; Score 54; DB 4; Length 119;  
Best Local Similarity 52.9%; Pred. No. 0.75;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKFOG 17  
|::|:|::|:|  
Db 50 WINPNSWTTNYAQKFOG 66

## RESULT 8

O8VCV5 PRELIMINARY; PRT; 481 AA.

AC Q8VCV5;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical 52.3 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Breast tumor;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC018455; AAH18455.1; -.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 4.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; 2.

KW Hypothetical protein.

SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 53.5%; Score 54; DB 11; Length 481;  
Best Local Similarity 58.8%; Pred. No. 3.7;

Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKFOG 17  
:|::|:|:|:|:|  
Db 69 YIDPYNGGSSYNQKFKG 85

## RESULT 9

O9UL92 PRELIMINARY; PRT; 124 AA.

AC Q9UL92;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035022; AAD56258.1; -.  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 1  
FT NON TER 1  
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 50.5%; Score 51; DB 4; Length 124;  
Best Local Similarity 56.2%; Pred. No. 2.3;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 IDPENGDGYPKFG 17  
Db 51 INPSGGSTSYAKFG 66

RESULT 10  
Q8K024 PRELIMINARY; PRT; 480 AA.

ID Q8K024  
AC Q8K024;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Similar to expressed sequence A1893585.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast tumor;  
RA Strausberg R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC029188; AAH29188.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IG; 3.  
DR SMART; SM00407; IGV; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
SQ SEQUENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;

Query Match 50.5%; Score 51; DB 11; Length 480;  
Best Local Similarity 52.9%; Pred. No. 11;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 WIDPENGDGYPKFG 17  
Db 69 WISPGDGSSEYNEKPKG 85

RESULT 11  
Q8NCB9 PRELIMINARY; PRT; 300 AA.

AC Q8NCB9;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein FLJ90364.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,  
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,  
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,  
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;  
RT "NEDO human cDNA sequencing project";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK074845; BAC11239.1; -.  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 300 AA; 33776 MW; 531993C757A82E49 CRC64;

Query Match 49.5%; Score 50; DB 4; Length 300;  
Best Local Similarity 46.7%; Pred. No. 9.2;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 WIDPENGDGYPKPF 15  
Db 60 WADPQISESNFSPKF 74

RESULT 12  
Q96KB3 PRELIMINARY; PRT; 350 AA.

ID Q96KB3  
AC Q96KB3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein FLJ14389.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,  
RA Magatsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Takiguchi S.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Saito K.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Masuho Y.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
RA Ninomiya K., Iwayanagi T.;  
RT "NEDO human cDNA sequencing project";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK027295; BAB55021.1; -.  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 350 AA; 39042 MW; 8BE1A31ECCFB343D CRC64;

Query Match 49.5%; Score 50; DB 4; Length 350;  
Best Local Similarity 46.7%; Pred. No. 11;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 WIDPENGDGYPKPF 15  
Db 110 WADPQISESNFSPKF 124

RESULT 13

Q8NBN1  
ID Q8NBN1, PRELIMINARY; PRT; 350 AA.  
AC Q8NBN1;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Hypothetical protein NT2RP2002907.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,  
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,  
RA Nagahari K., Sugano S., Isogai T.;  
RT "HRI human cDNA sequencing project."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK075408; BAC11601.1;  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 350 AA; 39095 MW; 2EB6A14B9BE83420 CRC64;

Query Match 49.5%; Score 50; DB 4; Length 350;  
Best Local Similarity 46.7%; Pred. No. 11;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKF 15  
| | | : | : | | |  
Db 110 WADPQISESNFSPKF 124

RESULT 14  
Q8K1J4  
ID Q8K1J4 PRELIMINARY; PRT; 350 AA.  
AC Q8K1J4;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Similar to nudix (Nucleoside diphosphate linked moiety X)-type motif  
DE 9.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC033921; AAH33921.1;  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
SQ SEQUENCE 350 AA; 38623 MW; 6FD9371307AB3366 CRC64;

Query Match 49.5%; Score 50; DB 11; Length 350;  
Best Local Similarity 46.7%; Pred. No. 11;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKF 15  
| | | : | : | | |  
Db 110 WADPQISESNFSPKF 124

RESULT 15  
Q8BVUS  
ID Q8BVUS PRELIMINARY; PRT; 350 AA.  
AC Q8BVUS;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Nudix.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK076500; BAC36366.1;  
SQ SEQUENCE 350 AA; 38604 MW; EDD9371307AB3373 CRC64;

Query Match 49.5%; Score 50; DB 11; Length 350;  
Best Local Similarity 46.7%; Pred. No. 11;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKF 15  
| | | : | : | | |  
Db 110 WADPQISESNFSPKF 124

Search completed: July 30, 2003, 09:42:32  
Job time : 16.2706 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 17 Seconds  
(without alignments)  
158.727 Million cell updates/sec

Title: US-09-865-198-2

Perfect score: 101

Sequence: 1 WIDPENGDSGYAPKFGQ 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	17	21	AAV97230
2	101	100.0	17	23	AAE25950
3	101	100.0	17	23	AAU74407
4	101	100.0	17	24	ABJ26719
5	101	100.0	117	21	AAV97235
6	101	100.0	117	23	AAE25955
7	101	100.0	117	23	AAU74412
8	101	100.0	117	24	ABJ26724
9	101	100.0	240	23	AAE25960

10	101	100.0	240	23	AAU74419	Antigen-binding pr
11	101	100.0	240	24	ABJ26731	VEGF binding relat
12	94	93.1	17	22	AAE13138	Humanised antibody
13	94	93.1	17	22	AAE25963	VEGF antagonist an
14	94	93.1	17	23	AAU74416	Heavy chain comple
15	94	93.1	17	24	ABJ26728	VEGF binding relat
16	94	93.1	117	22	AAE13143	Humanised antibody
17	94	93.1	117	22	AAE25965	VEGF antagonist an
18	94	93.1	117	23	AAU74417	Antigen-binding pr
19	94	93.1	117	24	ABJ26729	VEGF binding relat
20	94	93.1	135	23	AAE25965	Mouse anti-KDR p1C
21	94	93.1	136	22	AAE13145	Chimeric p1C11 hea
22	94	93.1	136	22	AAE25961	VEGF antagonist an
23	94	93.1	136	23	AAE28916	c-p1C11 vector hea
24	94	93.1	238	23	AAE25961	KDR binding immuno
25	94	93.1	238	23	AAE25963	KDR binding immuno
26	94	93.1	238	23	AAU74420	Antigen-binding pr
27	94	93.1	238	24	ABJ26732	VEGF binding relat
28	90	89.1	17	20	AAW89162	Anti-p53 monoclonal
29	90	89.1	20	21	AAV70794	Murine anti-p53 PA
30	90	89.1	112	20	AAW89173	Anti-p53 monoclonal
31	90	89.1	116	21	AAV70787	Murine anti-p53 mo
32	90	89.1	122	20	AAV39531	Humanised Murine C
33	90	89.1	124	15	AAE60565	Anti-carcinoembryo
34	90	89.1	124	15	AAE60566	Murine COL1 VH cha
35	90	89.1	124	20	AAV39528	Humanised Murine C
36	90	89.1	124	20	AAV39530	Humanised Murine C
37	90	89.1	124	20	AAV39536	Humanised Murine C
38	90	89.1	124	20	AAV39537	Humanised Murine C
39	90	89.1	124	20	AAV39538	Humanised Murine C
40	90	89.1	124	20	AAV39539	Humanised Murine C
41	90	89.1	124	20	AAV39540	Humanised Murine C
42	90	89.1	124	20	AAV39541	Humanised Murine C
43	90	89.1	124	20	AAV39542	Humanised Murine C
44	90	89.1	124	20	AAV39543	Humanised Murine C
45	90	89.1	124	23	ABB83941	Mouse monoclonal a

ALIGNMENTS

RESULT 1	
AAV97230	
ID AAV97230 standard; Protein; 17 AA.	
XX	
AC AAV97230;	
XX	
DT 19-DEC-2000 (first entry)	
XX	
DE Complementary determining region (CDRH2) of anti-SI (KDR) antibody.	
XX	
KW Immunoglobulin; antibody; complementary determining region; CDR;	
KW VEGF; vascular endothelial growth factor; KDR;	
KW kinase insert domain containing receptor; multivalent; monovalent;	
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;	
KW glioblastoma multiforme; hemangioblastoma; AIDS;	
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;	
KW acquired immune deficiency syndrome; AIDS; human.	
XX	
OS Homo sapiens.	
OS Synthetic.	
XX	
PN WO200044777-A1.	
XX	
PD 03-AUG-2000.	
XX	
PF 28-JAN-2000; 2000WO-US02180.	
XX	
PR 29-JAN-1999; 99US-0117726.	
XX	
PR 29-JAN-1999; 99US-0240736.	
XX	
PA (IMCL-) IMCLONE SYSTEMS INC.	
XX	

PI Zhu Z, Witte L;  
XX  
DR WPI; 2000-505966/45.  
DR N-PSDB; AAA53762.  
XX  
PT Novel immunoglobulin molecules binding kinase insert domain-containing  
PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growth  
XX  
PS Claim 3; Page 50; 55pp; English.  
XX  
CC New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Kaposi's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulins of the invention.  
XX  
SQ Sequence 17 AA;  
  
Query Match 100.0%; Score 101; DB 21; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WIDPENGDSGYAPKFG 17  
Db 1 WIDPENGDSGYAPKFG 17  
  
RESULT 2  
AAE25950  
ID AAE25950 standard; peptide; 17 AA.  
XX  
AC AAE25950;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Mouse anti-KDR p1C11 scFv antibody CDRH2 peptide.  
XX  
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; heavy chain complementarity determining region 2;  
KW CDRH2; angiogenesis; p1C11; scFv antibody.  
XX  
OS Mus musculus.  
XX  
PN US2002064528-A1.  
XX  
PD 30-MAY-2002.  
XX  
PF 12-OCT-2001; 2001US-0976787.  
XX  
PR 28-JAN-2000; 2000US-0493539.  
XX  
PA (ZHUZ/) ZHU Z.  
PA (WITT/) WITTE L...  
XX  
PI Zhu Z, Witte L;  
XX  
DR WPI; 2002-589175/63.  
DR N-PSDB; AAD42815.  
XX  
PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to

PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR  
XX  
PS Claim 3; Page 11; 34pp; English.  
XX  
CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody  
CC heavy chain complementarity determining region 2 (CDRH2).  
XX  
SQ Sequence 17 AA;  
  
Query Match 100.0%; Score 101; DB 23; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WIDPENGDSGYAPKFG 17  
Db 1 WIDPENGDSGYAPKFG 17  
  
RESULT 3  
AAU74407  
ID AAU74407 standard; peptide; 17 AA.  
XX  
AC AAU74407;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Heavy chain complementarity determining region H2 (CDRH2) version #1.  
XX  
KW Complementarity determining region; CDR; CDRH2; antigen; cytotoxic;  
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;  
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;  
KW antibody heavy chain variable domain.  
XX  
OS Mus sp.  
XX  
PN WO200190192-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US16924.  
XX  
PR 24-MAY-2000; 2000US-206749P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2002-106189/14.  
DR N-PSDB; AAS20278.  
XX  
PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides  
XX  
PS Claim 55; Page 56; 64pp; English.  
XX  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (C1 domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and



CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This peptide sequence represents the heavy chain variable domain  
CC complementarity determining region H2 (CDRH2) version #1 incorporated  
CC into an antigen-binding protein described in the method of the invention.  
XX  
SQ Sequence 17 AA;  
  
Query Match 100.0%; Score 101; DB 23; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WIDPENGDSGYAPKFOG 17  
Db 1 WIDPENGDSGYAPKFOG 17  
  
RESULT 4  
ABJ26719  
ID ABJ26719 standard; Peptide; 17 AA.  
XX  
AC ABJ26719;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE VEGF binding related peptide SEQ ID No 2.  
XX  
KM Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KM leukaemia cell; vascular endothelial growth factor; tumour;  
KM bispecific antigen-binding protein; mouse; murine.  
XX  
OS Mus sp.  
XX  
PN WO2003002144-A1.  
XX  
PD 09-JAN-2003.  
XX  
PF 26-JUN-2002; 2002WO-US20332.  
XX  
PR 26-JUN-2001; 2001US-301299P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2003-201468/19.  
DR N-PSDB; ABT23297.  
XX  
PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -  
XX  
PS Claim 6; Page 48; 98pp; English.  
XX  
CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse peptide relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX

SQ Sequence 17 AA;  
  
Query Match 100.0%; Score 101; DB 24; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WIDPENGDSGYAPKFOG 17  
Db 1 WIDPENGDSGYAPKFOG 17  
  
RESULT 5  
AA97235  
ID AA97235 standard; Protein; 117 AA.  
XX  
AC AA97235;  
XX  
DT 19-DEC-2000 (first entry)  
XX  
DE Variable heavy chain fragment of anti-SI(KDR) antibody.  
XX  
KM Immunoglobulin; antibody; complementary determining region; CDR;  
KM VEGF; vascular endothelial growth factor; KDR;  
KM kinase insert domain containing receptor; multivalent; monovalent;  
KM humanised antibody; chimeric antibody; tumour; diabody; triabody;  
KM glioblastoma multiforme; hemangioblastoma; AIDS;  
KM central nervous system neoplasms; AIDS associated Karpov's sarcoma;  
KM acquired immune deficiency syndrome; AIDS; human.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200044777-A1.  
XX  
PD 03-AUG-2000.  
XX  
PF 28-JAN-2000; 2000WO-US02180.  
XX  
PR 29-JAN-1999; 99US-0117726.  
XX  
PR 29-JAN-1999; 99US-0240736.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z, Witte L;  
XX  
DR WPI; 2000-505966/45.  
DR N-PSDB; AAA53767.  
XX  
PT Novel immunoglobulin molecules binding kinase insert domain-containing  
PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growth  
XX  
PS Claim 4; Page 50-51; 55pp; English.  
XX  
CC New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Karpov's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulins of the invention.  
XX  
SQ Sequence 117 AA;  
  
Query Match 100.0%; Score 101; DB 21; Length 117;

Best Local Similarity 100.0%; Pred. No. 7.9e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKFOG 17  
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 6  
AAE25955  
ID AAE25955 standard; Protein; 117 AA.

AC AAE25955;

DT 15-NOV-2002 (first entry)

DE Mouse anti-KDR p1C11 scFv antibody VH region #1.

KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
KW p1C11; scFv antibody.

OS Mus musculus.

PN US2002064528-A1.

PD 30-MAY-2002.

PF 12-OCT-2001; 2001US-0976787.

PR 28-JAN-2000; 2000US-0493539.

PA (ZHUZ/) ZHU Z.

PA (WITT/) WITTE L.

PI Zhu Z, Witte L;

DR WPI; 2002-589175/63.

DR N-PSDB; AAD42820.

PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR  
PS Claim 4; Page 11; 34pp; English.

CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (Flk)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody  
CC heavy chain variable region (VH).

SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 23; Length 117;  
Best Local Similarity 100.0%; Pred. No. 7.9e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKFOG 17  
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 7  
AAU74412  
ID AAU74412 standard; peptide; 117 AA.

AC AAU74412;

XX 26-MAR-2002 (first entry)

DE Antigen-binding protein heavy chain variable domain (VH) #1.  
XX Antigen-binding protein; antibody heavy chain variable domain;  
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;  
KW cell proliferation inhibitor.

OS Mus sp.

PN WO200190192-A2.

PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US16924.

PR 24-MAY-2000; 2000US-206749P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

DR WPI; 2002-106189/14.

DR N-PSDB; AAS20283.

PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides

PS Claim 57; Page 57; 64pp; English.

CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (CL domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This sequence represents a heavy chain variable domain (VH) incorporated  
CC into Fv, an engineered protein containing a heavy chain variable domain  
CC and a light chain variable domain in one polypeptide chain, described in  
CC the method of the invention.

SQ Sequence 117 AA;

Query Match 100.0%; Score 101; DB 23; Length 117;  
Best Local Similarity 100.0%; Pred. No. 7.9e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKFOG 17  
Db 50 WIDPENGDSGYAPKFOG 66

RESULT 8  
ABJ26724  
ID ABJ26724 standard; Protein; 117 AA.

AC ABJ26724;

XX 01-MAY-2003 (first entry)  
DT VEGF binding related protein SEQ ID No 7.  
XX  
DE  
XX  
XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.  
XX  
OS Mus sp.  
XX  
PN WO2003002144-A1.  
XX  
PD 09-JAN-2003.  
XX  
XX  
PF 26-JUN-2002; 2002WO-US20332.  
XX  
PR 26-JUN-2001; 2001US-301299P.  
XX  
XX (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2003-201468/19.  
DR N-PSDB; ABT23302.  
XX  
XX  
XX  
PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -  
XX  
XX  
PS Claim 7; Page 49; 98pp; English.  
XX  
CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse protein relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX  
SQ Sequence 117 AA;  
  
Query Match 100.0%; Score 101; DB 24; Length 117;  
Best Local Similarity 100.0%; Pred. No. 7.9e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WIDPENGDSGYAPKFOG 17  
Db 50 WIDPENGDSGYAPKFOG 66  
  
RESULT 9  
AAE25960  
ID AAE25960 standard; Protein; 240 AA.  
XX  
AC AAE25960;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE KDR binding immunoglobulin related mouse protein #1.  
XX  
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
KW pIC11; scFv antibody.  
XX  
OS Mus sp.  
XX  
PN US2002064528-A1.

XX 30-MAY-2002.  
PD  
XX 12-OCT-2001; 2001US-0976787.  
PF  
XX 28-JAN-2000; 2000US-0493539.  
PR  
XX (ZHUZ/) ZHU Z.  
PA (WITT/) WITTE L.  
XX  
XX Zhu Z, Witte L;  
XX  
XX WPI; 2002-589175/63.  
DR N-PSDB; AAD42824.  
XX  
XX  
XX Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR -  
XX  
XX  
PS Disclosure; Page 16-17; 34pp; English.  
XX  
XX  
CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is KDR binding immunoglobulin related  
CC mouse protein.  
XX  
SQ Sequence 240 AA;  
  
Query Match 100.0%; Score 101; DB 23; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WIDPENGDSGYAPKFOG 17  
Db 50 WIDPENGDSGYAPKFOG 66  
  
RESULT 10  
AAU74419  
ID AAU74419 standard; Protein; 240 AA.  
XX  
AC AAU74419;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Antigen-binding protein, single chain variable fragment version #1.  
XX  
XX  
KW Antigen-binding protein; single chain variable fragment; scFv; antigen;  
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;  
KW cell proliferation inhibitor.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT 1.117  
FT Region /label= VH  
FT /note= "Heavy chain variable domain. Specifically  
FT claimed in claim 57"  
FT  
FT Region 118..132  
FT /label= Linker  
FT /note= "15 amino acid linker joins the VH and VL  
FT regions of the single chain variable  
FT fragment protein. Encoded by AAS20285"  
FT 133..240  
FT /label= VL  
FT /note= "Light chain variable domain. Specifically

FT XX claimed in claim 57"  
XX PN WO200190192-A2.  
XX PD 29-NOV-2001.  
XX PF 24-MAY-2001; 2001WO-US16924.  
XX PR 24-MAY-2000; 2000US-206749P.  
XX PA (IMCL-) IMCLONE SYSTEMS INC.  
XX PI Zhu Z;  
XX DR WPI; 2002-106189/14.  
XX PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides  
XX PS  
XX PS Claim 63; Page 62; 64pp; English.  
XX CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (Cl domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This is the amino acid sequence of a single chain variable fragment  
CC (scFv), an engineered protein containing a variable light and variable  
CC heavy domain on one polypeptide, described in the method of the  
CC invention.  
XX SQ Sequence 240 AA;  
SQ Query Match 100.0%; Score 101; DB 23; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WIDPENGDSGYAPKFG 17  
Db 50 WIDPENGDSGYAPKFG 66  
RESULT 11  
ABJ26731  
ID ABJ26731 standard; Protein; 240 AA.  
XX AC ABJ26731;  
XX DT 01-MAY-2003 (first entry)  
XX DE VEGF binding related protein SEQ ID No 27.  
XX KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
XX bispecific antigen-binding protein; mouse; murine.  
OS Mus sp.  
XX

PN WO2003002144-A1.  
XX PD 09-JAN-2003.  
XX PF 26-JUN-2002; 2002WO-US20332.  
XX PR 26-JUN-2001; 2001US-301299P.  
XX PA (IMCL-) IMCLONE SYSTEMS INC.  
XX PI Zhu Z;  
XX DR WPI; 2003-201468/19.  
XX PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -  
XX PS  
XX PS Disclosure; Page 55-56; 98pp; English.  
XX CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse protein relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX SQ Sequence 240 AA;  
SQ Query Match 100.0%; Score 101; DB 24; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WIDPENGDSGYAPKFG 17  
Db 50 WIDPENGDSGYAPKFG 66  
RESULT 12  
AAE13138  
ID AAE13138 standard; peptide; 17 AA.  
XX AC AAE13138;  
XX DT 28-JAN-2002 (first entry)  
XX DE Humanised antibody murine heavy chain hypervariable region (VH) CDR2.  
XX KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytosstatic; heavy chain hypervariable region; VH; myelocytic leukaemia;  
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;  
KW Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.  
XX OS Mus sp.  
XX PN WO200174296-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US10504.  
XX PR 31-MAR-2000; 2000US-0540770.  
XX PA (IMCL-) IMCLONE SYSTEMS INC.  
PA (CORR ) CORNELL RES FOUND INC.  
XX PI Witte L, Rafii S;  
XX



DR WPI; 2001-662942/76.  
DR N-PSDB; AAD21664.  
XX  
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with  
PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
PS Claim 8; Page 14; 68pp; English.  
XX  
CC The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains mouse complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised  
CC antibody murine heavy chain hypervariable region (VH) CDR-2 used in the  
CC exemplification of the invention.  
XX  
SQ Sequence 17 AA;  
  
Query Match 93.1%; Score 94; DB 22; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 WIDPENGDSGYAPKFG 17  
Db 1 WIDPENGSDSYAPKFG 17  
|||||  
|  
  
RESULT 13  
AAB82704  
ID AAB82704 standard; Peptide; 17 AA.  
XX  
AC AAB82704;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE VEGF antagonist antibody IMC-1C11 VH CDR-2.  
XX  
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; heavy chain; CDR;  
KW complementarity determining region.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
PN WO200154723-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 29-JAN-2001; 2001WO-US02839.  
XX  
PR 28-JAN-2000; 2000US-0178791.  
PR 31-MAR-2000; 2000US-0539692.  
XX  
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Kerbel R;  
XX  
DR WPI; 2001-514531/56.  
XX  
PT Treating or controlling an angiogenic dependent condition (e.g. a

PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX  
PS Disclosure; Page 37; 42pp; English.  
XX  
CC The present sequence is that of complementarity determining region  
CC 2 of the heavy chain variable region (see also AAB82701) of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
SQ Sequence 17 AA;  
  
Query Match 93.1%; Score 94; DB 22; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 WIDPENGDSGYAPKFG 17  
Db 1 WIDPENGSDSYAPKFG 17  
|||||  
|  
  
RESULT 14  
AAU74416  
ID AAU74416 standard; peptide; 17 AA.  
XX  
AC AAU74416;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Heavy chain complementarity determining region H2 (CDRH2) version #2.  
XX  
KW Complementarity determining region; CDR; CDRH2; antigen; cytostatic;  
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;  
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;  
KW antibody heavy chain variable domain.  
XX  
OS SMus sp.  
XX  
PN WO200190192-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US16924.  
XX  
PR 24-MAY-2000; 2000US-206749P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2002-106189/14.  
DR N-PSDB; AAS20287.  
XX  
PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides -

XX Claim 59; Page 60; 64pp; English.  
PS  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (C1 domain), and P2 has an antigen-binding  
CC site located to the N terminus of the C1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This peptide sequence represents the heavy chain variable domain  
CC complementarity determining region H2 (CDRH2) version #2 incorporated  
CC into an antigen-binding protein described in the method of the invention.  
XX  
SQ Sequence 17 AA;

Query Match 93.1%; Score 94; DB 23; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 WIDPENGDSGYAPKFGG 17  
Db 1 WIDPENGDSGYAPKFGG 17

RESULT 15  
ID ABJ26728 standard; Peptide; 17 AA.  
XX  
AC ABJ26728;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE VEGF binding related peptide SEQ ID No 21.  
XX  
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.  
XX  
OS Mus sp.  
XX  
PN WO2003002144-A1.  
XX  
PD 09-JAN-2003.  
XX  
PF 26-JUN-2002; 2002WO-US20332.  
XX  
PR 26-JUN-2001; 2001US-301299P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2003-201468/19.  
XX  
PT New bispecific antibodies having antigen-binding sites specific for a  
PT first; vascular endothelial growth factor (VEGF) receptor and for a  
PT second; VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -  
XX  
PS Claim 10; Page 53; 98pp; English.

XX  
CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse peptide relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX  
SQ Sequence 17 AA;

Query Match 93.1%; Score 94; DB 24; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 WIDPENGDSGYAPKFGG 17  
Db 1 WIDPENGDSGYAPKFGG 17

Search completed: July 30, 2003, 09:36:45  
Job time : 18 secs





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; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-2
```

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Query Match          100.0%; Score 101; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 WIDPENGDSGYAPKFGG 17
        |||
Db      1 WIDPENGDSGYAPKFGG 17
```

## RESULT 3

```
US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7
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```
Query Match          100.0%; Score 101; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 WIDPENGDSGYAPKFGG 17
        |||
Db      50 WIDPENGDSGYAPKFGG 66
```

## RESULT 4

```
US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
```

```
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-7
```

```
Query Match          100.0%; Score 101; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 WIDPENGDSGYAPKFGG 17
        |||
Db      50 WIDPENGDSGYAPKFGG 66
```

## RESULT 5

```
US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28
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```
Query Match          100.0%; Score 101; DB 9; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 WIDPENGDSGYAPKFGG 17
        |||
Db      50 WIDPENGDSGYAPKFGG 66
```

## RESULT 6

```
US-09-865-198-27
; Sequence 27, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-27
```

```
Query Match          100.0%; Score 101; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 WIDPENGDSGYAPKFGG 17
        |||
Db      50 WIDPENGDSGYAPKFGG 66
```

RESULT 7  
US-09-976-787-22  
; Sequence 22, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 22  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-22

Query Match 93.1%; Score 94; DB 9; Length 17;  
Best Local Similarity 94.1%; Pred. No. 3.9e-08;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17  
|||  
Db 1 WIDPENGDSGYAPKFG 17

RESULT 8  
US-09-865-198-21  
; Sequence 21, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho  
; TITLE OF INVENTION: Production  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 21  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-21

Query Match 93.1%; Score 94; DB 10; Length 17;  
Best Local Similarity 94.1%; Pred. No. 3.9e-08;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17  
|||  
Db 1 WIDPENGDSGYAPKFG 17

RESULT 9  
US-09-976-787-23  
; Sequence 23, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505

; CURRENT APPLICATION NUMBER: US/09/976,787  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 23  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-23

Query Match 93.1%; Score 94; DB 9; Length 117;  
Best Local Similarity 94.1%; Pred. No. 2.9e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17  
|||  
Db 50 WIDPENGDSGYAPKFG 66

RESULT 10  
US-09-865-198-22  
; Sequence 22, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho  
; TITLE OF INVENTION: Production  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 22  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-22

Query Match 93.1%; Score 94; DB 10; Length 117;  
Best Local Similarity 94.1%; Pred. No. 2.9e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17  
|||  
Db 50 WIDPENGDSGYAPKFG 66

RESULT 11  
US-09-798-689-7  
; Sequence 7, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 08/326,552  
PRIOR FILING DATE: 1994-10-20  
PRIOR APPLICATION NUMBER: 08/196,041  
PRIOR FILING DATE: 1994-02-10  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Mouse  
US-09-798-689-7

Query Match 93.1%; Score 94; DB 11; Length 117;  
Best Local Similarity 94.1%; Pred. No. 2.9e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFGG 17  
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Db 50 WIDPENGDSGYAPKFGG 66

## RESULT 12

US-09-976-787-29  
Sequence 29, Application US/09976787  
Patent No. US20020064528A1  
GENERAL INFORMATION:  
APPLICANT: Zhu, Zhenping  
APPLICANT: Witte, Larry  
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
FILE REFERENCE: 11245/46505  
CURRENT APPLICATION NUMBER: US/09/976,787  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 09/493,539  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/117,726  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 29  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Mouse  
US-09-976-787-29

Query Match 93.1%; Score 94; DB 9; Length 238;  
Best Local Similarity 94.1%; Pred. No. 6.1e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFGG 17  
|||||  
Db 50 WIDPENGDSGYAPKFGG 66

## RESULT 13

US-09-865-198-28  
Sequence 28, Application US/09865198  
Patent No. US20020103345A1  
GENERAL INFORMATION:  
APPLICANT: Zhu, Zhenping  
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods  
FILE REFERENCE: 11245/47102  
CURRENT APPLICATION NUMBER: US/09/865,198  
CURRENT FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 60/206,749  
PRIOR FILING DATE: 2000-05-24  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 28  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Mouse  
US-09-865-198-28

Query Match 93.1%; Score 94; DB 10; Length 238;  
Best Local Similarity 94.1%; Pred. No. 6.1e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFGG 17  
|||||  
Db 50 WIDPENGDSGYAPKFGG 66

## RESULT 14

US-09-798-689-21  
Sequence 21, Application US/09798689  
Publication No. US20030103973A1  
GENERAL INFORMATION:  
APPLICANT: Rockwell, Patricia  
APPLICANT: Goldstein, Neil I.  
TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
CURRENT APPLICATION NUMBER: US/09/798,689  
CURRENT FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 09/401,163  
PRIOR FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: 08/967,113  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 08/706,804  
PRIOR FILING DATE: 1996-09-03  
PRIOR APPLICATION NUMBER: 08/476,533  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/326,552  
PRIOR FILING DATE: 1994-10-20  
PRIOR APPLICATION NUMBER: 08/196,041  
PRIOR FILING DATE: 1994-02-10  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Mouse  
US-09-798-689-21

Query Match 93.1%; Score 94; DB 11; Length 238;  
Best Local Similarity 94.1%; Pred. No. 6.1e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFGG 17  
|||||  
Db 50 WIDPENGDSGYAPKFGG 66

## RESULT 15

US-10-032-482-18  
Sequence 18, Application US/10032482  
Publication No. US20020197270A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Irwin  
APPLICANT: ROTTER, Varda  
APPLICANT: Wolkowicz, Roland  
APPLICANT: Ruiz, Pedro  
APPLICANT: EREZ-ALON, Neta  
APPLICANT: HERKEL, Johannes  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR  
FILE REFERENCE: COHEN42  
CURRENT APPLICATION NUMBER: US/10/032,482  
CURRENT FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: US/09/445,602  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: PCT/IL98/00266  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: IL 121041  
PRIOR FILING DATE: 1997-06-09

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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 17
; TYPE: prt
; ORGANISM: Mus musculus
US-10-032-482-18

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Query Match	89.1%;	Score 90;	DB 14;	Length 17;
Best Local Similarity	88.2%;	Pred. No. 1.6e-07;		
Matches 15; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0;

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    |||||: |||||
Db 1 WIDPENGDTFYAPKFOG 17
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 5.4784 Seconds  
(without alignments)  
131.295 Million cell updates/sec

Title: US-09-865-198-2  
Perfect score: 101  
Sequence: 1 WIDPENGDSGYAPKFG 17

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	90	89.1	124	1 US-08-017-570-6	Sequence 6, Appli
3	90	89.1	124	1 US-08-471-426-4	Sequence 4, Appli
4	90	89.1	124	1 US-08-471-426-6	Sequence 6, Appli
5	90	89.1	124	4 US-09-672-609-1	Sequence 1, Appli
6	90	89.1	124	4 US-09-672-609-3	Sequence 3, Appli
7	90	89.1	124	4 US-09-672-609-4	Sequence 4, Appli
8	90	89.1	124	4 US-09-672-609-5	Sequence 5, Appli
9	90	89.1	124	4 US-09-672-609-6	Sequence 6, Appli
10	90	89.1	124	4 US-09-672-609-7	Sequence 7, Appli
11	90	89.1	124	4 US-09-672-609-8	Sequence 8, Appli
12	90	89.1	124	4 US-09-672-609-9	Sequence 9, Appli
13	90	89.1	124	4 US-09-672-609-10	Sequence 10, Appli
14	90	89.1	124	4 US-09-672-609-11	Sequence 11, Appli
15	90	89.1	124	4 US-09-672-609-12	Sequence 12, Appli
16	90	89.1	124	4 US-09-025-403A-1	Sequence 1, Appli
17	90	89.1	124	4 US-09-025-403A-3	Sequence 3, Appli
18	90	89.1	124	4 US-09-025-403A-4	Sequence 4, Appli
19	90	89.1	124	4 US-09-025-403A-5	Sequence 5, Appli
20	90	89.1	124	4 US-09-025-403A-6	Sequence 6, Appli
21	90	89.1	124	4 US-09-025-403A-7	Sequence 7, Appli
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24	90	89.1	124	4 US-09-025-403A-10	Sequence 10, Appli
25	90	89.1	124	4 US-09-025-403A-11	Sequence 11, Appli
26	90	89.1	124	4 US-09-025-403A-12	Sequence 12, Appli
27	90	89.1	124	5 PCT-US94-01709-4	Sequence 4, Appli

28	90	89.1	124	5 PCT-US94-01709-6	Sequence 6, Appli
29	90	89.1	270	2 US-08-652-507-2	Sequence 2, Appli
30	90	89.1	535	4 US-08-983-035A-38	Sequence 38, Appli
31	90	89.1	553	2 US-08-661-052-16	Sequence 16, Appli
32	90	89.1	553	3 US-09-188-082-16	Sequence 16, Appli
33	90	89.1	553	4 US-09-364-088-16	Sequence 16, Appli
34	90	89.1	553	4 US-09-102-716-16	Sequence 16, Appli
35	86	85.1	17	3 US-09-171-945-31	Sequence 31, Appli
36	86	85.1	120	3 US-09-171-945-11	Sequence 11, Appli
37	86	85.1	120	3 US-09-171-945-55	Sequence 55, Appli
38	86	85.1	120	3 US-09-171-945-75	Sequence 75, Appli
39	86	85.1	120	3 US-09-171-945-79	Sequence 79, Appli
40	86	85.1	120	3 US-09-171-945-81	Sequence 81, Appli
41	86	85.1	120	3 US-09-171-945-85	Sequence 85, Appli
42	86	85.1	120	3 US-09-171-945-89	Sequence 89, Appli
43	86	85.1	120	3 US-09-171-945-91	Sequence 91, Appli
44	86	85.1	255	3 US-09-171-945-19	Sequence 19, Appli
45	86	85.1	255	3 US-09-171-945-57	Sequence 57, Appli

ALIGNMENTS

RESULT 1  
US-08-017-570-4  
; Sequence 4, Application US/08017570  
; Patent No. 5472693  
; GENERAL INFORMATION:  
; APPLICANT: GOURLIE, BRIAN B  
; APPLICANT: RIXON, MARK W  
; APPLICANT: MEZES, PETER S  
; APPLICANT: KAPLAN, DONALD A  
; APPLICANT: SCHLOM, JEFFREY  
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Duane C. Ulmer  
; STREET: P.O. Box 1967  
; CITY: Midland  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48641-1967  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/017,570  
; FILING DATE: 19930216  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ULMER, DUANE C  
; REGISTRATION NUMBER: 34,941  
; REFERENCE/DOCKET NUMBER: C-38,777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 636-8104  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 124 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-017-570-4

Query Match 89.1%; Score 90; DB 1; length 124;  
Best local Similarity 88.2%; Pred. No. 5.3e-07;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WIDPENGDSGYAPKFG 17  
Db 50 WIDPENGDTETAPKFG 66

## RESULT 2

US-08-017-570-6

; Sequence 6, Application US/08017570  
; Patent No. 5472693

; GENERAL INFORMATION:

; APPLICANT: GOURLIE, BRIAN B

; APPLICANT: RIXON, MARK W

; APPLICANT: MEZES, PETER S

; APPLICANT: KAPLAN, DONALD A

; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Duane C. Ulmer

; STREET: P.O. Box 1967

; CITY: Midland

; STATE: MI

; COUNTRY: US

; ZIP: 48641-1967

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/017,570

; FILING DATE: 19930216

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: ULMER, DUANE C

; REGISTRATION NUMBER: 34,941

; REFERENCE/DOCKET NUMBER: C-38,777

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (517) 636-8104

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 124 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-03-017-570-6

Query Match

Best local Similarity 89.1%; Score 90; DB 1; Length 124;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17

Db 50 WIDPENGDTETAPKFG 66

## RESULT 3

US-08-471-426-4

; Sequence 4, Application US/08471426  
; Patent No. 5808033

; GENERAL INFORMATION:

; APPLICANT: GOURLIE, BRIAN B

; APPLICANT: RIXON, MARK W

; APPLICANT: MEZES, PETER S

; APPLICANT: KAPLAN, DONALD A

; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Duane C. Ulmer

; STREET: P.O. Box 1967

; CITY: Midland

; STATE: MI

; COUNTRY: US

ZIP: 48641-1967

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,426

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/017,570

; FILING DATE: 16-FEB-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: ULMER, DUANE C

; REGISTRATION NUMBER: 34,941

; REFERENCE/DOCKET NUMBER: C-38,777

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (517) 636-8104

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 124 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-471-426-4

Query Match

Best local Similarity 89.1%; Score 90; DB 1; Length 124;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17

Db 50 WIDPENGDTETAPKFG 66

## RESULT 4

US-08-471-426-6

; Sequence 6, Application US/08471426  
; Patent No. 5808033

; GENERAL INFORMATION:

; APPLICANT: GOURLIE, BRIAN B

; APPLICANT: RIXON, MARK W

; APPLICANT: MEZES, PETER S

; APPLICANT: KAPLAN, DONALD A

; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Duane C. Ulmer

; STREET: P.O. Box 1967

; CITY: Midland

; STATE: MI

; COUNTRY: US

; ZIP: 48641-1967

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,426

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/017,570

; FILING DATE: 16-FEB-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: ULMER, DUANE C

; REGISTRATION NUMBER: 34,941

; REFERENCE/DOCKET NUMBER: C-38,777

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 124 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-471-426-6

Query Match 89.1%; Score 90; DB 1; Length 124;  
Best Local Similarity 88.2%; Pred. No. 5.3e-07;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17  
Db 50 WIDPENGDTYAPKFG 66

## RESULT 5

US-09-672-609-1  
; Sequence 1, Application US/09672609  
; Patent No. 6333405

## ; GENERAL INFORMATION:

; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.  
; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft word 97 SR-2  
; SEQ ID NO 1  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: Murine Col-1 VH  
; LOCATION: 1..124  
US-09-672-609-1

Query Match 89.1%; Score 90; DB 4; Length 124;  
Best Local Similarity 88.2%; Pred. No. 5.3e-07;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17  
Db 50 WIDPENGDTYAPKFG 66

## RESULT 6

US-09-672-609-3  
; Sequence 3, Application US/09672609  
; Patent No. 6333405

## ; GENERAL INFORMATION:

; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.  
; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft word 97 SR-2  
; SEQ ID NO 3

LENGTH: 124

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: Humanized COL-1 VH, HuVH

; LOCATION: 1..124

; OTHER INFORMATION: Humanized heavy chain variable region containing human  
; OTHER INFORMATION: NEMV VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,  
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98  
US-09-672-609-3

Query Match 89.1%; Score 90; DB 4; Length 124;  
Best Local Similarity 88.2%; Pred. No. 5.3e-07;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17  
Db 50 WIDPENGDTYAPKFG 66

## RESULT 7

US-09-672-609-4  
; Sequence 4, Application US/09672609  
; Patent No. 6333405

## ; GENERAL INFORMATION:

; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.  
; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft word 97 SR-2  
; SEQ ID NO 4  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Humanized COL-1 VH, HuVH  
; LOCATION: 1..124  
; OTHER INFORMATION: Humanized heavy chain variable region containing human  
; OTHER INFORMATION: NEMV VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,  
; OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98  
US-09-672-609-4

Query Match 89.1%; Score 90; DB 4; Length 124;  
Best Local Similarity 88.2%; Pred. No. 5.3e-07;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGDSGYAPKFG 17  
Db 50 WIDPENGDTYAPKFG 66

## RESULT 8

US-09-672-609-5  
; Sequence 5, Application US/09672609  
; Patent No. 6333405

## ; GENERAL INFORMATION:

; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.  
; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28

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; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 5
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHAT
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
US-09-672-609-5

Query Match      89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 WIDPENGDSGYAPKFG 17
Db      50 WIDPENGDTETAPKFG 66

RESULT 9
US-09-672-609-6
; Sequence 6, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Phillip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 6
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHAA
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Ala-79, Asn-97, and Thr-98
US-09-672-609-6

Query Match      89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 WIDPENGDSGYAPKFG 17
Db      50 WIDPENGDTETAPKFG 66

RESULT 10
US-09-672-609-7
; Sequence 7, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Phillip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
```

```
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 7
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Tyr-80, Asn-97, and Thr-98
US-09-672-609-7

Query Match      89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 WIDPENGDSGYAPKFG 17
Db      50 WIDPENGDTETAPKFG 66

RESULT 11
US-09-672-609-8
; Sequence 8, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Phillip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 8
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHATAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98
US-09-672-609-8

Query Match      89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 WIDPENGDSGYAPKFG 17
Db      50 WIDPENGDTETAPKFG 66

RESULT 12
US-09-672-609-9
; Sequence 9, Application US/09672609
; Patent No. 6333405
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 9
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHASTAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, Tyr-80, Asn-97, and
; OTHER INFORMATION: Thr-98
US-09-672-609-9
```

```
Query Match      89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WIDPENGDSGYAPKFOG 17
      |||||:|||||
Db      50 WIDPENGDTETAPKFOG 66
```

```
RESULT 13
US-09-672-609-10
; Sequence 10, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 10
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHT
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Thr-72, Asn-97, and Thr-98
US-09-672-609-10
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```
Query Match      89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 WIDPENGDSGYAPKFOG 17
      |||||:|||||
Db      50 WIDPENGDTETAPKFOG 66
```

```
RESULT 14
US-09-672-609-11
; Sequence 11, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 11
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHS
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region containing human
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
; OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Asn-97, and Thr-98
US-09-672-609-11
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```
Query Match      89.1%; Score 90; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 5.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 WIDPENGDSGYAPKFOG 17
      |||||:|||||
Db      50 WIDPENGDTETAPKFOG 66
```

```
RESULT 15
US-09-672-609-12
; Sequence 12, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 12
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Humanized COL-1 VH, HUVHSTAY
; LOCATION: 1..124
; OTHER INFORMATION: Humanized heavy chain variable region expressed from ATCC
; OTHER INFORMATION: CRL-12208, and containing human NEMM VH FRs, murine COL-1 VH CDRs
; OTHER INFORMATION: and Phe-27, Asn-28, Ile-29, Lys-30, Ser-76, Thr-78, Ala-79,
; OTHER INFORMATION: Tyr-80, Asn-97, and Thr-98
US-09-672-609-12
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```
Query Match      89.1%; Score 90; DB 4; Length 124;
```

Best Local Similarity 88.2%; Pred. No. 5.3e-07;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 WIDPENGDSGYAPKFOG 17  
|||:|||||  
Db 50 WIDPENGDTFYAPKFOG 66

Search completed: July 30, 2003, 09:38:27  
Job time : 5.4784 secs



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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 2.36545 Seconds  
(without alignments)  
325.245 Million cell updates/sec

Title: US-09-865-198-3  
Perfect score: 51  
Sequence: 1 YYGDYEGY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	41	80.4	435	2 D81272	hypothetical prote
2	40	78.4	542	2 S63222	MPA43 protein - ye
3	40	78.4	616	1 SYTMMT	methionine-tRNA li
4	40	78.4	1650	2 T18444	hypothetical prote
5	39	76.5	63	2 S44634	f22b7.4 protein -
6	38	74.5	595	2 B70402	hypothetical prote
7	38	74.5	660	2 E83656	methionyl-tRNA syn
8	38	74.5	3216	2 C90538	hypothetical prote
9	37	72.5	89	2 T19805	hypothetical prote
10	37	72.5	110	2 S13688	Ig heavy chain V r
11	37	72.5	154	1 A69012	conserved hypotet
12	37	72.5	271	2 S38115	hypothetical prote
13	37	72.5	542	2 B81910	probable ABC-trans
14	37	72.5	542	2 E81105	ABC transporter, A
15	37	72.5	564	2 T26053	hypothetical prote
16	37	72.5	633	2 T02673	heterogeneous nucl
17	37	72.5	730	2 A48832	cell surface glyco
18	37	72.5	1657	2 T19536	hypothetical prote
19	36	70.6	15	2 PH1366	Ig heavy chain DJ
20	36	70.6	120	2 A54256	Ig heavy chain V r
21	36	70.6	191	2 AE1218	alpha-ribazole-5'-
22	36	70.6	191	2 AH1571	alpha-ribazole-5'-
23	36	70.6	252	2 A95071	amino acid ABC tra
24	36	70.6	441	2 T49265	hypothetical prote
25	36	70.6	565	2 G90518	5'-nucleotidase pr
26	36	70.6	587	2 F69631	gamma-glutamyltran
27	36	70.6	656	2 T03473	acetate-CoA ligase
28	36	70.6	669	2 D72278	endo-1,4-beta-mann
29	36	70.6	831	2 AB3513	ATPase virB4 homol

30	36	70.6	851	2 T51545	receptor protein k
31	36	70.6	868	2 A84518	probable receptor-
32	36	70.6	914	1 JN0550	iodide peroxidase
33	36	70.6	914	1 S07047	iodide peroxidase
34	36	70.6	933	1 OPHUIT	iodide peroxidase
35	35	68.6	113	2 G82387	hypothetical prote
36	35	68.6	126	2 S16280	Ig heavy chain (38
37	35	68.6	145	2 S03844	dtDP-sugar epimera
38	35	68.6	186	2 AB1210	hypothetical prote
39	35	68.6	188	2 H91066	unknown protein en
40	35	68.6	201	2 H85910	hypothetical prote
41	35	68.6	376	2 S69529	ubiquinol-cytochro
42	35	68.6	386	2 T14243	probable transamin
43	35	68.6	398	2 A75128	probable transamin
44	35	68.6	401	2 D71003	homeotic protein 1
45	35	68.6	402	1 I61573	

ALIGNMENTS

RESULT 1

D81272  
hypothetical protein Cj1295 [imported] - Campylobacter jejuni (strain NCTC 11168)  
C/Species: Campylobacter jejuni  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
C/Accession: D81272  
R/Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell  
Nature 403, 665-668, 2000  
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hye  
A/Reference number: A81250; WUID:20150912; PMID:10688204  
A/Accession: D81272  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-435 <PAR>  
A/Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73722.1; PID:g696872  
A/Experimental source: serotype O2, strain NCTC 11168  
C/Genetics:  
A/Gene: Cj1295  
C/Superfamily: Campylobacter jejuni hypothetical protein Cj1295

Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps
80.4%;	85.7%;	6;	41;	2;	435;	0;	0;
Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	2	YGDYEGY 8					
Db	325	YGDYDGY 331					

RESULT 2

S63222  
MPA43 protein - yeast (Saccharomyces cerevisiae)  
N/Alternate names: protein N0875; protein YNL249c  
C/Species: Saccharomyces cerevisiae  
C/Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 06-Feb-1998  
C/Accession: S63222; S61594  
R/Sen-Gupta, M.; Gueldenier, U.; Beinbauer, J.; Fiedler, T.; Hegemann, J.H.  
submitted to the Protein Sequence Database, April 1996  
A/Reference number: S63220  
A/Accession: S63222  
A/Molecule type: DNA  
A/Residues: 1-542 <SEN>  
A/Cross-references: EMBL:Z71525; NID:g1302290; PID:e239640; PID:g1302291; MIPS:YNL249c  
A/Experimental source: strain S288C  
R/Boles, E.; Hettmann, C.; Zimmermann, F.K.  
submitted to the EMBL Data Library, December 1995  
A/Reference number: S61594  
A/Accession: S61594  
A/Molecule type: DNA  
A/Residues: 'YGD', 45, 'SR', 48, 'HGNTLA', 54-542 <BOU>  
A/Cross-references: EMBL:X94214; NID:g1122898; PID:e214032; PID:g1122899

C:Genetics:  
A:Gene: SGD:MPA43  
A:Cross-references: SGD:S0005193; MIPS:YNL249C  
A:Map position: 14L

Query Match 78.4%; Score 40; DB 2; Length 542;  
Best Local Similarity 85.7%; Pred. No. 25;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YYGDYEG 7  
:|||||  
Db 360 FYGDYEG 366

## RESULT 3

SYTMMT

methionine-tRNA ligase (EC 6.1.1.10) - *Thermus aquaticus*

N:Alternate names: methionyl-tRNA synthetase

C:Species: *Thermus aquaticus*

C&gt;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Dec-2002

C:Accession: A39517

R:Mureki, O.; Muramatsu, T.; Suzuki, K.; Kohda, D.; Matsuzawa, H.; Ohta, T.; Miyazawa, T.

J. Biol. Chem. 266, 3268-3277, 1991

A:Title: Methionyl-tRNA synthetase gene from an extreme thermophile, *Thermus thermophilus*.

A:Reference number: A39517; MUID:91131636; PMID:1993699

A:Accession: A39517

A:Molecule type: DNA

A:Residues: 1-616 &lt;NUR&gt;

A:Cross-references: GB:M64273; GB:J05744; NID:g155135; PIDN:AAA27510.1; PID:g155136

A:Experimental source: strain HB8, ATCC 27634

A&gt;Note: the authors translated the codon TAC for residue 323 as Thr

C:Genetics:

A:Gene: mets

C:Superfamily: methionyl-tRNA synthetase, dimer-forming

C:Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis

F:13,19,50,300/Active site: Tyr, His, Asp, Lys #status predicted

Query Match 78.4%; Score 40; DB 1; Length 616;  
Best Local Similarity 85.7%; Pred. No. 29;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YYGDYEG 7  
|||||  
Db 118 YGGEYEG 124

## RESULT 4

T18444

hypothetical protein C0385c - malaria parasite (*Plasmodium falciparum*)C:Species: *Plasmodium falciparum*

C&gt;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jun-2000

C:Accession: T18444

R:Lawson, D.; Bowman, S.; Barrell, B.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z18935

A:Accession: T18444

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1650 &lt;LAM&gt;

A:Cross-references: EMBL:Z98547; NID:e1325376; PID:e1427940; PIDN:CAB11112.2

C:Genetics:

A:Map position: 3

A:Introns: 1597/3; 1625/3

A&gt;Note: C0385c

Query Match 78.4%; Score 40; DB 2; Length 1650;  
Best Local Similarity 75.0%; Pred. No. 78;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YYGDYEG 8  
|||||  
Db 525 YFDDYEGY 532

## RESULT 5

S44634

f22b7.4 protein - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C&gt;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Sep-1997

C:Accession: S44634

R:Anderson, K.

submitted to the EMBL Data Library, March 1993

A:Description: Sequence of the C. elegans cosmid F22B7.

A:Reference number: S44628

A:Accession: S44634

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-63 &lt;AND&gt;

A:Cross-references: EMBL:L12018; NID:g156298; PID:g156305

C:Genetics:

A:Introns: 21/2

Query Match 76.5%; Score 39; DB 2; Length 63;  
Best Local Similarity 75.0%; Pred. No. 4.3;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YYGDYEGY 8  
|||||  
Db 56 YGGYNGY 63

## RESULT 6

B70402

hypothetical protein aq\_1185 - *Aquifex aeolicus*C:Species: *Aquifex aeolicus*

C&gt;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 04-Mar-2000

C:Accession: B70402

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: B70402

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-595 &lt;AQF&gt;

A:Cross-references: GB:AE000727; NID:g2983623; PIDN:AAC07204.1; PID:g2983636; GB:AE00065

A:Experimental source: strain VF5

C:Genetics:

A:Gene: aq\_1185

C:Superfamily: *Aquifex aeolicus* hypothetical protein aq\_1185

Query Match 74.5%; Score 38; DB 2; Length 595;  
Best Local Similarity 85.7%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 YGDYEGY 8  
|||||  
Db 159 YGDYTGX 165

## RESULT 7

E83656

methionyl-tRNA synthetase mets [imported] - *Bacillus halodurans* (strain C-125)C:Species: *Bacillus halodurans*

C&gt;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 23-Dec-2002

C:Accession: E83656

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: E83656

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-660 &lt;STO&gt;

A;Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03772.1; GSPDB:GN001538  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: mets  
C;Superfamily: methionyl-tRNA synthetase, dimer-forming

Query Match 74.5%; Score 38; DB 2; Length 660;  
Best Local Similarity 75.0%; Pred. No. 69;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||  
Db 121 YLGDYEGW 128

RESULT 8  
C90538  
hypothetical protein MYPV\_2110 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C;Species: Mycoplasma pulmonis  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001  
C;Accession: C90538  
R;Chambaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;  
Nucleic Acids Res. 29, 2145-2153, 2001  
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm  
A;Reference number: A99512; MUID:21267165; PMID:11353084  
A;Accession: C90538  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-3216 <KUR>

A;Cross-references: GB:AL445566; PID:g14089624; PIDN:CAC13384.1; GSPDB:GN00153  
A;Experimental source: strain UAB CTIP  
C;Genetics:  
A;Gene: MYPV\_2110  
A;Genetic code: SGC3

Query Match 74.5%; Score 38; DB 2; Length 3216;  
Best Local Similarity 75.0%; Pred. No. 3.4e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||  
Db 1978 YYVDYEGF 1985

RESULT 9  
T19805

hypothetical protein C37A5.8 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T19805

R;White, S.

submitted to the EMBL Data Library, March 1997

A;Reference number: Z19180

A;Accession: T19805

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-89 <WIL>

A;Cross-references: EMBL:Z92828; PIDN:CAB07335.1; GSPDB:GN00019; CESP:C37A5.8

A;Experimental source: clone C37A5

C;Genetics:

A;Gene: CESP:C37A5.8

A;Map position: 1

A;Introns: 52/2

Query Match 72.5%; Score 37; DB 2; Length 89;  
Best Local Similarity 75.0%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||  
Db 61 YYGGYGGY 68

RESULT 10  
S13688

Ig heavy chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 30-May-1997

C;Accession: S13688

R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

Eur. J. Immunol. 19, 1289-1295, 1989

A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl

A;Reference number: S13685; MUID:89338557; PMID:2503389

A;Accession: S13688

A;Molecule type: mRNA

A;Residues: 1-110 <PEN>

A;Cross-references: EMBL:X53341

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;10-93/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 110;  
Best Local Similarity 70.0%; Pred. No. 17;  
Matches 7; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 YY--GDYEGY 8  
|||  
Db 89 YYCXGDYDGY 98

RESULT 11  
A69012

conserved hypothetical protein MTH1091 - Methanobacterium thermoautotrophicum (strain De

C;Species: Methanobacterium thermoautotrophicum

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 14-Apr-2003

C;Accession: A69012

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: A69012

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-154 <MTH>

A;Cross-references: GB:AE000879; GB:AE000666; NID:g2622175; PIDN:AAB85580.1; PID:g262219

A;Experimental source: strain Delta H

C;Genetics:

A;Gene: MTH1091

A;Start codon: GTG

C;Superfamily: uncharacterized conserved protein

Query Match 72.5%; Score 37; DB 1; Length 154;  
Best Local Similarity 71.4%; Pred. No. 24;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEG 7  
:|  
Db 81 FYGDYDG 87

RESULT 12  
S38115

hypothetical protein YKR043c - yeast (Saccharomyces cerevisiae)

C;Species: Saccharomyces cerevisiae

C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 19-Apr-2002

C;Accession: S38115

R;Urrestarazu, L.A.; Jauniaux, J.C.

submitted to the Protein Sequence Database, March 1994

A;Reference number: S38097

A;Accession: S38115

A;Molecule type: DNA

A;Residues: 1-271 <URR>

A;Cross-references: EMBL:Z28268; NID:g486490; PID:g486491; GSPDB:GN00011; MIPS:YKR043C

A;Experimental source: strain S288C

C:Genetics:  
A:Gene: MIPS:YKR043c  
A:Cross-references: SGD:S0001751  
A:Map position: 11R  
C:Superfamily: phosphoglycerate mutase; phosphoglycerate mutase homology

Query Match 72.5%; Score 37; DB 2; Length 271;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 YGDYEG 7  
Db 102 YGDYEG 107

RESULT 13  
B81910  
probable ABC-transporter ATP-binding protein NMA1409 [imported] - Neisseria meningitidis  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: B81910  
R:Parthill, J.; Achtmann, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: B81910  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-542 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84649.1; PID:g738006  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1409  
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 72.5%; Score 37; DB 2; Length 542;  
Best Local Similarity 75.0%; Pred. No. 85;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YGDYEG 8  
Db 528 YLGDYEST 535

RESULT 14  
E81105  
ABC transporter, ATP-binding protein NMB1240 [imported] - Neisseria meningitidis (strain  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: E81105  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizze, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: E81105  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-542 <TET>  
A:Cross-references: GB:AE002472; GB:AE002098; NID:g7226475; PIDN:AAF41621.1; PID:g722648  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB1240  
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 72.5%; Score 37; DB 2; Length 542;  
Best Local Similarity 75.0%; Pred. No. 85;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YGDYEG 8

Db 528 YLGDYEST 535

RESULT 15  
T26053  
hypothetical protein W01C9.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T26053  
R:Sims, M.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: Z20143  
A:Accession: T26053  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-564 <WIL>  
A:Cross-references: EMBL:Z49969; PIDN:CAA90270.1; GSPDB:GN00020; CESP:W01C9.2  
A:Experimental source: clone W01C9  
C:Genetics:  
A:Gene: CESP:W01C9.2  
A:Map position: 2  
A:Introns: 30/1; 64/1; 100/3; 124/3; 229/3; 272/3; 536/2

Query Match 72.5%; Score 37; DB 2; Length 564;  
Best Local Similarity 85.7%; Pred. No. 88;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 YGDYEG 8  
Db 67 YGDYEDY 73

Search completed: July 30, 2003, 09:44:07  
Job time : 6.36545 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:35 ; Search time 1.24917 Seconds  
(without alignments)  
301.171 Million cell updates/sec

Title:	US-09-865-198-3
Perfect score:	51
Sequence:	1 YYGDYEGY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database : Swi88Prot\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	41	80.4	402	1	LHX5_HUMAN	Q9h2c1 homo sapien
2	41	80.4	402	1	LHX5_XENLA	P37137 xenopus lae
3	40	78.4	542	1	MP43_YEAST	P53583 saccharomyc
4	40	78.4	616	1	SYM_THETH	P23395 thermus the
5	39	76.5	63	1	YLM4_CAEEL	P34407 caenorhabdi
6	39	76.5	489	1	OCLN_POTTR	Q28793 potorous tr
7	38	74.5	660	1	SYM_BACHD	Q9kgk8 bacillus ha
8	37	72.5	271	1	YK23_YEAST	P36136 saccharomyc
9	37	72.5	394	1	ASSY_METAC	Q8tny5 methanosarc
10	37	72.5	399	1	LHX5_BRARE	P52889 brachydanic
11	37	72.5	446	1	SOX8_HUMAN	P57073 homo sapien
12	37	72.5	633	1	ROR_HUMAN	Q43390 homo sapien
13	37	72.5	730	1	G13A_DICDI	P34115 dictyostelli
14	36	70.6	587	1	GGT_BACSU	P54422 bacillus su
15	36	70.6	656	1	ACSA_RHOCA	O68040 rhodobacteri
16	36	70.6	914	1	PERT_MOUSE	P35419 mus musculu
17	36	70.6	914	1	PERT_RAT	P14650 rattus norv
18	36	70.6	933	1	PERT_HUMAN	P07202 homo sapien
19	35	68.6	321	1	KEPF_PASMU	Q9cpb2 pasteurella
20	35	68.6	376	1	YO23_BPPI	P51725 bacteriophag
21	35	68.6	386	1	CYB_TRIRU	Q92240 trichophytc
22	35	68.6	402	1	LHX5_MOUSE	P50459 mus musculu
23	35	68.6	405	1	LHX1_BRARE	Q90476 brachydanic
24	35	68.6	420	1	ANRX_HUMAN	Q9nxt5 homo sapien
25	35	68.6	428	1	RF4_KTULA	P09806 kluyveromyc
26	35	68.6	464	1	XKDK_BACSU	P54331 bacillus su
27	35	68.6	685	1	ERF2_YEAST	P05453 saccharomyc
28	35	68.6	919	1	AMY_STRLI	Q05884 streptomyc
29	35	68.6	1532	1	IGA_NEIGO	P09790 neisseria g
30	35	68.6	2358	1	MOKD_SCHPO	Q9y719 schizosacch
31	34	66.7	314	1	YG20_YEAST	P53257 saccharomyc
32	34	66.7	335	1	HTPX_ARCFU	Q30004 archaeoglob
33	34	66.7	344	1	ARGC_THETN	Q8r7b8 thermocanaer

34	34	66.7	497	1	SYM_AQUAE	O67298	aquifex aeo
35	34	66.7	649	1	SYM_BACST	P23920	bacillus st
36	34	66.7	657	1	SYM_STAM	Q99wb3	staphylococ
37	34	66.7	657	1	SYM_STAM	Q8ny00	staphylococ
38	34	66.7	664	1	SYM_LISIN	Q92f90	listeria in
39	34	66.7	664	1	SYM_LISMO	Q8yaf2	listeria mo
40	34	66.7	784	1	SK15_DROME	P40657	drosophila
41	34	66.7	972	1	UVRA_MYCTU	P94972	mycobacteri
42	34	66.7	3511	1	MY15_MOUSE	Q9qz24	mus musculuu
43	33.5	65.7	101	1	GP33_BPSP1	P06226	bacterioph
44	33.5	65.7	1224	1	ABLI_CAEEL	P03949	caenorhabditi
45	33	64.7	201	1	PDX_ARATH	Q9m7c0	arabidopsis

## ALIGNMENTS

```

RESULT 1
LHX5_HUMAN
ID_LHX5_HUMAN STANDARD; PRT; 402 AA.
AC Q9H2C1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx5.
GN LHX5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RX PubMed=11137295;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao Y., Hermesz E., Yarolin M.C., Westphal H.;
RT "Genomic structure, chromosomal localization and expression of the
RL human LIM-homeobox gene LHX5.";
CC Gene 260:95-101(2000).
CC -| FUNCTION: Plays an essential role in the regulation of neuronal
CC differentiation and migration during development of the central
CC nervous system.
CC -| SUBCELLULAR LOCATION: Nuclear (Probable).
CC -| TISSUE SPECIFICITY: Expressed in fetal brain and in various
CC regions of the adult central nervous system including the spinal
CC cord, the thalamus, and the cerebellum.
CC -| SIMILARITY: Contains 1 homeobox domain.
CC -| SIMILARITY: Contains 2 LIM zinc-binding domains.
CC -----
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CC -----
DR EMBL; AF291181; AAC36963.1; -.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T04180; -.
DR Genew; HGNC:14216; LHX5.
DR MIM; 605992; -.
DR GO; GO:0005634; C:nucleus; ISS.
DR GO; GO:0007417; P:central nervous system development; ISS.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM_homeo.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.

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DR PROSITE; PS00478; LIM\_DOMAIN\_1; 2.  
DR PROSITE; PS50023; LIM\_DOMAIN\_2; 2.  
KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;  
KM Metal-binding; Zinc; Transcription regulation.  
FT DOMAIN 3 61 LIM 1.  
FT DOMAIN 62 125 LIM 2.  
FT DNA\_BIND 180 239 HOMEBOX.  
SQ SEQUENCE 402 AA; 44405 MW; E880138A1A3FCA2A CRC64;  
  
Query Match 80.4%; Score 41; DB 1; Length 402;  
Best Local Similarity 85.7%; Pred. No. 8.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 YYGDYEG 7  
DB 278 YYGDYQG 284  
  
RESULT 2  
LHX5\_XENLA STANDARD; PRT; 402 AA.  
ID LHX5\_XENLA  
AC P37137;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE LIM/homeobox protein Lhx5 (Homeobox protein LIM-5) (XLIM-5) (XLIM-2A).  
GN LHX5 OR LIM5 OR LIM2A OR LIM-2A.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95377545; PubMed=7649385;  
RA Toyama R., Curtiss P.E., Otani H., Kimura M., David I.B., Taira M.;  
RT "The LIM class homeobox gene lim5: implied role in CNS patterning in  
RL Xenopus and zebrafish.";  
RN Dev. Biol. 170:583-593(1995).  
RN [2]  
RP SEQUENCE OF 188-225 FROM N.A.  
RX MEDLINE=92192449; PubMed=1347750;  
RA Taira M., Jamrich M., Good P.J., David I.B.;  
RT "The LIM domain-containing homeo box gene Xlim-1 is expressed  
RL specifically in the organizer region of Xenopus gastrula embryos.";  
RN Genes Dev. 6:356-366(1992).  
CC -!- FUNCTION: PROBABLY INVOLVED IN THE PATTERNING OF THE NERVOUS  
CC SYSTEM, IN PARTICULAR IN THE EARLY SPECIFICATION OF THE  
CC DIENCEPHALON.  
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).  
CC -!- SIMILARITY: Contains 1 homeobox domain.  
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.  
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CC -----  
DR EMBL; L42546; AAA99464.1; -;  
DR EMBL; Z11587; CAA77672.1; -;  
DR HSSP; P06601; 1FJL.  
DR TRANSFAC; T04209; -;  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR001781; LIM.  
DR InterPro; IPR007107; LIM\_homeo.  
DR Pfam; PF00046; homeobox\_1.  
DR Pfam; PF00412; LIM; 2.  
DR ProDom; PD000010; Homeobox; 1.  
DR ProDom; PD000094; LIM; 2.  
DR SMART; SM00389; HOX; 1.

DR SMART; SM00132; LIM; 2.  
DR PROSITE; PS00478; LIM\_DOMAIN\_1; 2.  
DR PROSITE; PS50023; LIM\_DOMAIN\_2; 2.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS50071; HOMEBOX\_2; 1.  
KW Homeobox; DNA-binding; Nuclear protein; Developmental protein;  
KM Repeat; LIM domain; Metal-binding; Zinc; Transcription regulation.  
FT DOMAIN 3 61 LIM 1.  
FT DOMAIN 62 125 LIM 2.  
FT DNA\_BIND 180 239 HOMEBOX.  
SQ SEQUENCE 402 AA; 44959 MW; A5852B94747E09F9 CRC64;  
  
Query Match 80.4%; Score 41; DB 1; Length 402;  
Best Local Similarity 85.7%; Pred. No. 8.4;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 YYGDYEG 7  
DB 278 YYGDYQG 284  
  
RESULT 3  
MP43\_YEAST STANDARD; PRT; 542 AA.  
ID MP43\_YEAST  
AC P53583;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE MPA43 protein.  
GN MPA43 OR YNL249C OR N0875.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C / FY1679;  
RX MEDLINE=97377992; PubMed=9234673;  
RA Sen-Gupta M., Gueldeher U., Beinhauer J.D., Fiedler T.A.,  
RA Hegemann J.H.;  
RT "Sequence analysis of the 33 kb long region between ORC5 and SUR1  
RT from the left arm of chromosome XIV from Saccharomyces cerevisiae.";  
RL Yeast 13:849-860(1997).  
RN [2]  
RP SEQUENCE OF 41-542 FROM N.A.  
RC STRAIN=ENT.WA-1A;  
RA Boles E., Hettmann C., Zimmermann F.K.;  
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
CC -----  
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CC -----  
DR EMBL; X96722; CAA65495.1; -;  
DR EMBL; Z71525; CAA96156.1; -;  
DR EMBL; X94214; CAA63905.1; -;  
DR PIR; S63222; S63222.  
DR SGD; S0005193; MPA43.  
DR CONFLICT 46 53 KSKWKFQW -> RSHGNLA (IN REF. 2).  
FT SEQUENCE 542 AA; 61667 MW; 830AA8D4E95365AD CRC64;  
SQ SEQUENCE 542 AA; 61667 MW; 830AA8D4E95365AD CRC64;

Query Match 78.4%; Score 40; DB 1; Length 542;  
Best Local Similarity 85.7%; Pred. No. 16;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 YYGDYEG 7  
DB 360 FYGDYEG 366



RESULT 4  
SYM\_THETH  
ID SYM THETH STANDARD; PRT; 616 AA.  
AC P23395;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)  
DE (METS).  
GN METG OR METS.  
OS Thermus thermophilus.  
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
OC Thermus.  
OX NCBI\_TaxID=274;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HB8 / ATCC 27634;  
RX MEDLINE=91131636; PubMed=1993699;  
RA Nureki O., Muramatsu T., Suzuki K., Kohda D., Matsuzawa H.,  
RA Ohta T., Miyazawa T., Yokoyama S.;  
RT "Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus  
RT thermophilus HB8. Molecular cloning, primary-structure analysis,  
RT expression in Escherichia coli, and site-directed mutagenesis.";  
RL J. Biol. Chem. 266:3268-3277(1991).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RC STRAIN=HB8 / ATCC 27634;  
RX MEDLINE=20139706; PubMed=10673435;  
RA Sugitara I., Nureki O., Uga-Ji-Yoshikawa Y., Kuwabara S., Shimada A.,  
RA Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;  
RT "The 2.0-A crystal structure of Thermus thermophilus methionyl-tRNA  
RT synthetase reveals two RNA-binding modules."  
RL Structure 8:197-208(2000).  
CC -1- FUNCTION: Is required not only for elongation of protein synthesis  
CC but also for the initiation of all mRNA translation through  
CC initiator tRNA(fMet) aminoacylation.  
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +  
CC -1- cofactor: Binds 1 zinc ion per subunit.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.  
CC MetG subfamily 2A.  
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.  
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CC -----  
DR EMBL; M64273; AAA27510.1; -.  
DR PDB; 1A8H; 04-MAY-99.  
DR HAMAP; MF\_01228; fused; 1.  
DR InterPro; IPR004495; MetG\_Cterm.  
DR InterPro; IPR002300; tRNA-synt\_1a.  
DR InterPro; IPR001412; tRNA-synt\_1.  
DR InterPro; IPR002304; tRNA-synt\_met.  
DR InterPro; IPR002547; tRNA\_bind.  
DR Pfam; PF00133; tRNA-synt\_1; 1.  
DR Pfam; PF01588; tRNA\_bind; 1.  
DR PIRSF; PIRSF001528; Mets dimerising; 1.  
DR PRINTS; PRO1041; TRNASYNTHMET.  
DR TIGRFAMs; TIGR00398; metG; 1.  
DR TIGRFAMs; TIGR00399; metG\_Cterm; 1.  
DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_I; FALSE\_NEG.  
DR PROSITE; PS50886; TRBD; 1.  
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
KW RNA-binding; tRNA-binding; Metal-binding; Zinc; 3D-structure.  
FT SITE 12 22 "HIGH" REGION.  
FT

FT SITE 297 301 "KMSKS" REGION.  
FT DOMAIN 518 616 TRNA-BINDING.  
FT METAL 127 127 ZINC.  
FT METAL 130 130 ZINC.  
FT METAL 144 144 ZINC.  
FT METAL 147 147 ZINC.  
FT BINDING 300 300 ATP (BY SIMILARITY).  
FT STRAND 4 13  
FT TURN 14 15  
FT HELIX 20 38  
FT TURN 39 40  
FT STRAND 42 50  
FT HELIX 54 62  
FT TURN 63 64  
FT HELIX 67 74  
FT TURN 75 75  
FT HELIX 76 84  
FT TURN 85 86  
FT STRAND 91 94  
FT TURN 95 96  
FT HELIX 98 113  
FT TURN 114 115  
FT STRAND 117 127  
FT TURN 128 131  
FT STRAND 132 134  
FT TURN 136 138  
FT STRAND 140 140  
FT TURN 141 142  
FT STRAND 143 143  
FT TURN 145 148  
FT STRAND 150 150  
FT STRAND 152 161  
FT HELIX 164 166  
FT HELIX 167 176  
FT TURN 178 179  
FT STRAND 181 181  
FT HELIX 184 193  
FT TURN 194 195  
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FT STRAND 204 206  
FT TURN 207 209  
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FT HELIX 227 230  
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FT HELIX 308 315  
FT HELIX 317 327  
FT TURN 330 331  
FT STRAND 334 335  
FT HELIX 338 367  
FT TURN 369 371  
FT STRAND 371 371  
FT STRAND 379 386  
FT HELIX 387 396  
FT TURN 397 398  
FT HELIX 400 421  
FT HELIX 423 429  
FT HELIX 431 452

FT TURN 453 455  
FT HELIX 457 466  
FT TURN 467 468  
FT HELIX 475 479  
FT STRAND 488 488  
SQ SEQUENCE 616 AA; 70638 MM; 053982C62558B72A CRC64;

Query Match 78.4%; Score 40; DB 1; Length 616;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYG DYEG 7  
Db 118 YG DYEG 124

RESULT 5  
YLM4\_CAEEL STANDARD; PRT; 63 AA.  
ID YLM4\_CAEEL  
AC P34407;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein F22B7.4 in chromosome III.  
GN F22B7.4.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Chordata; Rhabdita; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_Taxid=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=94150718; PubMed=7906398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
RA Parsons J., Perry C., Rifkin L., Roopra A., Saunders D., Showkhan R.,  
RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer B., Staden R.,  
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
RA Wohldman P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans."  
RL Nature 368:32-38(1994).

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CC EMBL; L12018; AAA65461.1; -.  
DR PIR; S44634; S44634.  
DR WormPep; F22B7.4; CE00157.  
KM Hypothetical protein.  
SQ SEQUENCE 63 AA; 6803 MM; 2F7579C4907024B0 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 63;  
Best Local Similarity 75.0%; Pred. No. 3.1;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YYG DYEG 8  
Db 56 YG DYNGY 63

RESULT 6  
OCLN\_POTTR

ID OCLN\_POTTR STANDARD; PRT; 489 AA.  
AC Q28793;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Occludin.  
GN OCLN.  
OS Potorous tridactylus (Potoroo).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Diprotodontia; Potoroidae; Potorous.  
OX NCBI\_Taxid=9310;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=96181088; PubMed=8601611;  
RA Ando-Akatsuka Y., Saitou M., Hirase T., Kishi M., Sakakibara A.,  
RA Itoh M., Yonemura S., Furuse M., Tsukita S.,  
RT "Interspecies diversity of the occludin sequence: cDNA cloning of  
RT human, mouse, dog, and rat-kangaroo homologues.";  
RL J. Cell Biol. 133:43-47(1996).

CC -1- FUNCTION: MAY PLAY A ROLE IN THE FORMATION AND REGULATION OF THE  
CC TIGHT JUNCTION (TJ) PARACELLULAR PERMEABILITY BARRIER. INTERACTS  
CC WITH ZO-1.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH  
CC EPITHELIAL AND ENDOTHELIAL CELLS.  
CC -1- DOMAIN: THE C-TERMINAL IS CYTOPLASMIC AND IS IMPORTANT FOR  
CC INTERACTION WITH ZO-1. NECESSARY FOR THE TIGHT JUNCTION  
CC LOCALIZATION. INVOLVED IN THE REGULATION OF THE PERMEABILITY  
CC BARRIER FUNCTION OF THE TIGHT JUNCTION (BY SIMILARITY).  
CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ELL / OCCLUDIN FAMILY.

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CC EMBL; U49183; AAC48565.1; -.  
DR InterPro; IPR002958; Occludin.  
DR Pfam; PF01284; MARVEL; 1.  
DR PRINTS; PR01258; OCCLUDIN.  
KW Tight junction; Transmembrane; Coiled coil; Phosphorylation.

FT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 52 74 POTENTIAL.  
FT DOMAIN 75 112 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 113 137 POTENTIAL.  
FT DOMAIN 138 147 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 148 172 POTENTIAL.  
FT DOMAIN 173 222 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 223 244 POTENTIAL.  
FT DOMAIN 245 489 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 76 107 TYR/GLY-RICH.  
FT DOMAIN 407 434 COILED COIL (POTENTIAL).  
SQ SEQUENCE 489 AA; 54075 MM; 4F0CA45A41094860 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 489;  
Best Local Similarity 75.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YYG DYEG 8  
Db 96 YG DYNGY 103

RESULT 7  
SYM\_BACHD STANDARD; PRT; 660 AA.  
ID SYM\_BACHD  
AC Q9K6K8;  
DT 28-FEB-2003 (Rel. 41, Created)

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
DE (MetRS).
GN METG OR METS OR BH0053.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Ogasawara N., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Is required not only for elongation of protein synthesis
CC but also for the initiation of all mRNA translation through
CC initiator tRNA(fMet) aminoacylation (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC MetG subfamily 2B.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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CC -----
DR EMBL; AP001507; BAB03772.1; -.
DR PIR; E83656; E83656.
DR HSSP; P23395; 1A8H.
DR HAMAP; MF_01228; fused; 1.
DR InterPro; IPR004495; MetG_Cterm.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR002547; tRNA_bind.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR Pfam; PF01588; tRNA_bind; 1.
DR PIRSF; PIRSF001528; MetRS_dimerising; 1.
DR PRINTS; PR01041; TRNASYNTHET.
DR TIGRFAMs; TIGR00398; metG; 1.
DR TIGRFAMs; TIGR00399; metG_C_term; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR PROSITE; PS50886; TRBD; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW RNA-binding; tRNA-binding; Complete proteome.
FT SITE 15 25 "HIGH" REGION.
FT SITE 311 315 "KMSKS" REGION.
FT DOMAIN 560 660 TRNA-BINDING.
FT BINDING 314 314 ATP (BY SIMILARITY).
SQ SEQUENCE 660 AA; 75191 MW; EC3408645728A536 CRC64;

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Query Match 74.5%; Score 38; DB 1; Length 660;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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CY 1 YG DYEGY 8
| | | | |
Db 121 YLGDYEGW 128

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RESULT 8  
YK23\_YEAST

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ID YK23 YEAST STANDARD; PRT; 271 AA.
AC P36136;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Hypothetical 31.0 kDa protein in GAP1-NAP1 intergenic region.
GN YKR043C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Urrestarazu L.A., Jauniaux J.-C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; Z28268; CAA82119.1; -.
DR PIR; S38115; S38115.
DR SGD; S0001751; YKR043C.
DR InterPro; IPR001345; PG/BPGM_mutase.
DR Pfam; PF00300; PGAM; 1.
KW Hypothetical protein.
SQ SEQUENCE 271 AA; 31022 MW; FF934DE2F5145C40 CRC64;

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Query Match 72.5%; Score 37; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 2 YG DYEG 7
| | | | |
Db 102 YG DYEG 107

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RESULT 9
ASSY_METAC STANDARD; PRT; 394 AA.
ID ASSY_METAC
AC O8TNY5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Argininosuccinate synthase (EC 6.3.4.5) (Citruiline--aspartate
DE ligase).
GN ARGG OR MA2142.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guess A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RL and physiological diversity.";
Genome Res. 12:532-542(2002).

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CC -1- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP +
CC diphosphate + L-argininosuccinate.
CC -1- PATHWAY: Arginine biosynthesis; seventh step.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SIMILARITY: Belongs to the argininosuccinate synthase family.
CC Subfamily 1.
-----
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-----
CC EMBL; AE010900; AAM05540.1; -.
CC HAMAP; MF_00005; -.
CC InterPro; IPR001518; Arginosuc_synth.
CC Pfam; PF00764; Arginosuc_synth; 1.
CC ProDom; PD003544; Arginosuc_synth; 1.
CC TIGRfam; TIGR00032; argG; 1.
CC PROSITE; PS00564; ARGININOSUCCIN SYN 1; 1.
CC PROSITE; PS00565; ARGININOSUCCIN SYN 2; 1.
CC Arginine biosynthesis; ligase; ATP-binding; Complete proteome.
CC KW Arginine biosynthesis; ligase; ATP-binding; Complete proteome.
CC SQ SEQUENCE 394 AA; 43994 MW; 2B995B9C138E7EF1 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GDYEGY 8
Db 81 GDYEGY 86

RESULT 10
LHX5_BRARE STANDARD; PRT; 399 AA.
AC P52889;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx5 (Homeobox protein LIM-5).
GN LHX5 OR LIM5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=95377545; PubMed=7649385;
RX Toyama R., Curtis P.E., Otani H., Kimura M., David I.B., Taira M.;
RT "The LIM class homeobox gene lim5: implied role in CNS patterning in
RT Xenopus and zebrafish.";
RL Dev. Biol. 170:583-593(1995).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE PATTERNING OF THE NERVOUS
CC SYSTEM, IN PARTICULAR IN THE EARLY SPECIFICATION OF THE
CC DIENCEPHALON.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
-----
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CC EMBL; L42547; AAA99465.1; -.
CC HSSP; P06601; 1FUL.
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DR ZFIN; ZDB-GENE-980526-484; lim5.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM_homeo.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM DOMAIN 1; 2.
DR PROSITE; PS50023; LIM DOMAIN 2; 2.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Developmental protein;
KW Repeat; LIM domain; Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 3 61 LIM 1.
FT DOMAIN 62 125 LIM 2.
FT DNA_BIND 180 239 HOMEBOX.
SQ SEQUENCE 399 AA; 44513 MW; C0D7B1B86D032DA CRC64;

Query Match 72.5%; Score 37; DB 1; Length 399;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGDEYEG 7
Db 278 YGDEYEG 284

RESULT 11
SOX8_HUMAN STANDARD; PRT; 446 AA.
ID P57073; Q9NZW2;
AC P57073; Q9NZW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transcription factor SOX-8.
GN SOX8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheng Y.-C., Badge R.M., Armour J.A.L., Scouting P.J.;
RT "SOX8: a newly identified human gene expressed in paediatric brain
RT tumours and a candidate for the mental retardation phenotype in
RT ATR-16.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21096910; PubMed=1157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.;
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Ellington A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 119-446 FROM N.A.
RX MEDLINE=20130119; PubMed=10662550;
RA Pfeifer D., Poulat F., Holinski-Feder E., Kooy F., Scherer G.;
RT "The SOX8 gene is located within 700 kb of the tip of chromosome 16p
RT and is deleted in a patient with ATR-16 syndrome.";
RL Genomics 63:108-116(2000).
CC -1- FUNCTION: MAY PLAY A ROLE IN CENTRAL NERVOUS SYSTEM, LIMB AND
CC FACIAL DEVELOPMENT. MAY BE INVOLVED IN MALE SEX DETERMINATION.
CC BINDS THE CONSENSUS MOTIF 5'-[AT][AT]CAA[AT]G-3' (BY SIMILARITY).
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CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Contains 1 HMG box domain.
CC -----
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CC -----
DR EMBL; AF226675; AAF35886.1; -.
DR EMBL; AE006465; AAK61260.1; -.
DR EMBL; Z99757; CAB75612.1; ALT_INIT.
DR EMBL; AF164104; AAF37424.1; -.
DR HSSP; P48436; ISX9.
DR TRNSFPAC; T04917; -.
DR Genew; HGNC:11203; SOX8.
DR MIM; 605923; -.
DR GO; GO:0003702; F:RNA polymerase II transcription factor acti. . . ; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. . . ; TAS.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 1.
DR SMART; SM00398; HMG; 1.
DR PROSITE; PS50118; HMG_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DNA_BIND 102 170 HMG_BOX.
SQ SEQUENCE 446 AA; 47314 MW; AE453359051A6DB3 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 446;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db 391 YYGAYPGY 398

RESULT 12
ROR_HUMAN STANDARD; PRT; 633 AA.
AC 043390;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heterogeneous nuclear ribonucleoprotein R (hnRNP R).
GN HNRPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98083170; PubMed=9421497;
RA Hassfeld W., Chan E.K.L., Mathison D.A., Portman D., Dreyfuss G.,
RA Steiner G., Tan E.M.;
RT "Molecular definition of heterogeneous nuclear ribonucleoprotein R
RT (hnRNP R) using autoimmune antibody: immunological relationship with
RT hnRNP P.";
RL Nucleic Acids Res. 26:439-445(1998).
CC -1- FUNCTION: COMPONENT OF RIBONUCLEOSOMES, WHICH ARE COMPLEXES OF AT
CC LEAST 20 OTHER DIFFERENT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS
CC (HNRNP). HNRNP PLAY AN IMPORTANT ROLE IN PROCESSING OF PRECURSOR
CC MRNA IN THE NUCLEUS.
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleoplasm.
CC -1- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
CC -----
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CC -----
DR EMBL; AF000364; AAC39540.1; -.
DR PIR; T02673; T02673.
DR HSSP; P09651; 1HA1.
DR Genew; HGNC:5047; HNRPR.
DR GK; 043390; -.
DR MIM; 607201; -.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0008436; F:heterogeneous nuclear ribonucleoprotein; TAS.
DR GO; GO:0003723; F:RNA binding activity; TAS.
DR GO; GO:0006397; P:RNA processing; TAS.
DR InterPro; IPR006535; HnrNP_R_Q.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 3.
DR SMART; SM00360; RRM; 3.
DR TIGRFAMs; TIGR01648; hnRNP-R-Q; 1.
DR PROSITE; PS50102; RRM; 3.
DR PROSITE; PS00030; RRM_RNP_1; 2.
KW Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat.
FT DOMAIN 1 153 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 412 418 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 165 244 RNA-BINDING (RRM) 1.
FT DOMAIN 246 328 RNA-BINDING (RRM) 2.
FT DOMAIN 341 411 RNA-BINDING (RRM) 3.
FT DOMAIN 447 567 RNA-BINDING (RGG-BOX).
FT DOMAIN 462 497 3 X 11 AA APPROXIMATE REPEATS OF D-D-Y-Y-
FT REPEAT 462 471 G-Y-D-Y-H-D-Y.
FT REPEAT 472 482 1 (APPROXIMATE).
FT REPEAT 488 497 2.
FT DOMAIN 579 633 GLN/ASN-RICH DOMAIN.
SQ SEQUENCE 633 AA; 70943 MW; 088341F6465ED46F CRC64;

Query Match 72.5%; Score 37; DB 1; Length 633;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db 470 YYDDYGY 477

RESULT 13
G13A_DICDI STANDARD; PRT; 730 AA.
AC P34115;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell surface glycoprotein gp138A precursor.
GN FUSA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-32.
RX STRAIN=AX3;
RX MEDLINE=93193972; PubMed=7680629;
RA Fang H., Higa M., Suzuki K., Aiba K., Urushihara H., Yanagisawa K.;
RT "Molecular cloning and characterization of two genes encoding gp138,
RT a cell surface glycoprotein involved in the sexual cell fusion of
RT Dictyostelium discoideum.";
RL Dev. Biol. 156:201-208(1993).
CC -1- FUNCTION: INVOLVED IN THE SEXUAL CELL FUSION OF D.DICOIDIUM.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT THE TIME OF ACQUISITION OF
CC FUSION COMPETENCE OF CELLS.
CC -1- PTM: THE SUGAR CHAINS MAY PLAY IMPORTANT ROLES IN CELL FUSION.
CC -1- PTM: The GPI-anchor contains a phosphoceramide moiety.
CC -1- MISCELLANEOUS: GP138A EXPRESSION IS MUCH HIGHER THAN THAT OF
CC GP138B AND MAY WELL BE THE MAJOR GENE FOR GP138 PRODUCT.

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CC -----
DR EMBL; D12883; BAA02287.1; -.
DR PIR; A48832; A48832.
DR DictyDb; DD03014; fusa.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF01833; TIG; 1.
KW Glycoprotein; Signal; Multigene family; GPI-anchor; Repeat.
FT SIGNAL 1 20
FT CHAIN 21 708
FT PROPEP 709 730
FT LIPID 708 708
FT DOMAIN 683 694
FT REPEAT 683 686
FT REPEAT 687 690
FT REPEAT 691 694
FT CARBOHYD 58 58
FT CARBOHYD 89 89
FT CARBOHYD 124 124
FT CARBOHYD 198 198
FT CARBOHYD 224 224
FT CARBOHYD 392 392
FT CARBOHYD 420 420
FT CARBOHYD 435 435
FT CARBOHYD 482 482
FT CARBOHYD 498 498
FT CARBOHYD 523 523
FT CARBOHYD 534 534
FT CARBOHYD 596 596
FT CARBOHYD 605 605
FT CARBOHYD 614 614
FT CARBOHYD 620 620
FT CARBOHYD 621 621
FT CARBOHYD 630 630
SQ SEQUENCE 730 AA; 80960 MW; C2BDB82BC24CD133 CRC64;

Query Match      72.5%; Score 37; DB 1; Length 730;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 YYGDEYEGY 8
DB 343 YNDYDEGY 350

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RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devane K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Frits C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Bianchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RT Nature 390:249-256 (1997).
RN [3]
RP SEQUENCE OF 36-52 AND 403-442, AND CHARACTERIZATION.
RC STRAIN=NR-1;
RA Ogawa Y., Hosoyama H., Hamano M., Motai H.;
RT "Purification and properties of gamma-glutamyltranspeptidase from
RT Bacillus subtilis (natto).";
RL Agric. Biol. Chem. 55:2971-2977 (1991).
CC -!- CATALYTIC ACTIVITY: (5-L-glutamyl)-peptide + an amino acid =
CC peptide + 5-L-glutamyl-amino acid.
CC -!- ENZYME REGULATION: INHIBITED BY GLUCOSE.
CC -!- PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, A
CC PATHWAY FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.
CC -!- SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHICH ARE
CC SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT THE END OF VEGETATIVE GROWTH.
CC -!- SIMILARITY: STRONG, TO OTHER GGT ENZYMES AND TO GL-7ACA ACYLASES.
CC -----
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CC -----
DR EMBL; U49358; AAC44233.1; -.
DR EMBL; Z99113; CAB13724.1; -.
DR EMBL; Z99114; CAB13734.1; -.
DR PIR; F69631; F69631.
DR MEROPS; T03.001; -.
DR Subtilist; BG1838; ggt.
DR InterPro; IPR000101; Gglutnsptdase.
DR Pfam; PF01019; G_glu_transpt; 1.
DR PRINTS; PR01210; GGTRANSPTASE.
DR TIGRams; TIGR00066; g_glu_trans; 1.
DR PROSITE; PS00462; G_GLU_TRANSPEPTIDASE; 1.
KW Transferase; Acyltransferase; Signal; Glutathione biosynthesis;

```



KW Zymogen; Complete proteome.  
FT SIGNAL; 1 28 POTENTIAL.  
FT CHAIN 29 402 GAMMA-GLUTAMYLTRANSPEPTIDASE LARGE CHAIN.  
FT CHAIN 403 587 GAMMA-GLUTAMYLTRANSPEPTIDASE SMALL CHAIN.  
FT BINDING 467 467 GAMMA-GLUTAMYL (POTENTIAL).  
FT CONFLICT 46 46 D -> V (IN REF. 3).  
SQ SEQUENCE 587 AA; 64189 MW; 6BF200CBA882C4F6 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 587;  
Best Local Similarity 71.4%; Pred. No. 83;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGDYEGY 8  
:||||:  
Db 277 WGDYQGY 283

RESULT 15  
ACSA\_RHOCA STANDARD; PRT; 656 AA.  
ID ACSA\_RHOCA  
AC 068040;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acy]-  
DE activating enzyme).  
GN ACS.  
OS Rhodobacter capsulatus (Rhodopsedomonas capsulata).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
OC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1061;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=SB1003 / St Louis;  
RX MEDLINE=97404404; PubMed=9256491;  
RA Vlack C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.;  
RT "Sequence of a 189-kb segment of the chromosome of Rhodobacter  
RT capsulatus SB1003."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).  
CC -!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +  
CC acetyl-CoA.  
CC -!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME  
CC FAMILY.  
CC

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CC -----

CC EMBL; AF010496; AAC16126.1; -.  
DR PIR; T03473; T03473.  
DR InterPro; IPR000873; AMP-bind.  
DR Pfam; PF00501; AMP-binding; 1.  
DR PRINTS; PR00154; AMPBINDING.  
DR PROSITE; PS00455; AMP\_BINDING; 1.  
KW Ligase.  
SQ SEQUENCE 656 AA; 72703 MW; 706EA969331D71C2 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 656;  
Best Local Similarity 62.5%; Pred. No. 92;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YGDYEGY 8  
|:|:|:  
Db 495 YFGQYRGY 502

Search completed: July 30, 2003, 09:45:02  
Job time : 4.24917 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 6.19269 Seconds  
(without alignments)  
333.364 Million cell updates/sec

Title: US-09-865-198-3  
Perfect score: 51  
Sequence: 1 YYGDYEGY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	82.4	138	17 Q8PT44	Q8PT44 methanosarc
2	41	80.4	101	16 Q8PEY8	Q8PEY8 xanthomonas
3	41	80.4	101	16 Q8P3U0	Q8P3U0 xanthomonas
4	41	80.4	435	16 Q9PN04	Q9PN04 campylobact
5	40	78.4	409	10 Q9LEB4	Q9LEB4 nicotiana p
6	40	78.4	1650	5 O77328	O77328 plasmodium
7	39	76.5	320	16 Q8EP40	Q8EP40 oceanobacil
8	39	76.5	465	16 Q8G5U5	Q8G5U5 bifidobacte
9	39	76.5	980	5 Q8IJ27	Q8IJ27 plasmodium
10	39	76.5	1881	17 Q8TUS7	Q8TUS7 methanosarc
11	38	74.5	387	10 Q9FPJ8	Q9FPJ8 arabidopsis
12	38	74.5	390	10 Q9FFU0	Q9FFU0 arabidopsis
13	38	74.5	595	16 O67245	O67245 aquifex aeo
14	38	74.5	3216	16 Q98QZ9	Q98QZ9 mycoplasma
15	37	72.5	68	9 Q8H9T7	Q8H9T7 pseudomonas
16	37	72.5	89	5 O62093	O62093 caenorhabdi

17	37	72.5	104	5 Q9U601	Q9U601 anisakis si
18	37	72.5	154	17 Q27163	Q27163 methanobact
19	37	72.5	212	5 Q8IRH6	Q8IRH6 drosophila
20	37	72.5	242	5 Q9W0H1	Q9W0H1 drosophila
21	37	72.5	242	5 Q8MZ31	Q8MZ31 drosophila
22	37	72.5	294	2 Q8VWN1	Q8VWN1 vibrio chol
23	37	72.5	294	2 Q8GJ09	Q8GJ09 escherichia
24	37	72.5	300	5 Q9W098	Q9W098 drosophila
25	37	72.5	300	5 Q8MZP7	Q8MZP7 drosophila
26	37	72.5	307	11 Q8BL32	Q8BL32 mus musculu
27	37	72.5	376	4 Q9H719	Q9H719 homo sapien
28	37	72.5	542	16 Q9JZ89	Q9JZ89 neisseria m
29	37	72.5	542	16 Q9JUB3	Q9JUB3 neisseria m
30	37	72.5	564	5 Q23118	Q23118 caenorhabdi
31	37	72.5	601	11 Q99KG1	Q99KG1 mus musculu
32	37	72.5	620	17 Q96XC8	Q96XC8 sulfolobus
33	37	72.5	632	11 Q8VHM5	Q8VHM5 mus musculu
34	37	72.5	636	4 Q9BV64	Q9BV64 homo sapien
35	37	72.5	1657	5 P90761	P90761 caenorhabdi
36	36	70.6	191	16 Q92CQ8	Q92CQ8 listeria in
37	36	70.6	191	16 Q8Y7X0	Q8Y7X0 listeria in
38	36	70.6	252	16 Q97S13	Q97S13 streptococc
39	36	70.6	299	17 Q8TL35	Q8TL35 methanosarc
40	36	70.6	307	17 Q8TTD1	Q8TTD1 methanosarc
41	36	70.6	313	11 Q8BXC4	Q8BXC4 mus musculu
42	36	70.6	313	11 Q8BL81	Q8BL81 mus musculu
43	36	70.6	335	5 Q8SZN5	Q8SZN5 drosophila
44	36	70.6	335	5 Q9V5P1	Q9V5P1 drosophila
45	36	70.6	441	10 Q9LX71	Q9LX71 arabidopsis

ALIGNMENTS

RESULT 1

ID	Q8PT44	PRELIMINARY;	PRT;	138 AA.
AC	Q8PT44;			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-OCT-2002 (Tremblrel. 22, Last annotation update)			
DE	Conserved protein.			
GN	MM2874.			
OS	Methanosarcina mazel (Methanosarcina frisia).			
OC	Archaea; Euryarchaeota; Methanococci; Methanosarcinales;			
OC	Methanosarcinaceae; Methanosarcina.			
OX	NCBI_TaxID=2209;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;			
RX	MEDLINE=22120827; PubMed=12125824;			
RA	Deppeleier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,			
RA	Martinez-Arias R., Henne A., Wieser A., Baumeier S., Jacobi C.,			
RA	Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,			
RA	Fritz H.-J., Gottschalk G.;			
RT	"The genome of Methanosarcina mazel: evidence for lateral gene			
RT	transfer between Bacteria and Archaea."			
RL	J. Mol. Microbiol. Biotechnol. 4:453-461(2002).			
DR	EMBL; AE013538; AAM32570.1; -.			
KW	Complete proteome.			
SQ	SEQUENCE 138 AA; 15664 MW; E500398EAD066078 CRC64;			

Query Match 82.4%; Score 42; DB 17; Length 138;  
Best Local Similarity 75.0%; Pred. No. 9.1;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
Db 75 FYGDYSGY 82

RESULT 2

Q8PEY8 PRELIMINARY; PRT; 101 AA.  
AC Q8PEY8;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Hypothetical protein XAC4200.  
GN XAC4200.  
OS Xanthomonas axonopodis (pv. citri).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xanthomonas.  
OX NCBI\_TaxID=92829;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=306 / ATCC 13902 / XV.101;  
RX MEDLINE=22022145; PubMed=12024217;  
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
Camarotte G., Canavan F., Cardozo J., Chambergo F., Ciapina L.P.,  
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,  
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
Spincola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,  
Setubal J.C., Kitajima J.P.,  
RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
RT host specificities."  
RL Nature 417:459-463(2002).  
DR EMBL; AE012071; AAM39035.1; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 101 AA; 11468 MW; AD363D0264EBD629 CRC64;  
Query Match 80.4%; Score 41; DB 16; Length 101;  
Best Local Similarity 75.0%; Pred. No. 9.6; Mismatches 1; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YG DYEGY 8  
Db 39 YFADYEGY 46  
RESULT 3  
ID Q8P3J0 PRELIMINARY; PRT; 101 AA.  
AC Q8P3J0;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Hypothetical protein XCC4081.  
GN XCC4081.  
OS Xanthomonas campestris (pv. campestris).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xanthomonas.  
OX NCBI\_TaxID=340;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33913 / NCPPB 528;  
RX MEDLINE=22022145; PubMed=12024217;  
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
Camarotte G., Canavan F., Cardozo J., Chambergo F., Ciapina L.P.,  
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,  
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
Spincola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,  
Setubal J.C., Kitajima J.P.,  
RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
RT host specificities."  
RL Nature 417:459-463(2002).  
DR EMBL; AE012531; AAM43302.1; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 101 AA; 11503 MW; 578C1C9ED8E1404D CRC64;  
Query Match 80.4%; Score 41; DB 16; Length 101;  
Best Local Similarity 75.0%; Pred. No. 9.6; Mismatches 1; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YG DYEGY 8  
Db 39 YFADYEGY 46  
RESULT 4  
ID Q9PN04 PRELIMINARY; PRT; 435 AA.  
AC Q9PN04;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Hypothetical protein Cj1295.  
GN Cj1295.  
OS Campylobacter jejuni.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Campylobacteraceae; Campylobacter.  
OX NCBI\_TaxID=197;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCTC 11168;  
RX MEDLINE=20150912; PubMed=10688204;  
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,  
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,  
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,  
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,  
Whitehead S., Barrell B.G.,  
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni  
RT reveals hypervariable sequences."  
RL Nature 403:665-668(2000).  
DR EMBL; AL139078; CAB73722.1; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 435 AA; 49948 MW; 1DFD6DD270C0877 CRC64;  
Query Match 80.4%; Score 41; DB 16; Length 435;  
Best Local Similarity 85.7%; Pred. No. 48; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YG DYEGY 8  
Db 325 YG DYDGY 331  
RESULT 5  
ID Q9LEB4 PRELIMINARY; PRT; 409 AA.  
AC Q9LEB4;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE RNA binding protein 45.  
GN RBP45.  
OS Nicotiana glauca (Leadwort-leaved tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.

```
OX NCBI_TaxID=4092;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20555308; PubMed=11105760;
RA Lorkovic Z.J., Wiczorek Kirk D.A., Klahre U., Hemmings-Mieszcak M.,
RA Filipowicz W.;
RT "RBP45 and RBP47, two oligouridylylate-specific hnRNP-like proteins
RT interacting with poly(A)+ RNA in nuclei of plant cells.";
RL RNA 6:1610-1624(2000).
DR EMBL; AJ292767; CAC01237.1; -.
DR HSSP; P11940; 1CVJ.
DR ANU-2DPAGE; Q9LEB4; -.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 3.
DR SMART; SM00360; RRM; 3.
DR PROSITE; PS50102; RRM; 3.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 409 AA; 45243 MW; 145EE701A89AF01D CRC64;

Query Match
Best Local Similarity 78.4%; Score 40; DB 10; Length 409;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db 394 YYGNYPGY 401

RESULT 6
O77328 PRELIMINARY; PRT; 1650 AA.
ID O77328;
AC O77328;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative serine/threonine protein kinase.
GN PFC0385C, MAL3P3.12.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sultston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT falciparum.";
RL Nature 400:532-538(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; Z98547; CAB1112.2; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1650 AA; 193755 MW; D70FE19C5C640B5A CRC64;

Query Match
Best Local Similarity 78.4%; Score 40; DB 5; Length 1650;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
```

```
Db 525 YFDYEGY 532

RESULT 7
Q8EPA0 PRELIMINARY; PRT; 320 AA.
ID Q8EPA0;
AC Q8EPA0;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE 2-keto-3-deoxygluconate kinase (EC 2.7.1.45).
GN KDGK OR OB2213.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 11309;
RX MEDLINE=2220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; AP004600; BAC14169.1; -.
KW Kinase; Transferase; Complete proteome.
SQ SEQUENCE 320 AA; 35224 MW; 264E9D41C54C09FE CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 16; Length 320;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db 293 YVGDEYGF 300

RESULT 8
Q8G5U5 PRELIMINARY; PRT; 465 AA.
ID Q8G5U5;
AC Q8G5U5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Possible cyclomaltoextrinase or neopullulanase.
GN BL0907.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaalen M.-C., Desiere F., Borx P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014712; AAN24720.1; -.
KW Complete proteome.
SQ SEQUENCE 465 AA; 51674 MW; 18FE7AA673E4DE0A CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 16; Length 465;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db 356 YVGDEQGY 363
```

```
RESULT 9
Q8IJ27 PRELIMINARY; PRT; 980 AA.
AC Q8IJ27;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE Hypothetical protein.
GN PF10_0373.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berrihan M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RA "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014834; AAN35570.1; -.
KW Hypothetical protein.
SQ SEQUENCE 980 AA; 116175 MW; 172F14BD1A18F31F CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 5; Length 980;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEG 7
Db 44 YYGDYNG 50

RESULT 10
Q8TJS7 PRELIMINARY; PRT; 1881 AA.
AC Q8TJS7;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Cell surface protein.
GN MA3700.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atwood D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tittell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hederich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RA "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:532-542(2002).
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DR EMBL; AE011081; AAM07055.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000413; Integrin alpha.
DR InterPro; IPR000601; PKD_domain.
DR Pfam; PF01839; EG-GAP; 5.
DR Pfam; PF00801; PKD; 6.
DR SMART; SM00089; PKD; 7.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS50093; PKD; 4.
KW Complete proteome.
SQ SEQUENCE 1881 AA; 201366 MW; 836514E38E842A49 CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 17; Length 1881;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db 165 HYGDYVGY 172

RESULT 11
Q9FPJ8 PRELIMINARY; PRT; 387 AA.
AC Q9FPJ8;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE AT5G54900.
GN AT5G54900/MEG8 17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin P., Chao Q., Brooks S., Chen H., Cheuk R., Johnson-Hopson C.,
RA Khan S., Kim C.J., Bawser L., Chung M.K., Goldsmith A.D.,
RA Jones T., Karlin-Neumann G., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H.,
RA Southwick A., Toriumi M., Yamada K., Yu G., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cdna clones."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF324983; AAG40335.1; -.
DR HSSP; P11940; 1CVJ.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 3.
DR SMART; SM00360; RRM; 3.
DR PROSITE; PS50102; RRM; 3.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 387 AA; 42324 MW; D6CF4F66DFD78DB0 CRC64;

Query Match
Best Local Similarity 74.5%; Score 38; DB 10; Length 387;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
Db 372 YYGGYTG 379

RESULT 12
Q9FFU0 PRELIMINARY; PRT; 390 AA.
AC Q9FFU0;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Similarity to polyadenylate-binding protein 5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```



OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC euosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=97471969; PubMed=9330910;  
 RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,  
 Miyajima N., Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence  
 features of the 1.6 Mb regions covered by twenty physically assigned  
 RT pl clones.";  
 RL DNA Res. 4:215-230(1997).  
 DR EMBL; AB005232; BAB08769.1; -.  
 DR HSSP; P11940; 1CVJ.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR Pfam; PF00076; rim; 3.  
 DR SMART; SM00360; RRM; 3.  
 DR PROSITE; PS50102; RRM; 3.  
 DR PROSITE; PS00030; RRM\_RNP\_1; 1.  
 SQ SEQUENCE 390 AA; 42652 MW; DD03B776CF4F66DF CRC64;

Query Match 74.5%; Score 38; DB 10; Length 390;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YG DYEGY 8  
 Db 372 YG GYTGX 379

## RESULT 13

O67245 PRELIMINARY; PRT; 595 AA.  
 AC O67245;  
 DT 01-AUG-1998 (TReMBLrel. 07, Created)  
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Hypothetical protein AQ\_1185.  
 GN AQ\_1185.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VR5;  
 RX MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjay M., Huber R.,  
 Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus.";  
 RL Nature 392:353-358(1998).  
 DR EMBL; AE000727; AAC07204.1; -.  
 DR InterPro; IPR001440; TPR.  
 DR Pfam; PF00515; TPR; 2.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 595 AA; 71080 MW; F8373F5603427F24 CRC64;

Query Match 74.5%; Score 38; DB 16; Length 595;  
 Best Local Similarity 85.7%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YG DYEGY 8  
 Db 159 YG DYTGX 165

## RESULT 14

O98QZ9 PRELIMINARY; PRT; 3216 AA.  
 AC O98QZ9;  
 DT 01-OCT-2001 (TReMBLrel. 18, Created)

DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)  
 DE Hypothetical protein MYPU\_2110.  
 GN MYPU\_2110.  
 OS Mycoplasma pulmonis.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=2107;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UAB CTIP;  
 RX MEDLINE=21267165; PubMed=11353084;  
 RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,  
 Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,  
 Blanchard A.;  
 RT "The complete genome sequence of the murine respiratory pathogen  
 RT Mycoplasma pulmonis.";  
 RL Nucleic Acids Res. 29:2145-2153(2001).  
 DR EMBL; AL445563; CAC13384.1; -.  
 DR Mypulist; MYPU\_2110; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 3216 AA; 359419 MW; A62ED95756BDB90C CRC64;

Query Match 74.5%; Score 38; DB 16; Length 3216;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YG DYEGY 8  
 Db 1978 YV DYEGF 1985

## RESULT 15

O8H9T7 PRELIMINARY; PRT; 68 AA.  
 AC O8H9T7;  
 DT 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE ORF23318.  
 GN ORF23318.  
 OS Pseudomonas aeruginosa phage Pap3.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
 OC T7-like viruses.  
 OX NCBI\_TaxID=188350;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hu F.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa phage Pap3.";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY078382; AAL85549.1; -.  
 SQ SEQUENCE 68 AA; 7787 MW; D292B2B7E6EB0E41 CRC64;

Query Match 72.5%; Score 37; DB 9; Length 68;  
 Best Local Similarity 62.5%; Pred. No. 31;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YG DYEGY 8  
 Db 55 FYGDWRGX 62

Search completed: July 30, 2003, 09:42:35  
 Job time : 9.3038 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 8 Seconds  
(without alignments)  
158.727 Million cell updates/sec

Title: US-09-865-198-3  
Perfect score: 51  
Sequence: 1 YTGDIYEGY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	8	21	AA97231
2	51	100.0	8	22	AAE13139
3	51	100.0	8	22	AAB82705
4	51	100.0	8	23	AAE25951
5	51	100.0	8	23	AAU74408
6	51	100.0	8	24	ABJ26720
7	51	100.0	117	21	AA97235
8	51	100.0	117	22	AAE13143
9	51	100.0	117	22	AAB82709

10	51	100.0	117	23	AAE25955	Mouse anti-KDR p1c
11	51	100.0	117	23	AAU74412	Antigen-binding pr
12	51	100.0	117	23	AAU74417	Antigen-binding pr
13	51	100.0	117	24	ABJ26724	VEGF binding relat
14	51	100.0	117	24	ABJ26729	VEGF binding relat
15	51	100.0	135	23	AAE25965	Mouse anti-KDR p1c
16	51	100.0	136	22	AAE13145	Chimeric p1c11 hea
17	51	100.0	136	22	AAB82701	VEGF antagonist an
18	51	100.0	136	23	AAE28916	c-p1c11 vector hea
19	51	100.0	238	23	AAE25961	KDR binding immuno
20	51	100.0	238	23	AAE25963	KDR binding immuno
21	51	100.0	238	23	AAU74420	Antigen-binding pr
22	51	100.0	238	24	ABJ26732	VEGF binding relat
23	51	100.0	240	23	AAE25960	KDR binding immuno
24	51	100.0	240	23	AAU74419	Antigen-binding pr
25	51	100.0	240	24	ABJ26731	VEGF binding relat
26	39	76.5	11	17	AA92576	VLA-4 binding pept
27	39	76.5	439	23	ABR38866	A. niger secr. Ami
28	39	76.5	465	23	ABP65782	Bifidobacterium lo
29	38	74.5	120	12	AA13721	Control fusion pro
30	38	74.5	322	23	AAE15536	Beta vulgaris RNA
31	38	74.5	364	21	AAE28667	Arabidopsis thalia
32	38	74.5	364	21	AAE37706	Arabidopsis thalia
33	38	74.5	365	21	AAE28666	Arabidopsis thalia
34	38	74.5	365	21	AAE37705	Arabidopsis thalia
35	38	74.5	387	21	AAE28665	Arabidopsis thalia
36	38	74.5	387	21	AAE37704	Arabidopsis thalia
37	38	74.5	564	21	AAE36226	Arabidopsis thalia
38	38	74.5	738	21	AAE36225	Arabidopsis thalia
39	38	74.5	745	21	AAE36224	Arabidopsis thalia
40	37	72.5	74	23	ABE79657	Chronic lymphocyte
41	37	72.5	248	22	ABE59150	Drosophila melanog
42	37	72.5	264	20	AAE41480	Fragment of human
43	37	72.5	279	22	ABE93805	Human protein sequ
44	37	72.5	300	22	ABE57949	Drosophila melanog
45	37	72.5	485	22	ABE22097	Novel human diagno

ALIGNMENTS

RESULT 1	
AA97231	
AA97231 standard; Protein; 8 AA.	
XX	
AC	AA97231;
XX	
DT	19-DEC-2000 (first entry)
XX	
DE	Complementary determining region (CDRH3) of anti-SI(KDR) antibody.
XX	
KW	Immunoglobulin; antibody; complementary determining region; CDR;
KW	VEGF; vascular endothelial growth factor; KDR;
KW	kinase insert domain containing receptor; multivalent; monovalent;
KW	humanised antibody; chimeric antibody; tumour; diabydy; triabydy;
KW	glioblastoma multiforme; hemangioblastoma; AIDS;
KW	central nervous system neoplasms; AIDS associated Karpoti's sarcoma;
KW	acquired immune deficiency syndrome; AIDS; human.
XX	
OS	Homo sapiens.
XX	
OS	Synthetic.
XX	
PN	WO200044777-A1.
XX	
PD	03-AUG-2000.
XX	
PF	28-JAN-2000; 2000WO-US02180.
XX	
PR	29-JAN-1999; 99US-0117726.
XX	
PR	29-JAN-1999; 99US-0240736.
XX	
PA	(IMCL-) IMCLONE SYSTEMS INC.
XX	

PI Zhu Z, Witte L;  
XX  
DR WPI; 2000-505966/45.  
DR N-PSDB; AAA53763.  
XX  
PT Novel immunoglobulin molecules binding kinase insert domain-containing  
PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growth  
XX  
PS Claim 3; Page 50; 55pp; English.  
XX  
CC New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Kaposi's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulins of the invention.  
XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 21; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYG DYEGY 8  
|||  
DB 1 YYG DYEGY 8

RESULT 2  
AAE13139  
ID AAE13139 standard; peptide; 8 AA.  
XX  
AC AAE13139;  
XX  
DT 28-JAN-2002 (first entry)  
XX  
DE Humanised antibody murine heavy chain hypervariable region (VH) CDR3.  
XX  
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytosolic; heavy chain hypervariable region; VH; myelocytic leukaemia;  
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;  
KW Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.  
XX  
OS Mus sp.  
XX  
PN WO200174296-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US10504.  
XX  
PR 31-MAR-2000; 2000US-0540770.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Witte L, Rafil S;  
XX  
DR WPI; 2001-662942/76.  
DR N-PSDB; AAD21665.  
XX  
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with

PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
PS Claim 8; Page 14; 68pp; English.  
XX  
CC The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains mouse complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised  
CC antibody murine heavy chain hypervariable region (VH) CDR-3 used in the  
CC exemplification of the invention.  
XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYG DYEGY 8  
|||  
DB 1 YYG DYEGY 8

RESULT 3  
AAB82705  
ID AAB82705 standard; Peptide; 8 AA.  
XX  
AC AAB82705;  
XX  
DT 15-OCT-2001 (first entry).  
XX  
DE VEGF antagonist antibody IMC-1C11 VH CDR-3.  
XX  
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; heavy chain; CDR;  
KW complementarity determining region.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
PN WO200154723-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 29-JAN-2001; 2001WO-US02839.  
XX  
PR 28-JAN-2000; 2000US-0178791.  
XX  
PR 31-MAR-2000; 2000US-0539692.  
XX  
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Kerbel R;  
XX  
DR WPI; 2001-514531/56.  
XX  
PT Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX  
PS Disclosure; Page 37; 42pp; English.

XX The present sequence is that of complementarity determining region  
CC 3 of the heavy chain variable region (see also AAB82701) of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

Sequence 8 AA;

Query Match 100.0%; Score 51; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
|||  
1 YYGDYEGY 8

RESULT 4  
AAE25951

ID AAE25951 standard; peptide; 8 AA.

AAE25951;

15-NOV-2002 (first entry)

Mouse anti-KDR p1C11 scFv antibody CDRH3 peptide.

Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
VEGF; tumour growth; heavy chain complementarity determining region 3;  
CDRH3; angiogenesis; p1C11; scFv antibody.

Mus musculus.

US2002064528-A1.

30-MAY-2002.

12-OCT-2001; 2001US-0976787.

28-JAN-2000; 2000US-0493539.

(ZHUZ/) ZHU Z.  
(WITT/) WITTE L.

Zhu Z, Witte L;

WPI; 2002-589175/63.

N-PSDB; AAD42816.

Novel immunoglobulin molecule for reducing tumor growth, binds to  
kinase insert domain-containing receptor with an affinity comparable to  
human vascular endothelial growth factor, and neutralizes activation of  
KDR

Claim 3; Page 11; 34pp; English.

CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody  
CC heavy chain complementarity determining region 3 (CDRH3) protein.

Sequence 8 AA;

Query Match 100.0%; Score 51; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
|||  
1 YYGDYEGY 8

RESULT 5  
AAU74408

ID AAU74408 standard; peptide; 8 AA.

AAU74408;

26-MAR-2002 (first entry)

Heavy chain complementarity determining region H3 (CDRH3).

Complementarity determining region; CDR; CDRH3; antigen; cytostatic;  
angiogenesis inhibitor; vascular endothelial growth factor receptor;  
VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;  
antibody heavy chain variable domain.

Mus sp.

WO200190192-A2.

29-NOV-2001.

24-MAY-2001; 2001WO-US16924.

24-MAY-2000; 2000US-206749P.

(IMCL-) IMCLONE SYSTEMS INC.

Zhu Z;

WPI; 2002-106189/14.

N-PSDB; AAS20279.

New bispecific immunoglobulin-like antigen-binding protein for reducing  
tumour growth and for inhibiting angiogenesis, comprises a complex of  
two polypeptides and two second polypeptides

Claim 55; Page 56; 64pp; English.

The invention describes an antigen-binding protein (I) comprising a  
complex of two polypeptides (P1) and two second polypeptides (P2) which  
are stably associated in an immunoglobulin like complex. P1 has an  
antigen-binding site located to the N terminus of immunoglobulin (Ig)  
light chain constant domain (CL domain), and P2 has an antigen-binding  
site located to the N terminus of the CH1 domain. (I) is useful for:  
neutralising the activation of a vascular endothelial growth factor  
(VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
reducing endothelial cell proliferation; blocking interaction of a protein and  
its ligand; promoting interactions between immune cells and target cells;  
and in vivo and in vitro for investigative, diagnostic or treatment  
methods. The design of (I) provides for efficient production so that  
substantially all of the antigen-binding proteins produced are assembled  
in the desired configuration. (I) is bivalent and bispecific, homogeneous



CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This peptide sequence represents the heavy chain variable domain  
CC complementarity determining region H3 (CDRH3) incorporated into an  
CC antigen-binding protein described in the method of the invention.

XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
1  
Db 1 YYGDYEGY 8

RESULT 6  
ABJ26720

ID ABJ26720 standard; Peptide; 8 AA.

AC ABJ26720;

DT 01-MAY-2003 (first entry)

DE VEGF binding related peptide SEQ ID No 3.

KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.

OS Mus sp.

PN WO2003002144-A1.

PD 09-JAN-2003.

PF 26-JUN-2002; 2002WO-US20332.

PR 26-JUN-2001; 2001US-301299P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

DR WPI; 2003-201468/19.

DR N-PSDB; ABT23298.

PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -

PS Claim 6; Page 48; 98pp; English.

CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse peptide relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.

XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 24; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
1  
Db 1 YYGDYEGY 8

RESULT 7  
AA97235

ID AA97235 standard; Protein; 117 AA.

AC AA97235;

DT 19-DEC-2000 (first entry)

DE Variable heavy chain fragment of anti-SI (KDR) antibody.

KW Immunoglobulin; antibody; complementary determining region; CDR;  
KW VEGF; vascular endothelial growth factor; KDR;  
KW kinase insert domain containing receptor; multivalent; monovalent;  
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;  
KW glioblastoma multiforme; hemangioblastoma; AIDS;  
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;  
KW acquired immune deficiency syndrome; AIDS; human.

OS Homo sapiens.

OS Synthetic.

PN WO200044777-A1.

PD 03-AUG-2000.

PF 28-JAN-2000; 2000WO-US02180.

PR 29-JAN-1999; 99US-0117726.

PR 29-JAN-1999; 99US-0240736.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z, Witte L;

DR WPI; 2000-505966/45.

DR N-PSDB; AAA53767.

PT Novel immunoglobulin molecules binding kinase insert domain-containing  
PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growth

PS Claim 4; Page 50-51; 55pp; English.

CC New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Kaposi's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulins of the invention.

XX  
SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 21; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
1  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db 99 YYG DYEGY 106

RESULT 8  
ID AAE13143 standard; Protein; 117 AA.  
XX AAE13143;  
AC AAE13143;  
XX 28-JAN-2002 (first entry)  
DT 28-JAN-2002 (first entry)  
XX Humanised antibody heavy chain fragment.  
DE Humanised antibody heavy chain fragment.  
XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytosstatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;  
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;  
KW human; chimeric.  
XX Chimeric - Homo sapiens.  
OS Chimeric - Mus sp.  
XX WO200174296-A2.  
PN 11-OCT-2001.  
PD 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US10504.  
PF 30-MAR-2001; 2000US-0540770.  
PR 31-MAR-2000; 2000US-0540770.  
XX (IMCL-) IMCLONE SYSTEMS INC.  
PA (CORR ) CORNELL RES FOUND INC.  
XX Witte L, Rafi S;  
PI WPI; 2001-662942/76.  
XX N-PSDB; AAD21669.  
DR N-PSDB; AAD21669.  
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with  
PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
XX Claim 8; Page 15; 68pp; English.  
PS  
XX The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains mouse complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised  
CC antibody heavy chain frgament used in the exemplification of the  
CC invention.  
XX  
XX Sequence 117 AA;  
SQ

Query Match 100.0%; Score 51; DB 22; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
| | | | | | | |  
Db 99 YYGDYEGY 106

RESULT 9  
ID AAB82709 standard; Protein; 117 AA.  
XX

AC AAB82709;  
XX 15-OCT-2001 (first entry)  
DT 15-OCT-2001 (first entry)  
XX VEGF antagonist antibody IMC-1C11 heavy chain variable region.  
DE VEGF antagonist antibody IMC-1C11 heavy chain variable region.  
XX IMC-1C11, chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; heavy chain.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 26..35  
FT /label= CDR-H1  
FT /note= "complementarity determining region 1"  
FT 50..66  
FT /label= CDR-H2  
FT /note= "complementarity determining region 2"  
FT 99..106  
FT /label= CDR-H3  
FT /note= "complementarity determining region 3"  
XX  
XX WO200154723-A1.  
PN 02-AUG-2001.  
PD 02-AUG-2001.  
XX 29-JAN-2001; 2001WO-US02839.  
PF 28-JAN-2000; 2000US-0178791.  
PR 31-MAR-2000; 2000US-0539692.  
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX Kerbel R;  
PI WPI; 2001-514531/56.  
XX N-PSDB; AAH26405.  
DR  
XX Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX  
XX Disclosure; Page 38; 42pp; English.  
PS  
XX The present sequence is that of the heavy chain variable region of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
XX Sequence 117 AA;  
SQ

Query Match 100.0%; Score 51; DB 22; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
|||  
Db 99 YYGDYEGY 106

RESULT 10

AAE25955  
ID AAE25955 standard; Protein; 117 AA.

AC AAE25955;

DT 15-NOV-2002 (first entry)

DE Mouse anti-KDR p1C11 scFv antibody VH region #1.

XX  
KM Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KM foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KM VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
KM p1C11; scFv antibody.

OS Mus musculus.

PN US2002064528-A1.

PD 30-MAY-2002.

PF 12-OCT-2001; 2001US-0976787.

PR 28-JAN-2000; 2000US-0493539.

PA (ZHUZ/) ZHU Z.

XX (WITT/) WITTE L.

PI Zhu Z, Witte L;

DR WPI; 2002-589175/63.

DR N-PSDB; AAD42820.

PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR

PS Claim 4; Page 11; 34pp; English.

CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody  
CC heavy chain variable region (VH).

SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 23; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
|||  
Db 99 YYGDYEGY 106

RESULT 11

AAU74412

ID AAU74412 standard; peptide; 117 AA.

XX

AC AAU74412;  
XX 26-MAR-2002 (first entry)

DE Antigen-binding protein heavy chain variable domain (VH) #1.

XX  
KM Antigen-binding protein; antibody heavy chain variable domain;  
KM cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KM vascular endothelial growth factor receptor; VEGF;  
KM cell proliferation inhibitor.

OS Mus sp.

PN WO200190192-A2.

PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US16924.

PR 24-MAY-2000; 2000US-206749P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

DR WPI; 2002-106189/14.

DR N-PSDB; AAS20283.

PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides

PS Claim 57; Page 57; 64pp; English.

CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This sequence represents a heavy chain variable domain (VH) incorporated  
CC into Fv, an engineered protein containing a heavy chain variable domain  
CC and a light chain variable domain in one polypeptide chain, described in  
CC the method of the invention.

SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 23; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
|||  
Db 99 YYGDYEGY 106

RESULT 12

AAU74417

ID AAU74417 standard; peptide; 117 AA.

XX

AC AAU74417;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Antigen-binding protein heavy chain variable domain (VH) #2.  
XX  
KW Antigen-binding protein; antibody heavy chain variable domain;  
KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;  
KW cell proliferation inhibitor.  
XX  
OS Mus sp.  
XX  
PN WO200190192-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US16924.  
XX  
PR 24-MAY-2000; 2000US-206749P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2002-106189/14.  
DR N-PSDB; AAS20288.  
XX  
PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides -  
XX  
PS Claim 61; Page 60; 64pp; English.  
XX  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (C1 domain), and P2 has an antigen-binding  
CC site located to the N terminus of the C1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This sequence represents a heavy chain variable domain (VH) incorporated  
CC into Fv, an engineered protein containing a heavy chain variable domain  
CC and a light chain variable domain in one polypeptide chain, described in  
CC the method of the invention.  
XX  
SQ Sequence 117 AA;  
QY  
Db 1 YYG DYEGY 8  
99 YYG DYEGY 106

Query Match 100.0%; Score 51; DB 23; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13  
ABJ26724  
ID ABJ26724 standard; Protein; 117 AA.  
XX

AC ABJ26724;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE VEGF binding related protein SEQ ID No 7.  
XX  
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.  
XX  
OS Mus sp.  
XX  
PN WO2003002144-A1.  
XX  
PD 09-JAN-2003.  
XX  
PF 26-JUN-2002; 2002WO-US20332.  
XX  
PR 26-JUN-2001; 2001US-301299P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2003-201468/19.  
DR N-PSDB; ABT23302.  
XX  
PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -  
XX  
PS Claim 7; Page 49; 98pp; English.  
XX  
CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse protein relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX  
SQ Sequence 117 AA;  
QY  
Db 1 YYG DYEGY 8  
99 YYG DYEGY 106

Query Match 100.0%; Score 51; DB 24; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
ABJ26729  
ID ABJ26729 standard; Protein; 117 AA.  
XX  
AC ABJ26729;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE VEGF binding related protein SEQ ID No 22.  
XX  
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.  
XX  
OS Mus sp.  
XX  
PN WO2003002144-A1.  
XX

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XX 09-JAN-2003.
PD
XX 26-JUN-2002; 2002WO-US20332.
PF
XX 26-JUN-2001; 2001US-301299P.
PR
XX (IMCL-) IMCLONE SYSTEMS INC.
PA
XX Zhu Z;
PI
XX WPI; 2003-201468/19.
DR N-PSDB; ABT23307.
XX
PT New bispecific antibodies having antigen-binding sites specific for a
PT first vascular endothelial growth factor (VEGF) receptor and for a
PT second VEGF receptor, useful for inhibiting migration of leukemia
PT cells, or for treating tumors -
XX
XX Disclosure; Page 53; 98pp; English.
XX
CC The invention relates to a novel antibody having a first antigen binding
CC site specific for a first vascular endothelial growth factor (VEGF)
CC receptor and a second antigen-binding site specific for a second VEGF
CC receptor. The bispecific antigen-binding proteins block activation of the
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
CC cellular functions such as mitogenesis of vascular endothelial cells
CC and migration of leukaemia cells. The antibodies are useful for treating
CC tumours and for in vivo or in vitro for investigative and diagnostic
CC methods. This sequence represents a mouse protein relating to the
CC bispecific antibodies that bind to the VEGF receptors of the invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 51; DB 24; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
   |||||
   99 YYGDYEGY 106

Db

RESULT 15
AAE25965
ID AAE25965 standard; Protein; 135 AA.
XX
AC AAE25965;
XX
DT 15-NOV-2002 (first entry)
XX
DE Mouse anti-KDR p1C11 scFv antibody VH region #2.
XX
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;
KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;
KW p1C11; scFv antibody.
XX
OS Mus musculus.
XX
FH Key
FH Peptide 1.19
FT /label= Signal-peptide
FT 20.135
FT Protein /note= "Mouse p1C11 scFv antibody mature VH region"
FT Region 45.54
FT /note= "Heavy chain complementarity
FT determining region 1 (CDR-H1)"
FT 69.85
FT /note= "Heavy chain complementarity
FT determining region 2 (CDR-H2)"
FT 118.125
FT Region "
FT /note= "Heavy chain complementarity
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FT determining region 3 (CDR-H3)"
XX
XX US2002064528-A1.
PN
XX 30-MAY-2002.
PD
XX 12-OCT-2001; 2001US-0976787.
PF
XX 28-JAN-2000; 2000US-0493539.
PR
XX (ZHUZ/) ZHU Z.
PA (WITT/) WITTE L.
XX
PI Zhu Z, Witte L;
XX
XX WPI; 2002-589175/63.
DR N-PSDB; AAD42832.
XX
PT Novel immunoglobulin molecule for reducing tumor growth, binds to
PT kinase insert domain-containing receptor with an affinity comparable to
PT human vascular endothelial growth factor, and neutralizes activation of
PT KDR -
XX
XX Disclosure; Fig 4; 34pp; English.
XX
CC The present invention relates to novel immunoglobulin molecules that bind
CC to kinase insert domain-containing receptor (KDR) (a human homologue of
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable
CC to human vascular endothelial growth factor (VEGF) and that neutralises
CC activation of KDR. Sequences of the invention are useful for neutralising
CC the activation of KDR, for reducing tumour growth and for inhibiting
CC angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody
CC heavy chain variable region (VH).
XX
SQ Sequence 135 AA;

Query Match 100.0%; Score 51; DB 23; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8
   |||||
   118 YYGDYEGY 125

Db

Search completed: July 30, 2003, 09:36:45
Job time : 8 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:42:53 ; Search time 9.83389 Seconds  
(without alignments)  
96.613 Million cell updates/sec

Title: US-09-865-198-3  
Perfect score: 51  
Sequence: 1 YYGDYEGY 8

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	8	9	US-09-976-787-3 Sequence 3, Appli
2	51	100.0	8	10	US-09-865-198-3 Sequence 3, Appli
3	51	100.0	8	11	US-09-798-689-3 Sequence 3, Appli
4	51	100.0	117	9	US-09-976-787-7 Sequence 7, Appli
5	51	100.0	117	9	US-09-976-787-23 Sequence 23, Appli
6	51	100.0	117	10	US-09-865-198-7 Sequence 22, Appli
7	51	100.0	117	10	US-09-865-198-22 Sequence 22, Appli
8	51	100.0	117	11	US-09-798-689-7 Sequence 7, Appli
9	51	100.0	238	9	US-09-976-787-29 Sequence 29, Appli
10	51	100.0	238	10	US-09-865-198-28 Sequence 28, Appli
11	51	100.0	238	11	US-09-798-689-21 Sequence 21, Appli
12	51	100.0	240	9	US-09-976-787-28 Sequence 28, Appli
13	51	100.0	240	10	US-09-865-198-27 Sequence 27, Appli
14	37	72.5	335	10	US-09-821-687-11 Sequence 11, Appli
15	37	72.5	522	15	US-10-156-761-9497 Sequence 9497, Ap

	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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	633	633	663	663	680	680	68.6	68.6	68.6	68.6	1806	119	404	619	652	657	657	666	677	61	148	148	148	148	148	148	148	148	148	148
	10	11	14	15	14	15	15	11	10	15	15	10	15	10	9	9	9	9	9	US-10-231-778-215	US-09-946-374-336	US-10-052-586-360	US-10-176-758-360	US-10-175-737-360	US-10-173-706-360	US-10-175-738-360	US-10-175-752-360	US-10-176-482-360	US-10-176-757-360	
	Sequence 10, Appli	Sequence 128, App	Sequence 61, Appli	Sequence 61, Appli	Sequence 25, Appli	Sequence 25, Appli	Sequence 990, App	Sequence 990, App	Sequence 4492, App	Sequence 188, App	Sequence 13509, A	Sequence 5696, App	Sequence 11573, A	Sequence 2, Appli	Sequence 5896, App	Sequence 12135, A	Sequence 13013, A	Sequence 4933, App	Sequence 10663, A	Sequence 215, App	Sequence 336, App	Sequence 360, App	Sequence 360, App	Sequence 360, App	Sequence 360, App	Sequence 360, App	Sequence 360, App	Sequence 360, App	Sequence 360, App	

## ALIGNMENTS

RESULT 1  
US-09-976-787-3  
Sequence 3, Application US/09976787  
Patent No. US20020064528A1  
GENERAL INFORMATION:  
APPLICANT: Znu, Zhenping  
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
FILE REFERENCE: 11245/46505  
CURRENT APPLICATION NUMBER: US/09/976, 787  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 09/493, 539  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/117, 726  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 3  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-976-787-3

Query Match 100.0%; Score 51; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
DB 1 YYGDYEGY 8

RESULT 2  
US-09-865-198-3  
Sequence 3, Application US/09865198  
Patent No. US20020103345A1  
GENERAL INFORMATION:  
APPLICANT: Znu, Zhenping



```
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-3
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Query Match      100.0%; Score 51; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. NO. 4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 YYGDYEGY 8
        |||||
Db      1 YYGDYEGY 8
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## RESULT 3

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US-09-798-689-3
; Sequence 3, Application US/09798689
; Publication No. US20030103973A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-3
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Query Match      100.0%; Score 51; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. NO. 4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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        |||||
Db      1 YYGDYEGY 8
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## RESULT 4

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US-09-976-787-7
; Sequence 7, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
```

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; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-7
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Query Match      100.0%; Score 51; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. NO. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 YYGDYEGY 8
        |||||
Db      99 YYGDYEGY 106
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## RESULT 5

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US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23
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Query Match      100.0%; Score 51; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. NO. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 YYGDYEGY 8
        |||||
Db      99 YYGDYEGY 106
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## RESULT 6

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US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
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; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-7

Query Match 100.0%; Score 51; DB 10; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||  
Db 99 YYGDYEGY 106

## RESULT 7

US-09-865-198-22  
; Sequence 22, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; PRIOR FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 22  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-22

Query Match 100.0%; Score 51; DB 10; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||  
Db 99 YYGDYEGY 106

## RESULT 8

US-09-798-689-7  
; Sequence 7, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CTP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/326,552  
; PRIOR FILING DATE: 1994-10-20  
; PRIOR APPLICATION NUMBER: 08/196,041  
; PRIOR FILING DATE: 1994-02-10  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mouse

US-09-798-689-7

Query Match 100.0%; Score 51; DB 11; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||  
Db 99 YYGDYEGY 106

## RESULT 9

US-09-976-787-29  
; Sequence 29, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 29  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-29

Query Match 100.0%; Score 51; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.49;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||  
Db 99 YYGDYEGY 106

## RESULT 10

US-09-865-198-28  
; Sequence 28, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; PRIOR FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 28  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-28

Query Match 100.0%; Score 51; DB 10; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.49;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||  
Db 99 YYGDYEGY 106

## RESULT 11

US-09-798-689-21  
; Sequence 21, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; PRIORITY FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/326,552  
; PRIOR FILING DATE: 1994-10-20  
; PRIOR APPLICATION NUMBER: 08/196,041  
; PRIOR FILING DATE: 1994-02-10  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-798-689-21

Query Match 100.0%; Score 51; DB 11; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.49;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDIYEGY 8

Db 99 YYGDIYEGY 106

## RESULT 12

US-09-976-787-28  
; Sequence 28, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; PRIORITY FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 28  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-28

Query Match 100.0%; Score 51; DB 9; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDIYEGY 8

Db 99 YYGDIYEGY 106

## RESULT 13

US-09-865-198-27  
; Sequence 27, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; PRIORITY FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 27  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-27

Query Match 100.0%; Score 51; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYGDIYEGY 8

Db 99 YYGDIYEGY 106

## RESULT 14

US-09-821-687-11  
; Sequence 11, Application US/09821687  
; Patent No. US20020106724A1  
; GENERAL INFORMATION:  
; APPLICANT: MIKOSHIBA, KATSUHIKO  
; TITLE OF INVENTION: RNA-BINDING PROTEIN  
; FILE REFERENCE: 081356/0162  
; CURRENT APPLICATION NUMBER: US/09/821,687  
; PRIORITY FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: JP 2000-299812  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; OTHER INFORMATION: Description of Unknown Organism: m-hmrNPR  
US-09-821-687-11

Query Match 72.5%; Score 37; DB 10; Length 335;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDIYEGY 8

Db 172 YYDDYYGY 179

## RESULT 15

US-10-156-761-9497  
; Sequence 9497, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 9497  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-9497

Query Match 72.5%; Score 37; DB 15; Length 522;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDYEGY 8  
|||  
Db 333 GDYEGY 338

Search completed: July 30, 2003, 10:20:28  
Job time : 9.83389 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 2.57807 Seconds  
(without alignments)  
131.295 Million cell updates/sec

Title: US-09-865-198-3.  
Perfect score: 51  
Sequence: 1 YYGDYEGY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTus\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	76.5	11	3	US-08-467-580-43
2	39	76.5	11	5	PCT-US95-08516-43
3	36	70.6	525	3	US-09-113-750A-35
4	36	70.6	663	4	US-09-134-078-61
5	36	70.6	680	4	US-09-134-078-25
6	36	70.6	933	2	US-08-313-200-1
7	36	70.6	933	4	US-09-251-039-2
8	36	70.6	933	5	PCT-US93-03837-1
9	35	68.6	359	4	US-09-646-028-16
10	35	68.6	361	4	US-09-646-028-13
11	35	68.6	374	4	US-09-646-028-15
12	35	68.6	1507	6	5268270-2
13	34	66.7	116	2	US-08-888-366-12
14	34	66.7	139	3	US-09-136-315-2
15	34	66.7	139	3	US-09-136-315-6
16	34	66.7	213	4	US-09-252-991A-27051
17	34	66.7	301	4	US-09-328-352-4356
18	34	66.7	660	4	US-09-134-001C-3350
19	34	66.7	674	4	US-09-107-532A-6201
20	33.5	65.7	261	2	US-07-857-224B-61
21	33	64.7	11	3	US-08-467-580-42
22	33	64.7	11	5	PCT-US95-08516-42
23	33	64.7	120	4	US-09-252-991A-32408
24	33	64.7	174	4	US-09-522-714-28
25	33	64.7	369	4	US-09-328-352-5757
26	33	64.7	371	1	US-08-225-477B-8
27	33	64.7	371	5	PCT-US95-04353-8

28	33	64.7	389	4	US-09-055-765-13	Sequence 13, Appl
29	33	64.7	400	3	US-09-264-097-6	Sequence 6, Appl
30	33	64.7	402	4	US-09-055-765-14	Sequence 14, Appl
31	33	64.7	405	4	US-09-291-023A-20	Sequence 20, Appl
32	33	64.7	485	2	US-08-446-803-1	Sequence 1, Appl
33	33	64.7	485	2	US-08-446-803-2	Sequence 2, Appl
34	33	64.7	485	2	US-08-861-837-1	Sequence 1, Appl
35	33	64.7	485	2	US-08-861-837-2	Sequence 2, Appl
36	33	64.7	485	2	US-08-600-908A-12	Sequence 12, Appl
37	33	64.7	485	3	US-08-683-838A-12	Sequence 12, Appl
38	33	64.7	485	3	US-08-600-656-1	Sequence 1, Appl
39	33	64.7	485	3	US-08-600-656-2	Sequence 2, Appl
40	33	64.7	485	3	US-08-600-656-7	Sequence 7, Appl
41	33	64.7	485	3	US-09-170-670-1	Sequence 1, Appl
42	33	64.7	485	3	US-09-170-670-2	Sequence 2, Appl
43	33	64.7	485	3	US-09-170-670-6	Sequence 6, Appl
44	33	64.7	485	3	US-09-170-670-7	Sequence 7, Appl
45	33	64.7	485	3	US-09-170-670-8	Sequence 8, Appl

## ALIGNMENTS

## RESULT 1

US-08-467-580-43  
Sequence 43, Application US/08467580B  
Patent No. 6001809

## GENERAL INFORMATION:

APPLICANT: Thorsett, Eugene D  
APPLICANT: Yednock, Theodore A  
APPLICANT: Pleiss, Michael A  
TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion  
FILE REFERENCE: 123-US-CIP1  
CURRENT APPLICATION NUMBER: US/08/467,580B  
EARLIER FILING DATE: 1995-06-06  
EARLIER APPLICATION NUMBER: 08/273,055  
NUMBER OF SEQ ID NOS: 163  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 43  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide  
OTHER INFORMATION: derived from VCAM-1  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: ACETYLATION  
US-08-467-580-43

Query Match 76.5%; Score 39; DB 3; Length 11;  
Best Local Similarity 75.0%; Pred. No. 2.2;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
DB 3 YYGNYGGY 10

## RESULT 2

PCT-US95-08516-43  
Sequence 43, Application PC/TUS9508516

## GENERAL INFORMATION:

APPLICANT: ATHENA NEUROSCIENCES, INC.  
TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION  
NUMBER OF SEQUENCES: 157  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ATHENA NEUROSCIENCES, INC.  
STREET: 800 Gateway Blvd.  
CITY: South San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08516  
FILING DATE: 10-JUL-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/273,055  
FILING DATE: 11-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MOOI, LESLIE A.  
REGISTRATION NUMBER: 37,047  
REFERENCE/DOCKET NUMBER: 002010-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 877-0900  
TELEFAX: (415) 877-3620  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-08516-43

Query Match 76.5%; Score 39; DB 5; Length 11;  
Best Local Similarity 75.0%; Pred. No. 2.2;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||:|  
Db 3 YYGNYGY 10

## RESULT 3

US-09-113-750A-35  
Sequence 35, Application US/09113750A  
Patent No. 6294176  
GENERAL INFORMATION:  
APPLICANT: David E. Junker and Mark D. Cochran  
TITLE OF INVENTION: Recombinant Raccoonpox virus  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/113,750A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 55744  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 262-0400  
TELEFAX: (212) 664-0525  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 525 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-113-750A-35

Query Match 70.6%; Score 36; DB 3; Length 525;  
Best Local Similarity 75.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||:|  
Db 71 YSGDYENY 78

## RESULT 4

US-09-134-078-61  
Sequence 61, Application US/09134078  
Patent No. 6368844  
GENERAL INFORMATION:  
APPLICANT: Bylina, Edward J.  
TITLE OF INVENTION: GLYCOSIDASE ENZYMES  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
STREET: 4365 Executive Drive, Suite 1600  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92121

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,078  
FILING DATE: 13-AUG-1998  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/949,026  
FILING DATE: 10-OCT-1997  
APPLICATION NUMBER: 60/056,916  
FILING DATE: 06-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/024002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858/677-1456  
TELEFAX: 858/677-1465  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 663 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-134-078-61

Query Match 70.6%; Score 36; DB 4; Length 663;  
Best Local Similarity 62.5%; Pred. No. 3.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
|||:|  
Db 361 YYPDYDGF 368

## RESULT 5

US-09-134-078-25  
Sequence 25, Application US/09134078  
Patent No. 6368844

GENERAL INFORMATION:  
APPLICANT: Bylina, Edward J.  
TITLE OF INVENTION: GLYCOSIDASE ENZYMES  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
STREET: 4365 Executive Drive, Suite 1600  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,078  
FILING DATE: 13-AUG-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/949,026  
FILING DATE: 10-OCT-1997  
APPLICATION NUMBER: 60/056,916  
FILING DATE: 06-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/024002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858/677-1456  
TELEFAX: 858/677-1465  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 680 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-134-078-25

Query Match 70.6%; Score 36; DB 4; Length 680;  
Best Local Similarity 62.5%; Pred. No. 3.5e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YYGDYEGY 8  
Db 378 YYPDYDGF 385

RESULT 6  
US-08-313-200-1  
Sequence 1, Application US/08313200  
Patent No. 5998153  
GENERAL INFORMATION:  
APPLICANT: Baker, James R.  
APPLICANT: Koenig, Ronald J.  
TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/313,200

FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 20344-20658.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 933 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
DEVELOPMENTAL STAGE: Mature  
TISSUE TYPE: Thyroid gland(from people with Grave's  
TISSUE TYPE: disease)  
IMMEDIATE SOURCE:  
CLONE: pHTPO-2.8  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: join(1..3, 456..631)  
OTHER INFORMATION: /note= "TPO region within fusion  
OTHER INFORMATION: plasmid: TPO(delta4-455)"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
OTHER INFORMATION: /note= "C-terminal truncation:  
OTHER INFORMATION: TPO(1-120)"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..400  
OTHER INFORMATION: /note= "TPO epitopic region within  
OTHER INFORMATION: fusion protein: MBP-TPO (AA 1-400)"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..455  
OTHER INFORMATION: /note= "C-terminal truncation-  
OTHER INFORMATION: TPO(1-455) or N-terminal half of TPO"  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..631  
OTHER INFORMATION: /note= "C-terminal truncation:  
OTHER INFORMATION: TPO(1-631)"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 266..281  
OTHER INFORMATION: /note= "TPO epitopic or binding  
OTHER INFORMATION: region"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 376..631  
OTHER INFORMATION: /note= "TPO epitopic region within  
OTHER INFORMATION: fusion protein: MBP-TPO (AA 376-631)"  
FEATURE:  
NAME/KEY: Region  
LOCATION: join(455..532, 590..933)  
OTHER INFORMATION: /note= "alternatively spliced  
OTHER INFORMATION: C-terminus of TPO"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 455..933  
OTHER INFORMATION: /note= "TPO C-terminus containing  
OTHER INFORMATION: binding region"  
FEATURE:

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1 NAME/KEY: Region
2 LOCATION: 456..631 /note= "TPO binding or epitopic
3 OTHER INFORMATION: region"
4 FEATURE:
5 NAME/KEY: Region
6 LOCATION: 456..633 /note= "TPO binding or epitopic
7 OTHER INFORMATION: region"
8 FEATURE:
9 NAME/KEY: Region
10 LOCATION: 456..933 /note= "TPO region within maltose
11 OTHER INFORMATION: binding fusion protein"
12 FEATURE:
13 NAME/KEY: Region
14 LOCATION: 457..517 /note= "non-reactive fragment"
15 OTHER INFORMATION:
16 FEATURE:
17 NAME/KEY: Region
18 LOCATION: 457..633 /note= "TPO region within fusion
19 OTHER INFORMATION: plasmid pMalTPO"
20 FEATURE:
21 NAME/KEY: Region
22 LOCATION: 457..933 /note= "TPO binding region within
23 OTHER INFORMATION: plasmid pMalTPO"
24 FEATURE:
25 NAME/KEY: Region
26 LOCATION: 465..933 /note= "TPO binding region of
27 OTHER INFORMATION: maltose binding region fusion construct"
28 FEATURE:
29 NAME/KEY: Region
30 LOCATION: 513..633 /note= "recombinant TPO"
31 OTHER INFORMATION:
32 FEATURE:
33 NAME/KEY: Region
34 LOCATION: 517..630 /note= "TPO binding or epitopic
35 OTHER INFORMATION: region"
36 FEATURE:
37 NAME/KEY: Region
38 LOCATION: 517..633 /note= "TPO binding or epitopic
39 OTHER INFORMATION: region"
40 FEATURE:
41 NAME/KEY: Region
42 LOCATION: 573..633 /note= "TPO binding or epitopic
43 OTHER INFORMATION: region"
44 FEATURE:
45 NAME/KEY: Region
46 LOCATION: 590..611 /note= "TPO region within maltose
47 OTHER INFORMATION: binding fusion protein"
48 FEATURE:
49 NAME/KEY: Region
50 LOCATION: 590..615 /note= "TPO binding or epitopic
51 OTHER INFORMATION: region"
52 FEATURE:
53 NAME/KEY: Binding-site
54 LOCATION: 590..675 /note= "TPO binding or epitopic
55 OTHER INFORMATION: region"
56 FEATURE:

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; NAME/KEY: Region
; LOCATION: 592..613 /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; OTHER INFORMATION:
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; NAME/KEY: Region
; LOCATION: 596..611
; OTHER INFORMATION: /note= "Tpo region within fusion
; OTHER INFORMATION: protein"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 602..615
; OTHER INFORMATION: /note= "TPO region containing
; OTHER INFORMATION: divergent sequences"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 611..615
; OTHER INFORMATION: /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 631..933
; OTHER INFORMATION: /note= "TPO binding or epitopic
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 632..933
; OTHER INFORMATION: /note= "TPO region within maltose
; OTHER INFORMATION: binding fusion protein"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 633..768
; OTHER INFORMATION: /note= "TPO binding or epitopic
; OTHER INFORMATION:

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Query Match	70.6%	Score 36;	DB 2;	Length 933;
Best Local Similarity	75.0%	Pred. No. 4.7e+02;		
Matches 6; Conservative	0;	Mismatches 2;	Indels 0;	Caps 0;

QY	1	YYGDYEGY	8
Db	466	YVGPYEGY	473

## RESULT 7

```

US-09-251-039-2
/ Sequence 2, Application US/09251039
/ Patent No. 6528059
/ GENERAL INFORMATION:
/ APPLICANT: Baker, James R.
/ APPLICANT: Koenig, Ronald J.
/ APPLICANT: University of Michigan
/ TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
/ FILE REFERENCE: 203442065801
/ CURRENT APPLICATION NUMBER: US/09/251, 039
/ CURRENT FILING DATE: 1999-02-18
/ EARLIER APPLICATION NUMBER: 08/313, 200
/ EARLIER FILING DATE: 1994-11-08
/ EARLIER APPLICATION NUMBER: 07/885, 656
/ EARLIER FILING DATE: 1992-05-19
/ EARLIER APPLICATION NUMBER: PCT/US93/03837
/ EARLIER FILING DATE: 1993-04-22
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 933
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-251-039-2

```

Query Match	70.6%;	Score 36;	DB 4;	Length 933;
Best Local Similarity	75.0%;	Pred. No. 4.7e+02;		
Matches	6;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;

OY 1 YYGDYEGY 8  
| | | | |  
Db 466 YVGPEYEGY 473

## RESULT 8

PCT-US93-03837-1  
; Sequence 1, Application PC/TUS9303837  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Jr., James R.  
; APPLICANT: Koenig, Ronald J.  
; TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/03837  
; FILING DATE: 19930422  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lewak, Anna M.  
; REGISTRATION NUMBER: 33006  
; REFERENCE/DOCKET NUMBER: 2115-00656PPA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (313) 641-1600  
; TELEFAX: (313) 641-0270  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 933 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; DEVELOPMENTAL STAGE: Mature  
; TISSUE TYPE: Thyroid gland (from people with Grave's  
; DISEASE)  
; IMMEDIATE SOURCE:  
; CLONE: pHTPO-2.8  
; PUBLICATION INFORMATION:  
; AUTHORS: Kimura, S.  
; AUTHORS: Kotani, T.  
; AUTHORS: McBride, O. W.  
; AUTHORS: Umeki, K.  
; AUTHORS: Nakayama, T.  
; AUTHORS: Ohtaki, S.  
; AUTHORS: Hirai, K.  
; TITLE: Human thyroid peroxidase: Complete cDNA and  
; TITLE: protein sequence, chromosome mapping, and  
; TITLE: identification of two alternately spliced mRNAs  
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.  
; VOLUME: 84  
; PAGES: 5555-5559  
; DATE: 1987  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 3048  
; PCT-US93-03837-1

Query Match 70.6%; Score 36; DB 5; Length 933;  
Best Local Similarity 75.0%; Pred. No. 4.7e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
| | | | |  
Db 466 YVGPEYEGY 473

## RESULT 9

US-09-646-028-16  
; Sequence 16, Application US/09646028  
; Patent No. 6562347  
; GENERAL INFORMATION:  
; APPLICANT: Kwak, Larry  
; APPLICANT: Biragyn, Arya  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES  
; FILE REFERENCE: 14014.0316/P  
; CURRENT APPLICATION NUMBER: US/09/646,028  
; PRIOR FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/077,745  
; PRIOR FILING DATE: 1998-03-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 359  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-16

Query Match 68.6%; Score 35; DB 4; Length 359;  
Best Local Similarity 75.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
| | | | |  
Db 194 YDGSYEGY 201

## RESULT 10

US-09-646-028-13  
; Sequence 13, Application US/09646028  
; Patent No. 6562347  
; GENERAL INFORMATION:  
; APPLICANT: Kwak, Larry  
; APPLICANT: Biragyn, Arya  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES  
; FILE REFERENCE: 14014.0316/P  
; CURRENT APPLICATION NUMBER: US/09/646,028  
; PRIOR FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/077,745  
; PRIOR FILING DATE: 1998-03-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-13

Query Match 68.6%; Score 35; DB 4; Length 361;  
Best Local Similarity 75.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
| | | | |  
Db 196 YDGSYEGY 203

RESULT 11  
US-09-646-028-15



; Sequence 15, Application US/09646028  
; Patent No. 6562347  
; GENERAL INFORMATION:  
; APPLICANT: Kwak, Larry  
; APPLICANT: Biragyn, Arya  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
; FILE REFERENCE: 14014.0316/P  
; CURRENT APPLICATION NUMBER: US/09/646,028  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/077,745  
; PRIOR FILING DATE: 1998-03-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-15.

Query Match 68.6%; Score 35; DB 4; Length 374;  
Best Local Similarity 75.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
Db 319 YDGSYEGY 326

RESULT 12  
5268270-2  
; Patent No. 5268270  
; APPLICANT: Meyer, Thomas F.; Halter, Roman; Pohlner, Johannes  
; TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM  
; NEGATIVE HOST CELLS  
; NUMBER OF SEQUENCES: 6  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/171,872  
; FILING DATE: 01-JUL-1987  
; SEQ ID NO: 2  
; LENGTH: 1507  
5268270-2

Query Match 68.6%; Score 35; DB 6; Length 1507;  
Best Local Similarity 62.5%; Pred. No. 1.1e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
Db 110 YYGQYNGH 117

RESULT 13  
US-08-888-366-12  
; Sequence 12, Application US/08888366  
; Patent No. 5972656  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Osvaldo  
; APPLICANT: Wylie, Dwane E.  
; APPLICANT: Wagner, Fred W.  
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/888,366  
; FILING DATE: 03-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/187,407  
; FILING DATE: 27-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,542  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/493,299  
; FILING DATE: 14-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/324,392  
; FILING DATE: 14-MAR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.39USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-888-366-12.

Query Match 66.7%; Score 34; DB 2; Length 116;  
Best Local Similarity 62.5%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
Db 96 YXGNYEWF 103

RESULT 14  
US-09-136-315-2  
; Sequence 2, Application US/09136315B  
; Patent No. 6228360  
; GENERAL INFORMATION:  
; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND  
; TITLE OF INVENTION: FACTOR MONOCLONAL ANTIBODY  
; FILE REFERENCE: 0010-0933-0  
; CURRENT APPLICATION NUMBER: US/09/136,315B  
; CURRENT FILING DATE: 1998-08-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 139  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-136-315-2

Query Match 66.7%; Score 34; DB 3; Length 139;  
Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YYGDYEGY 8  
Db 119 YXGSYGGF 126

RESULT 15

US-09-136-315-6  
 ; Sequence 6, Application US/09136315B  
 ; Patent No. 6228360  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CO, MAN SUNG  
 ; APPLICANT: VASQUEZ, MAXIMILIANO  
 ; TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND  
 ; FILE REFERENCE: 0010-0933-0  
 ; CURRENT APPLICATION NUMBER: US/09/136,315B  
 ; CURRENT FILING DATE: 1998-08-19  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 139  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA  
 US-09-136-315-6

Query Match 66.7%; Score 34; DB 3; Length 139;  
 Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YYGDYEGY 8  
 |||||  
 Db 119 YGSGYGGF 126

Search completed: July 30, 2003, 09:38:28  
 Job time : 3.57807 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 10 Seconds  
(without alignments)  
158.727 Million cell updates/sec

Title: US-09-865-198-4  
Perfect score: 48  
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	10	18	AAW27424
2	48	100.0	10	19	AAW73169
3	48	100.0	10	20	AAV28390
4	48	100.0	10	21	AAV97232
5	48	100.0	10	21	AAV77582
6	48	100.0	10	21	AAV77588
7	48	100.0	10	22	AAE13140
8	48	100.0	10	22	AAB82706
9	48	100.0	10	22	AAB83163

10	48	100.0	10	22	AAB78851	Anti-human Flt-1 a
11	48	100.0	10	22	AAB78857	Anti-human Flt-1 a
12	48	100.0	10	23	AAE25952	Mouse anti-KDR p1c
13	48	100.0	10	23	AAU74409	Light chain comple
14	48	100.0	10	23	AAU70361	Mouse kappa VI lig
15	48	100.0	10	24	ABJ26721	VEGF binding relat
16	48	100.0	55	24	ABU56871	BoNT/A Hc binding
17	48	100.0	55	24	ABU56877	BoNT/A Hc binding
18	48	100.0	55	24	ABU56878	BoNT/A Hc binding
19	48	100.0	55	24	ABU56882	BoNT/A Hc binding
20	48	100.0	96	22	AAU08982	Single-chain antib
21	48	100.0	99	22	AAU08981	Single-chain antib
22	48	100.0	102	11	AAU07321	VK domain of antib
23	48	100.0	102	17	AAW14489	Monoclonal antibod
24	48	100.0	102	17	AAU99872	Monoclonal antibod
25	48	100.0	103	13	AAU26002	L-chain variable r
26	48	100.0	105	17	AAW03182	Guy's 13 anti-Stre
27	48	100.0	106	22	AAE13144	Humanised antibody
28	48	100.0	106	23	ABJ10396	Anti-mesothelin Fv
29	48	100.0	106	23	ABJ10397	Mutant anti-mesoth
30	48	100.0	106	23	AAU99519	Humanised antibody
31	48	100.0	106	23	AAU99521	Humanised antibody
32	48	100.0	106	23	AAU99523	Humanised antibody
33	48	100.0	106	23	AAU99524	Humanised antibody
34	48	100.0	106	23	AAU99525	Humanised antibody
35	48	100.0	106	23	AAU99526	Humanised antibody
36	48	100.0	106	23	AAU99527	Humanised antibody
37	48	100.0	106	23	AAU99539	Humanised antibody
38	48	100.0	106	23	AAU99540	Humanised antibody
39	48	100.0	106	23	AAU99541	Humanised antibody
40	48	100.0	106	23	AAU99542	Humanised antibody
41	48	100.0	106	23	AAU99543	Humanised antibody
42	48	100.0	106	23	AAU99544	Humanised antibody
43	48	100.0	106	23	AAU99545	Humanised antibody
44	48	100.0	106	23	AAU99546	Humanised antibody
45	48	100.0	106	23	AAU99547	Humanised antibody

ALIGNMENTS

RESULT 1  
ID AAW27424 standard; peptide; 10 AA.  
AAW27424;  
AC AAW27424;  
XX  
DT 19-DEC-1997 (first entry)  
XX  
DE CDR1 from light chain variable region of KM1486 antibody.  
XX  
KW Complementarity determining region; CDR; light chain; treatment;  
KW variable region; murine; mouse; human; interleukin 5; IL-5;  
KW receptor; alpha chain; monoclonal antibody; hybridoma; detection;  
KW assay; diagnosis; allergic respiratory disease; chronic bronchitis;  
XX  
OS Mus spp.  
XX  
PN W09710354-A1.  
XX  
PD 20-MAR-1997.  
XX  
PF 11-SEP-1996; 96WO-JP02588.  
XX  
PR 11-SEP-1995; 95JP-0232384.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Anazawa H, Furuya A, Hanai N, Iida A, Koike M;  
XX Nakamura K, Takatsu K;  
DR WPI; 1997-202249/18.  
XX

PT Antibody against alpha-chain of human interleukin 5 receptor -  
PT useful for diagnosis and treatment of respiratory allergic diseases,  
PT e.g. chronic bronchitis  
XX  
PS Claim 10; Page 165; 238pp; Japanese.  
XX  
CC The present sequence is complementarity determining region 1 (CDR1)  
CC from the light chain variable region of the murine anti-human  
CC interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal  
CC antibody (Mab) KM1486. KM1486 is produced by the hybridoma  
CC FERM BP-5651, which was prepared by immunising Balb/c mice with  
CC hIL-5R alpha, fusing spleen cells obtained from the mice with mouse  
CC myeloma P3-U1 cells and screening the resultant hybridomas. The Mab  
CC can be used to detect or assay for hIL-5R alpha and cells  
CC expressing it on their surface, especially to diagnose allergic  
CC respiratory diseases, e.g. chronic bronchitis. It can also be used  
CC to treat such diseases.  
XX  
SQ Sequence 10 AA;  
  
Query Match 100.0%; Score 48; DB 18; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 SASSSVSYMH.10  
DB 1 SASSSVSYMH 10  
  
RESULT 2  
AAW73169  
ID AAW73169 standard; peptide; 10 AA.  
XX  
AC AAW73169;  
XX  
DT 22-JAN-1999 (first entry)  
XX  
DE CDR1 of light chain of ganglioside GM2 targeting antibody.  
XX  
KW Ganglioside GM2; antibody; complementarity determining region; cancer;  
KW anti-tumour agent.  
XX  
OS Homo sapiens.  
XX  
PN JP10257893-A.  
XX  
PD 29-SEP-1998.  
XX  
PF 19-MAR-1997; 97JP-0066981.  
XX  
PR 19-MAR-1997; 97JP-0066981.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
DR WPI; 1998-575904/49.  
XX  
XX  
PT A human type complementarity determining region transplanted  
PT antibody against ganglioside GM2 - useful as an anti-tumour agent  
PT and as a diagnostic for related cancers  
XX  
PS Claim 1; Page 29; 66pp; Japanese.  
XX  
CC This sequence represents a complementarity determining region (CDR) from  
CC the heavy chain of the antibody of the invention. The antibody of the  
CC invention is a human CDR transplanted antibody that reacts specifically  
CC with ganglioside GM2. DNA encoding the antibody, and vectors and  
CC transformants containing it, can be used for the recombinant production  
CC of the antibody. The antibody itself can be used as an anti-tumour agent  
CC or as a diagnostic tool for related cancers. The antibody has antitumour  
CC activity against ganglioside GM2 positive cells.  
XX  
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 19; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 SASSSVSYMH 10  
DB 1 SASSSVSYMH 10  
  
RESULT 3  
AA28390  
ID AAY28390 standard; Protein; 10 AA.  
XX  
AC AAY28390;  
XX  
DT 04-NOV-1999 (first entry)  
XX  
DE Peptide fragment from the human anti-GM2 light chain in REI.  
XX  
KW antibody; REI; complementarity determining region; CDR;  
KW chimeric; light chain; heavy chain.  
XX  
OS Homo sapiens.  
XX  
PN US5939532-A.  
XX  
PD 17-AUG-1999.  
XX  
PF 07-JUN-1995; 95US-0483528.  
XX  
PR 07-JUN-1995; 95US-0483528.  
PR 07-SEP-1993; 93US-0116778.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;  
PI Shitara K;  
XX  
DR WPI; 1999-468416/39.  
XX  
PT Chimeric human antibody expression vectors  
XX  
PS Example 2; Column 157; 188pp; English.  
XX  
CC The sequences AAY28390 to AAY28392 replace the CDR regions of the NEMM  
CC DNA and they produce AAY28394, the hKM796L human anti-GM2 antibody light  
CC chain.  
CC Chimeric human antibodies of the invention are useful in the treatment  
CC of cancer, especially that which is of neural ectodermal origin.  
CC In contrast to prior art constructs based on mouse monoclonal  
CC antibodies, the chimeric human antibodies do not cause anti-mouse  
CC immunoglobulin production.  
CC The chimeric human antibodies have a prolonged half-life and a reduced  
CC frequency of adverse effects when compared to mouse monoclonal  
CC antibodies.  
XX  
SQ Sequence 10 AA;  
  
Query Match 100.0%; Score 48; DB 20; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 SASSSVSYMH 10  
DB 1 SASSSVSYMH 10  
  
RESULT 4  
AAY97232  
ID AAY97232 standard; Protein; 10 AA.  
XX  
AC AAY97232;  
XX



DT 19-DEC-2000 (first entry)  
XX  
DE Complementary determining region (CDRL1) of anti-SI(KDR) antibody.  
XX  
KW Immunoglobulin; antibody; complementary determining region; CDR;  
KW VEGF; vascular endothelial growth factor; KDR;  
KW kinase insert domain containing receptor; multivalent; monovalent;  
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;  
KW glioblastoma multiforme; hemangioblastoma; AIDS;  
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;  
KW acquired immune deficiency syndrome; AIDS; human.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200044777-A1.  
XX  
PD 03-AUG-2000.  
XX  
PF 28-JAN-2000; 2000WO-US02180.  
XX  
PR 29-JAN-1999; 99US-0117726.  
PR 29-JAN-1999; 99US-0240736.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z, Witte L;  
XX  
DR WPI; 2000-505966/45.  
DR N-PSDB; AAA53764.  
XX  
PT Novel immunoglobulin molecules binding kinase insert domain-containing  
PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growth  
XX  
PS Claim 3; Page 50; 55pp; English.  
XX  
CC New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Kaposi's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulins of the invention.  
XX  
SQ Sequence 10 AA;  
QY  
Db 1 SASSSVSYMH 10  
1 SASSSVSYMH 10

Query Match 100.0%; Score 48; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
ID AAY77582 standard; peptide; 10 AA.  
XX  
AC AAY77582;  
XX  
DT 08-MAY-2000 (first entry)  
XX  
DE Anti-human VEGF receptor Flt-1 antibody CDR peptide sequence.

XX  
KW Antibody; human; vascular endothelial growth factor; VEGF receptor;  
KW Flt-1; neovascularisation; cell proliferation; metastasis; tumour;  
KW rheumatoid arthritis; retinopathy; psoriasis.  
XX  
OS Mus musculus.  
XX  
PN WO9960025-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-JP02661.  
XX  
PR 20-MAY-1998; 98JP-0139000.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Shitara K, Ito M, Kawada Y, Nakamura K;  
XX  
DR WPI; 2000-072431/06.  
XX  
PT Gene recombinant antibodies, useful for diagnosis and as remedies for  
PT diseases due to abnormal neovascularization e.g. proliferation or  
PT metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy  
PT and psoriasis  
XX  
PS Claim 10; Page 159; 210pp; Japanese.  
XX  
CC The invention relates to a gene recombinant antibody that has specific  
CC reaction with human vascular endothelial growth factor (VEGF) receptor  
CC Flt-1. The antibodies are useful for diagnosis and as remedies for  
CC diseases due to abnormal neovascularisation such as proliferation or  
CC metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic  
CC retinopathy, premature retinopathy and psoriasis.  
XX  
SQ Sequence 10 AA;  
QY  
Db 1 SASSSVSYMH 10  
1 SASSSVSYMH 10

Query Match 100.0%; Score 48; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
ID AAY77588 standard; peptide; 10 AA.  
XX  
AC AAY77588;  
XX  
DT 08-MAY-2000 (first entry)  
XX  
DE Anti-human VEGF receptor Flt-1 antibody CDR peptide sequence.  
XX  
KW Antibody; human; vascular endothelial growth factor; VEGF receptor;  
KW Flt-1; neovascularisation; cell proliferation; metastasis; tumour;  
KW rheumatoid arthritis; retinopathy; psoriasis.  
XX  
OS Mus musculus.  
XX  
PN WO9960025-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-JP02661.  
XX  
PR 20-MAY-1998; 98JP-0139000.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Shitara K, Ito M, Kawada Y, Nakamura K;

XX WPI; 2000-072431/06.  
DR  
XX  
PT Gene recombinant antibodies, useful for diagnosis and as remedies for  
PT diseases due to abnormal neovascularization e.g. proliferation or  
PT metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy  
PT and psoriasis  
XX  
PS Claim 10; Page 161; 210pp; Japanese.  
XX  
CC The invention relates to a gene recombinant antibody that has specific  
CC reaction with human vascular endothelial growth factor (VEGF) receptor  
CC Flt-1. The antibodies are useful for diagnosis and as remedies for  
CC diseases due to abnormal neovascularisation such as proliferation or  
CC metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic  
CC retinopathy, premature retinopathy and psoriasis.  
XX  
SQ Sequence 10 AA;  
OY  
Query Match 100.0%; Score 48; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 SASSSVSYMH 10  
1 SASSSVSYMH 10  
RESULT 7  
AAE13140  
ID AAE13140 standard; peptide; 10 AA.  
AC AAE13140;  
XX 28-JAN-2002 (first entry)  
DT  
XX Humanised antibody murine light chain hypervariable region (VL) CDR1.  
DE  
XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytosolic; light chain hypervariable region; VL; myelocytic leukaemia;  
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;  
KW Hodgkin's disease; complementarity determining region-1; CDR-1; mouse.  
XX  
OS Mus sp.  
XX WO200174296-A2.  
PN  
XX 11-OCT-2001.  
PD  
XX 30-MAR-2001; 2001WO-US10504.  
PF  
XX 31-MAR-2000; 2000US-0540770.  
PR  
XX (IMCL-) IMCLONE SYSTEMS INC.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Witte L, Rafii S;  
XX  
DR WPI; 2001-662942/76.  
DR N-PSDB; AAD21666.  
XX  
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with  
PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
PS Claim 8; Page 14; 68pp; English.  
XX  
XX The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised

CC mouse variable region contains mouse complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised  
CC antibody murine light chain hypervariable region (VL) CDR-1 used in the  
CC exemplification of the invention.  
XX  
SQ Sequence 10 AA;  
OY  
Query Match 100.0%; Score 48; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 SASSSVSYMH 10  
1 SASSSVSYMH 10  
RESULT 8  
AAB82706  
ID AAB82706 standard; Peptide; 10 AA.  
AC AAB82706;  
XX 15-OCT-2001 (first entry)  
DT  
XX VEGF antagonist antibody IMC-1C11 VL CDR-1.  
DE  
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; light chain; CDR;  
KW complementarity determining region.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX WO200154723-A1.  
PN  
XX 02-AUG-2001.  
PD  
XX 29-JAN-2001; 2001WO-US02839.  
PF  
XX 28-JAN-2000; 2000US-0178791.  
PR 31-MAR-2000; 2000US-0539692.  
XX  
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Kerbel R;  
XX  
DR WPI; 2001-514531/56.  
DR  
XX  
XX Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX  
PS Disclosure; Page 37; 42pp; English.  
XX  
XX The present sequence is that of complementarity determining region  
CC 1 of the light chain variable region (see also AAB82702) of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an

CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
|||  
Db 1 SASSSVSVMH 10

RESULT 9  
AAB83163  
ID AAB83163 standard; peptide; 10 AA.

AC AAB83163;

DT 02-JUL-2001 (first entry)

XX Mouse ganglioside GM2 antibody light chain variable region CDR1.

KW Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer;  
KM complementarity determining region; CDR.

OS Mus sp.

PN WO200123431-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP06775.

PR 30-SEP-1999; 99JP-0278292.

PA (KYOW ) KYOWA HAKKO KOGYO KK.

PI Hanai N, Nakamura K, Niwa R;

DR WPI; 2001-266142/27.

PT Monoclonal antibodies against ganglioside GM2 combined with drugs,  
PT radioisotopes or proteins for treatment and diagnosis of cancer -

PS Claim 4; Page 71; 80pp; Japanese.

CC The present invention relates to derivatives of an antibody against  
CC ganglioside GM2. The antibody may be a monoclonal antibody or its  
CC fragments. The antibody is combined with a radioactive isotope,  
CC protein or small drug in the treatment and diagnosis of cancer.

SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
|||  
Db 1 SASSSVSVMH 10

RESULT 10  
AAB78851  
ID AAB78851 standard; Peptide; 10 AA.  
XX  
AC AAB78851;  
DT 20-APR-2001 (first entry)  
XX  
XX Anti-human Flt-1 antibody KM1732 L chain V region CDR 1 peptide.  
DE  
XX  
XX Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;  
KW vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;  
KM delayed hypersensitivity; malignant tumour; arteriosclerosis.  
XX  
KW Mus musculus.

PN WO200079275-A1.

PD 28-DEC-2000.

PF 16-JUN-2000; 2000WO-JP03957.

PR 17-JUN-1999; 99JP-0171709.

PA (KYOW ) KYOWA HAKKO KOGYO KK.

PI Shtara K, Shibuya M;

DR WPI; 2001-080847/09.

PT Substances binding to human vascular endothelial growth factor receptor  
PT Flt-1, used for diagnosis and treatment of inflammatory diseases,  
PT arteriosclerosis, cancer and delayed hypersensitivity -

PS Example 3; Page 127; 164pp; Japanese.

CC This invention relates to a reagent for detecting differentiation of  
CC monocytes and macrophages from haematopoietic stem cells, containing a  
CC substance which binds to human vascular endothelial growth factor (VEGF)  
CC receptor Flt-1. The invention also includes a method for diagnosing a  
CC disease in which the differentiation of monocytes and macrophages is  
CC implicated, using the reagent, and an agent for the treatment of diseases  
CC diagnosed using the method, containing a substance which binds to Flt-1  
CC or a substance which inhibits the signal transduction of Flt-1. Diseases  
CC which may be diagnosed or treated include inflammation, delayed  
CC hypersensitivity, malignant tumours and arteriosclerosis.  
CC AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences  
CC encoding anti-human Flt-1 monoclonal antibody fragments, and  
CC oligonucleotides used in the construction of the antibody. The monoclonal  
CC antibody is used in the reagent of the invention. PCR primers AAF70245 -  
CC AAF78870 (excluding AAF70251) are used in the isolation of the antibody  
CC DNA sequences. Protein sequences AAB78848 - AAB78870 represent fragments  
CC of the anti-human Flt-1 antibody.

SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
|||  
Db 1 SASSSVSVMH 10

RESULT 11  
AAB78857  
ID AAB78857 standard; Peptide; 10 AA.

AC AAB78857;

DT 20-APR-2001 (first entry)

DE Anti-human Flt-1 antibody KM1750 L chain V region CDR 1 peptide.  
XX  
KW Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;  
KW vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;  
KW delayed hypersensitivity; malignant tumour; arteriosclerosis.  
XX  
OS Mus musculus.  
XX  
PN WO200079275-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 16-JUN-2000; 2000WO-JP03957.  
XX  
PR 17-JUN-1999; 99JP-0171709.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Shitara K, Shibuya M;  
XX  
DR WPI; 2001-080847/09.  
XX  
PT Substances binding to human vascular endothelial growth factor receptor  
PT Flt-1, used for diagnosis and treatment of inflammatory diseases,  
PT arteriosclerosis, cancer and delayed hypersensitivity -  
XX  
PS Example 3; Page 128; 164pp; Japanese.  
XX  
CC This invention relates to a reagent for detecting differentiation of  
CC monocytes and macrophages from haematopoietic stem cells, containing a  
CC substance which binds to human vascular endothelial growth factor (VEGF)  
CC receptor Flt-1. The invention also includes a method for diagnosing a  
CC disease in which the differentiation of monocytes and macrophages is  
CC implicated, using the reagent, and an agent for the treatment of diseases  
CC diagnosed using the method, containing a substance which binds to Flt-1  
CC or a substance which inhibits the signal transduction of Flt-1. Diseases  
CC which may be diagnosed or treated include inflammation, delayed  
CC hypersensitivity, malignant tumours and arteriosclerosis.  
CC AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences  
CC encoding anti-human Flt-1 monoclonal antibody fragments, and  
CC oligonucleotides used in the construction of the antibody. The monoclonal  
CC antibody is used in the reagent of the invention. PCR primers AAF70245 -  
CC AAF78870 (excluding AAF70251) are used in the isolation of the antibody  
CC DNA sequences. Protein sequences AAB78848 - AAB78870 represent fragments  
CC of the anti-human Flt-1 antibody.  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 100.0%; Score 48; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10  
XX  
RESULT 12  
AAE25952  
ID AAE25952 standard; peptide; 10 AA.  
XX  
AC AAE25952;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Mouse anti-KDR pIC11 scFv antibody CDR1 peptide.  
XX  
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; light chain complementarity determining region 1;  
KW CDR1; angiogenesis; pIC11; scFv antibody.  
XX  
OS Mus musculus.

XX  
PN US2002064528-A1.  
XX  
PD 30-MAY-2002.  
XX  
PF 12-OCT-2001; 2001US-0976787.  
XX  
PR 28-JAN-2000; 2000US-0493539.  
XX  
PA (ZHUZ/) ZHU Z.  
PA (WITT/) WITTE L.  
XX  
PI Zhu Z, Witte L;  
XX  
DR WPI; 2002-589175/63.  
DR N-PSDB; AAD42817.  
XX  
PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR -  
XX  
PS Claim 3; Page 11; 34pp; English.  
XX  
CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR pIC11 scFv antibody  
CC light chain complementarity determining region 1 (CDRL1).  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 100.0%; Score 48; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10  
XX  
RESULT 13  
AAU74409  
ID AAU74409 standard; peptide; 10 AA.  
XX  
AC AAU74409;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Light chain complementarity determining region L1 (CDRL1).  
XX  
KW Complementarity determining region; CDR; CDR1; antigen; cytostatic;  
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;  
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;  
KW antibody light chain variable domain.  
XX  
OS Mus sp.  
XX  
PN WO200190192-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US16924.  
XX  
PR 24-MAY-2000; 2000US-206749P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX



DR WPI; 2002-106189/14.  
DR N-PSDE; AAS20280.  
XX  
PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides  
XX  
PS Claim 55; Page 56; 64pp; English.  
XX  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (CL domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This peptide sequence represents the light chain variable domain  
CC complementarity determining region L1 (CDRL1) incorporated into an  
CC antigen-binding protein described in the method of the invention.  
XX  
SQ Sequence 10 AA;  
QY  
Query Match 100.0%; Score 48; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 SASSSSVSYMH 10  
1 SASSSSVSYMH 10  
RESULT 14  
AAU70361  
ID AAU70361 standard; Peptide; 10 AA.  
XX  
AC AAU70361;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Mouse Kappa VI light chain CDR1.  
XX  
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
KW complementarity determining region; framework region; IgBP;  
KW transgenic plant; immunoglobulin binding protein array;  
KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.  
XX  
OS Mus musculus.  
XX  
PN WO200183806-A1.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14349.  
XX  
PR 02-MAY-2000; 2000US-0563222.  
XX  
PA (EPIC-) EPICYTE PHARM INC.  
XX  
PI Hiatt AC, Hein MB;  
XX  
DR WPI; 2002-055482/07.

XX  
PT Preparing immunoglobulin binding protein array in plant cells by  
PT transforming the cells with different polynucleotides encoding binding  
PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array  
XX  
PS Disclosure; Page 14; 129pp; English.  
XX  
CC The invention relates to transforming a population of cells (e.g. plant  
CC cells), comprising using a library of two different polynucleotides  
CC encoding different immunoglobulin binding protein (IgBP) polypeptides  
CC that specifically bind to a ligand or form one or more disulphide bonds  
CC with polypeptides in transfected cells, to generate an IgBP that  
CC binds to a ligand, and transformed plant cells are selected, and  
CC preparing an IgBP array in plant cells. At least one peptide sequence has  
CC at least 75% sequence identity to a framework region (FR) of a native  
CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.  
CC The method is useful for preparing an immunoglobulin binding protein  
CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic  
CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)  
CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The  
CC CHBP is useful for discovery of e.g. screening assays of IgBPs having  
CC desired characteristics. The present sequence is a mammalian  
CC immunoglobulin derived peptide that may be incorporated into an IgBP of  
CC the invention.  
XX  
SQ Sequence 10 AA;  
QY  
Query Match 100.0%; Score 48; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 SASSSSVSYMH 10  
1 SASSSSVSYMH 10  
RESULT 15  
ABJ26721  
ID ABJ26721 standard; Peptide; 10 AA.  
XX  
AC ABJ26721;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE VEGF binding related peptide SEQ ID No 4.  
XX  
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.  
XX  
OS Mus sp.  
XX  
PN WO2003002144-A1.  
XX  
PD 09-JAN-2003.  
XX  
PF 26-JUN-2002; 2002WO-US20332.  
XX  
PR 26-JUN-2001; 2001US-301299P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2003-201468/19.  
DR N-PSDB; ABT23299.  
XX  
PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors  
XX



PS Claim 6; Page 48; 98pp; English.  
XX  
CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse peptide relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX  
SQ Sequence 10 AA;

Query Match 100.0%; Score 48; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10  
|||  
Db 1 SASSSVSYMH 10

Search completed: July 30, 2003, 09:36:46  
Job time : 11 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 2.95681 Seconds  
(without alignments)  
325.245 Million cell updates/sec

Title: US-09-865-198-4  
Perfect score: 48  
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	91	2	S17629	Ig kappa chain V r
2	48	100.0	91	2	S17637	Ig kappa chain V r
3	48	100.0	91	2	S17639	Ig kappa chain V r
4	48	100.0	94	2	S20650	Ig heavy chain V r
5	48	100.0	94	2	S20653	Ig heavy chain V r
6	48	100.0	97	2	S26341	Ig light chain V r
7	48	100.0	97	2	PH1084	Ig light chain V r
8	48	100.0	99	2	D38601	Ig kappa chain V r
9	48	100.0	100	2	S29590	Ig kappa chain V r
10	48	100.0	102	2	S11115	Ig kappa chain V r
11	48	100.0	102	2	S24214	Ig kappa chain V r
12	48	100.0	103	2	S29591	Ig kappa chain V r
13	48	100.0	104	2	B49049	Ig kappa chain V r
14	48	100.0	106	2	B54378	Ig light chain V r
15	48	100.0	106	2	PS0071	Ig kappa chain V r
16	48	100.0	106	2	PS0072	Ig kappa chain V r
17	48	100.0	106	2	S11114	Ig kappa chain V r
18	48	100.0	106	2	S11120	Ig kappa chain V r
19	48	100.0	107	1	KVMSX4	Ig kappa chain V r
20	48	100.0	107	2	A30562	Ig kappa chain V r
21	48	100.0	107	2	B30562	Ig kappa chain V r
22	48	100.0	107	2	PT0395	Ig light chain V r
23	48	100.0	107	2	PT0398	Ig light chain V r
24	48	100.0	107	2	PT0399	Ig light chain V r
25	48	100.0	107	2	PT0400	Ig light chain V r
26	48	100.0	107	2	PT0401	Ig light chain V r
27	48	100.0	107	2	PT0402	Ig light chain V r
28	48	100.0	107	2	PT0403	Ig light chain V r
29	48	100.0	107	2	S11112	Ig kappa chain V r

30	48	100.0	107	2	S11113	Ig kappa chain V r
31	48	100.0	107	2	S11116	Ig kappa chain V r
32	48	100.0	107	2	S11117	Ig kappa chain V r
33	48	100.0	107	2	S11118	Ig kappa chain V r
34	48	100.0	107	2	S11119	Ig kappa chain V r
35	48	100.0	107	2	S11121	Ig kappa chain V r
36	48	100.0	107	2	S11123	Ig kappa chain V r
37	48	100.0	107	2	PT0406	Ig kappa chain V r
38	48	100.0	108	2	G30560	Ig kappa chain V r
39	48	100.0	130	1	JL0079	Ig kappa chain pre
40	48	100.0	140	2	PL0013	Ig kappa chain pre
41	47	97.9	107	2	PD0011	Ig kappa chain V r
42	47	97.9	107	2	PC4405	Ig kappa chain V r
43	45	93.8	76	2	A48784	Ig kappa V regions
44	45	93.8	91	2	S17626	Ig kappa chain V r
45	44	91.7	91	2	S17628	Ig kappa chain V r

ALIGNMENTS

RESULT 1  
S17629  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S17629  
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352:624-628, 1991  
A/Title: Making antibody fragments using phage display libraries.  
A/Reference number: S17230; MUID:91326098; PMID:1907718  
A/Accession: S17629  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-91 <CLA>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSYMH 10  
Db 16 SASSSVSYMH 25

RESULT 2  
S17637  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S17637  
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A/Title: Making antibody fragments using phage display libraries.  
A/Reference number: S17230; MUID:91326098; PMID:1907718  
A/Accession: S17637  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-91 <CLA>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSYMH 10  
Db 16 SASSSVSYMH 25

## RESULT 3

S17639  
Ig kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S17639  
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A:Title: Making antibody fragments using phage display libraries.  
A:Reference number: S17230; MUID:91326098; PMID:1907718  
A:Accession: S17639  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-91 <CLAS>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;16-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
|||||  
Db 16 SASSSVSVMH 25

## RESULT 4

S20650  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S20650  
R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.  
submitted to the EMBL Data Library, February 1992  
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react  
A:Reference number: S20639  
A:Accession: S20650  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-94 <LOS>  
A:Cross-references: EMBL:X65006; NID:g52645; PIDN:CAA46139.1; PID:g52646  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 0.0082;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
|||||  
Db 24 SASSSVSVMH 33

## RESULT 5

S20653  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S20653  
R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.  
submitted to the EMBL Data Library, February 1992  
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react  
A:Reference number: S20639  
A:Accession: S20653  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-94 <LOS>  
A:Cross-references: EMBL:X65009; NID:g52651; PIDN:CAA46142.1; PID:g52652  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 0.0082;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
|||||  
Db 24 SASSSVSVMH 33

## RESULT 6

S26341  
Ig light chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 20-Jun-2000  
C:Accession: S26341; S78448  
R:Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e  
A:Reference number: S26309; MUID:91341421; PMID:1908510  
A:Accession: S26341  
A:Molecule type: mRNA  
A:Residues: 1-97 <STA>  
A:Cross-references: EMBL:X59179  
R:Caton, A.J.  
submitted to the EMBL Data Library, April 1991  
A:Reference number: S78447  
A:Accession: S78448  
A:Molecule type: mRNA  
A:Residues: 1-39, 'R', '41-97', 'L' <CAT>  
A:Cross-references: EMBL:X59179; NID:g52311; PIDN:CAA41889.1; PID:g2334060  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;11-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.0085;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
|||||  
Db 19 SASSSVSVMH 28

## RESULT 7

PHI084  
Ig light chain V region (clone 202.61) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PHI084  
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PHI084  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-97 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.0085;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
|||||  
Db 24 SASSSVSVMH 33

RESULT 8

D38601  
Ig kappa chain V region (6A7) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 21-Jan-2000  
C/Accession: D38601  
R/Goshorn, S.C.; Retzel, E.; Jemerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A/Title: Common structural features among monoclonal antibodies binding the same antigen  
A/Reference number: A38601; MUID:91115823; PMID:1703527  
A/Accession: D38601  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-99 <GOS>  
A/Cross-references: GB:M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;8-81/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 99;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
|||||

Db 16 SASSSVSVMH 25

RESULT 9

S29590  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S29590  
R/Kavaler, J.  
submitted to the EMBL Data Library, April 1991  
A/Reference number: S26459  
A/Accession: S29590  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-100 <KAV>  
A/Cross-references: EMBL:X59093; NID:g52225; PIDN:CAA41819.1; PID:g52226  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 100;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
|||||

Db 24 SASSSVSVMH 33

RESULT 10

S1115  
Ig kappa chain V region (clone NO2-20.5.3) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
C/Accession: S1115  
R/Karttunen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.  
Nature 304, 320-324, 1983  
A/Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazalone  
A/Reference number: S07331; MUID:83271467; PMID:6877353  
A/Accession: S1115  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-102 <KAA>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 102;  
Best Local Similarity 100.0%; Pred. No. 0.009;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
|||||

Db 24 SASSSVSVMH 33

RESULT 11

S24214  
Ig kappa chain - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S24214  
R/Shimizu, T.; Iwasato, T.; Yamagishi, H.  
J. Exp. Med. 173, 1065-1072, 1991  
A/Title: Deletions of immunoglobulin C(kappa) region characterized by the circular excis  
A/Reference number: S24214; MUID:91217618; PMID:1902500  
A/Accession: S24214  
A/Status: preliminary; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-102 <SHI>  
A/Cross-references: EMBL:X58204  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;14-87/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 102;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
|||||

Db 22 SASSSVSVMH 31

RESULT 12

S29591  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S29591  
R/Kavaler, J.  
submitted to the EMBL Data Library, April 1991  
A/Reference number: S26459  
A/Accession: S29591  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-103 <KAV>  
A/Cross-references: EMBL:X59094; NID:g52227; PIDN:CAA41820.1; PID:g52228  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-88/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 103;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
|||||

Db 23 SASSSVSVMH 32

RESULT 13

B49049  
Ig kappa chain V region (anti-idiotypic) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C/Accession: B49049  
R/Armandoia, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.  
Eur. J. Immunol. 22, 2893-2899, 1992  
A/Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen

A;Reference number: A49049; MUID:93049629; PMID:1425914  
A;Accession: B49049  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-104 <ARM>  
A;Experimental source: BALB/c  
A;Note: sequence extracted from NCBI backbone (NCBIN:118298, NCBIPI:118299)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 0.0092;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
|||  
Db 24 SASSSVSVMH 33

RESULT 14

B54378  
Ig light chain V region anti-triplex DNA - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: B54378  
R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.  
J. Biol. Chem. 269, 7019-7023, 1994  
A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluoresc  
A;Reference number: A54378; MUID:94165109; PMID:7509814  
A;Accession: B54378  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-106 <AGA>  
A;Cross-references: GB:S68985; NID:g545746; PIDN:AAB30096.1; PID:g545747  
A;Experimental source: spleen and myeloma cell line MOPC 315.43  
A;Note: sequence inconsistent with nucleotide translation  
A;Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIPI:144175)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 0.0094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
|||  
Db 24 SASSSVSVMH 33

RESULT 15

PS0071  
Ig kappa chain V region (38C13.V8) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
C;Accession: PS0071  
R;Levy, S.; Campbell, M.J.; Levy, R.  
J. Exp. Med. 170, 1-13, 1989  
A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangeme  
A;Reference number: A92781; MUID:89310348; PMID:2501443  
A;Accession: PS0071  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-106 <LEV>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 0.0094;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
|||  
Db 24 SASSSVSVMH 33

Search completed: July 30, 2003, 09:44:07  
Job time : 2.95681 secs



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: July 30, 2003, 09:31:35 ; Search time 1.56146 Seconds  
(without alignments)  
301.171 Million cell updates/sec

Title:	US-09-865-198-4
Perfect score:	48
Sequence:	1 SASSSVSYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 beqs, 47026705 residues

Total number of hits satisfying chosen parameters: 1278633

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	107	1	KV6A_MOUSE	P01675 mus musculus
2	48	100.0	107	1	KV6B_MOUSE	P01676 mus musculus
3	48	100.0	107	1	KV6C_MOUSE	P01677 mus musculus
4	48	100.0	107	1	KV6D_MOUSE	P01678 mus musculus
5	48	100.0	107	1	KV6F_MOUSE	P04940 mus musculus
6	48	100.0	107	1	KV6G_MOUSE	P04941 mus musculus
7	48	100.0	107	1	KV6H_MOUSE	P04942 mus musculus
8	48	100.0	107	1	KV6I_MOUSE	P04943 mus musculus
9	48	100.0	107	1	KV6J_MOUSE	P04944 mus musculus
10	42	87.5	108	1	KV6K_MOUSE	P04945 mus musculus
11	36	75.0	107	1	KV6E_MOUSE	P01679 mus musculus
12	35	72.9	720	1	GT11_SCHPO	P014367 echizosacch
13	34	70.8	129	1	KV4A_MOUSE	P01680 mus musculus
14	34	70.8	270	1	ALYS_BPRIT	Q38135 bacterioph
15	34	70.8	731	1	BGAL_MALDO	P48981 malus domes
16	33	68.8	271	1	RRF_SPIOL	P82231 spinacia ol
17	33	68.8	405	1	CBG_HUMAN	P08185 homo sapien
18	32	66.7	394	1	DUG4_HUMAN	Q13115 homo sapien
19	32	66.7	933	1	SIAP_CAMEF	P35827 campylobact
20	31	64.6	230	1	YIME_BACSU	Q31727 bacillus su
21	31	64.6	318	1	ATH4_ARATH	P922953 arabidopsi
22	31	64.6	363	1	SERC_LISMO	Q8y310 listeria mo
23	31	64.6	377	1	Y835_METJA	Q58245 methanococc
24	31	64.6	460	1	MYIN_HELPJ	Q9zkw7 helicobacte
25	31	64.6	461	1	MYIN_HELPY	O25551 helicobacte
26	31	64.6	989	1	PTP3_DICDI	P54637 dictyostelli
27	31	64.6	1380	1	ZMS1_YEAST	P46974 saccharomyc
28	31	64.6	1520	1	PMPD_CHIMU	Q9p1b0 chlamydia m
29	30	62.5	218	1	NUKM_ARATH	Q42577 arabidopsis
30	30	62.5	367	1	CCR3_MOUSE	O88410 mus musculu
31	30	62.5	368	1	CCR3_HUMAN	P49682 homo sapien
32	30	62.5	380	1	CYB_IACVV	O48089 lacerta viv
33	30	62.5	383	1	CBG_RABIT	P23775 oryctolagus

## ALIGNMENTS

	34	35	36	37	38	39	40	41	42	43	44	45
	30	62.5	418	1	HLT_VIBPA	Q99289	vibrio	para				
	30	62.5	435	1	FUT9_ARATH	Q9x177	arabidopsis					
	30	62.5	447	1	COBB_METTH	O27509	methanobact					
	30	62.5	448	1	PADL_ECOLI	P10384	escherichia					
	30	62.5	461	1	NORM_VIBCH	Q9krn4	vibrio	chol				
	30	62.5	481	1	HH_DROHY	P56674	drosophila					
	30	62.5	584	1	LAM1_CHICK	P14731	gallus	gall				
	30	62.5	585	1	LAM1_HUMAN	P20700	homo	sapient				
	30	62.5	586	1	LAM1_RAT	P70615	rattus	norv				
	30	62.5	587	1	LAM1_MOUSE	P14733	mus	musculus				
	30	62.5	647	1	DPG1_CHICK	Q92076	gallus	gall				
	30	62.5	878	1	MSH4_YEAST	P40965	saccharomyc					

## RESULT 1

ID	KV6A_MOUSE	STANDARD;	PRT;	107 AA.
AC	P01675;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, last sequence update)		
DT	15-JUL-1999	(Rel. 38, last annotation update)		
DE	Ig kappa chain V-VI region XRPC 44.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			

RP SEQ

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RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "K Chain variable regions from three galactan binding myeloma
RT proteins.";
RL Biochemistry 17:5555-5559(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
CC PIR; A90420; KVMX4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;

Query Match 100.0%; Score 48; DB 1; length 107;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
   |||||
   |||||
   |||||
DB 24 SASSSVSYMH 33

RESULT 2
KV6B_MOUSE
ID KV6B_MOUSE STANDARD; PRT; 107 AA.
AC P01676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

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DT 15-JUL-1999 (Rel. 38, Last annotation update).  
DE Ig kappa chain V-VI region XRPC 24.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79082830; PubMed=103573;  
RA Rao D.N., Rudikoff S., Potter M.;  
RT "k Chain variable regions from three galactan binding myeloma  
RT proteins.";  
RL Biochemistry 17:5555-5559(1978).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BIND GALACTAN.  
CC HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 34 48 FRAMEWORK-2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 56 87 FRAMEWORK-3.  
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 97 106 FRAMEWORK-4.  
FT DISULFID 23 87 BY SIMILARITY.  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11584 MW; 36E6D022A5EC34D7 CRC64;  
Query Match 100.0%; Score 48; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33  
RESULT 3  
KV6C\_MOUSE STANDARD; PRT; 107 AA.  
ID \_KV6C\_MOUSE  
AC P01677;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-VI region TEPC 601/TEPC 191.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE (TEPC 601).  
RX MEDLINE=79082830; PubMed=103573;  
RA Rao D.N., Rudikoff S., Potter M.;  
RT "k Chain variable regions from three galactan binding myeloma  
RT proteins.";  
RL Biochemistry 17:5555-5559(1978).  
RN [2]  
RP SEQUENCE (TEPC 191).  
RX MEDLINE=81054757; PubMed=6776525;  
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;  
RT "Kappa Chain joining segments and structural diversity of antibody  
RT combining sites.";  
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).  
CC -1- MISCELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.  
CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS  
CC THAT BIND GALACTAN.  
DR HSSP; P01679; 2FBJ.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 34 48 FRAMEWORK-2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 56 87 FRAMEWORK-3.  
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 97 106 FRAMEWORK-4.  
FT DISULFID 23 87 BY SIMILARITY.  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11568 MW; 203CD752A5EC34D7 CRC64;  
Query Match 100.0%; Score 48; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33  
RESULT 4  
KV6D\_MOUSE STANDARD; PRT; 107 AA.  
ID \_KV6D\_MOUSE  
AC P01678;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-VI region SAPC 10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81054757; PubMed=6776525;  
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;  
RT "Kappa Chain joining segments and structural diversity of antibody  
RT combining sites.";  
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BIND GALACTAN.  
CC HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 34 48 FRAMEWORK-2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 56 87 FRAMEWORK-3.  
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 97 106 FRAMEWORK-4.  
FT DISULFID 23 87 BY SIMILARITY.  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;  
Query Match 100.0%; Score 48; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33

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Db      24 SASSSVSYMH 33

RESULT 5
KV6F_MOUSE      STANDARD;      PRT;      107 AA.
ID   KV6F_MOUSE      P04940;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-VI region NQ2-17.4.1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=83271467; PubMed=6877353;
RA      Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT      "mRNA sequences define an unusually restricted Igg response to 2-
RT      phenylloxazolone and its early diversification.";
RL      Nature 304:320-324(1983).
CC      -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; K00735; AAA38680.1; -.
DR      HSSP; P01679; 2FBJ.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Hybridoma.
FT      DOMAIN 1 23 FRAMEWORK-1.
FT      DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN 34 48 FRAMEWORK-2.
FT      DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN 56 87 FRAMEWORK-3.
FT      DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT      DOMAIN 97 106 FRAMEWORK-4.
FT      DISULFID 23 87 BY SIMILARITY.
FT      NON TER 107 107
SQ      SEQUENCE 107 AA; 11561 MW; 6F694284ECFA68E6 CRC64;

Query Match      100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 SASSSVSYMH 10
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Db      24 SASSSVSYMH 33

RESULT 6
KV6G_MOUSE      STANDARD;      PRT;      107 AA.
ID   KV6G_MOUSE      P04941;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-VI region NQ2-48.2.2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;

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RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=83271467; PubMed=6877353;
RA      Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT      "mRNA sequences define an unusually restricted Igg response to 2-
RT      phenylloxazolone and its early diversification.";
RL      Nature 304:320-324(1983).
CC      -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; K00737; AAA38682.1; -.
DR      HSSP; P01679; 2FBJ.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Hybridoma.
FT      DOMAIN 1 23 FRAMEWORK-1.
FT      DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN 34 48 FRAMEWORK-2.
FT      DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN 56 87 FRAMEWORK-3.
FT      DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT      DOMAIN 97 106 FRAMEWORK-4.
FT      DISULFID 23 87 BY SIMILARITY.
FT      NON TER 107 107
SQ      SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;

Query Match      100.0%; Score 48; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 SASSSVSYMH 10
      |||||
Db      24 SASSSVSYMH 33

RESULT 7
KV6H_MOUSE      STANDARD;      PRT;      107 AA.
ID   KV6H_MOUSE      P04942;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-VI region NQ5-61.1.2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=83271467; PubMed=6877353;
RA      Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT      "mRNA sequences define an unusually restricted Igg response to 2-
RT      phenylloxazolone and its early diversification.";
RL      Nature 304:320-324(1983).
CC      -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC      -----
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CC EMBL; K00739; AAA38684.1; -.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 34 48 FRAMEWORK-2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 56 87 FRAMEWORK-3.  
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 97 106 FRAMEWORK-4.  
FT DISULFID 23 87 BY SIMILARITY.  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11605 MW; CA6C4284ECFCB550 CRC64;  
  
Query Match 100.0%; Score 48; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33  
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RESULT 8  
KV6I MOUSE STANDARD; PRT; 107 AA.  
AC P04943;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-VI region NQ6-8.3.1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83271467; PubMed=6877353;  
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;  
RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."  
RL Nature 304:320-324(1983).  
CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.  
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-----  
CC EMBL; K00740; AAA38685.1; -.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 34 48 FRAMEWORK-2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 56 87 FRAMEWORK-3.  
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 97 106 FRAMEWORK-4.  
FT DISULFID 23 87 BY SIMILARITY.  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECFC8E6 CRC64;  
  
Query Match 100.0%; Score 48; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33  
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RESULT 9  
KV6J MOUSE STANDARD; PRT; 107 AA.  
AC P04944;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-VI region NQ5-78.2.6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83271467; PubMed=6877353;  
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;  
RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."  
RL Nature 304:320-324(1983).  
CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.  
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CC EMBL; K00744; AAA38689.1; -.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 34 48 FRAMEWORK-2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 56 87 FRAMEWORK-3.  
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 97 106 FRAMEWORK-4.  
FT DISULFID 23 87 BY SIMILARITY.  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11611 MW; A38290781F3C30D3 CRC64;  
  
Query Match 100.0%; Score 48; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33



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RESULT 10
KV6K_MOUSE
ID KV6K_MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RT Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
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CC -----
DR EMBL; K00746; AAA38691.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 34 48 FRAMEWORK-2.
FT DOMAIN 4 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 56 87 FRAMEWORK-3.
FT DOMAIN 6 88 98 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 99 108 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;

Query Match
Best Local Similarity 87.5%; Score 42; DB 1; Length 108;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSYMY 33

RESULT 11
KV6E_MOUSE
ID KV6E_MOUSE STANDARD; PRT; 107 AA.
AC P01679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-VI region J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;

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RA Rudikoff S., Rao D.N., Glandemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
RT combining sites.";
RT Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=88217852; PubMed=3449853;
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
RT study at 2.6-A resolution.";
RL Proteins 1:74-80(1986).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR PIR; A01942; KVMJS5.
DR PDB; 2FBJ; 15-OCT-90.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 34 48 FRAMEWORK-2.
FT DOMAIN 4 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 56 87 FRAMEWORK-3.
FT DOMAIN 6 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 97 106 FRAMEWORK-4.
FT DISULFID 23 87
FT STRAND 4 7
FT STRAND 10 14
FT TURN 15 16
FT STRAND 19 25
FT STRAND 31 37
FT TURN 39 40
FT STRAND 44 48
FT TURN 49 51
FT STRAND 52 53
FT TURN 55 56
FT TURN 59 60
FT STRAND 61 66
FT TURN 67 68
FT STRAND 69 74
FT HELIX 79 81
FT STRAND 83 91
FT TURN 92 93
FT STRAND 94 97
FT STRAND 101 107
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11502 MW; EA30C9A3E903979C CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 1; Length 107;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10
Db 24 SASSSVSSLH 33

RESULT 12
GT1I_SCHPO
ID GT1I_SCHPO STANDARD; PRT; 720 AA.
AC O14367;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucanate transport inducer 1.
GN GT1I OR SPAC1751.01C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

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OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=SP011;
RX MEDLINE=98039718; PubMed=9372449;
RA Caspari T.;
RT "Onset of gluconate-H+ symport in Schizosaccharomyces pombe is
RT regulated by the kinases Wisl and Pkal, and requires the gtl1+ gene
RT product.";
RL J. Cell Sci. 110:2599-2608(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Hoizer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerruttl L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakowski G.V., Ussey D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Promotes the onset of gluconate uptake upon glucose
CC starvation.
CC -!- SIMILARITY: IN THE N-TERMINAL REGION; TO S.POMBE PAC2.
CC -----
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CC -----
CC
CC EMBL; X92655; CAA63345.1; -.
CC DR EMBL; AL133154; CAB61447.1; -.
CC DR PIR; T43327; T43327.
CC DR GenedB_SPombe; SPAC1751.01c; -.
CC KW Transport.
CC FT DOMAIN
CC SQ SEQUENCE 720 AA; 78725 MW; 5CC2CD58ACE7CD87 CRC64;
OY 2 ASSSVSYMH 10
Db 255 SSSSLSYLH 263
Query Match 72.9%; Score 35; DB 1; Length 720;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

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ID KV4A_MOUSE STANDARD; PRT; 129 AA.
AC P01680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82115300; PubMed=6799208;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";
RL Cell 26:57-66(1981).
CC -!- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE
CC NORMAL KAPPA CHAIN S107.
CC -----
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CC -----
CC
CC EMBL; J00577; AAA38780.1; -.
CC DR EMBL; V00780; CAA24157.1; -.
CC DR PIR; A01943; KVM57B.
CC DR HSSP; P01679; 2FBJ.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR003596; Ig_V.
CC DR Pfam; PF00047; ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC KW Immunoglobulin V region; Signal.
CC FT SIGNAL 1 22
CC FT CHAIN 23 129 IG KAPPA CHAIN V-IV REGION S107B.
CC FT DOMAIN 23 45 FRAMEWORK-1.
CC FT DOMAIN 46 57 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 58 72 FRAMEWORK-2.
CC FT DOMAIN 73 79 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 80 111 FRAMEWORK-3.
CC FT DOMAIN 112 118 COMPLEMENTARITY-DETERMINING-3.
CC FT DOMAIN 119 128 FRAMEWORK-4.
CC FT DISULFID 45 111 BY SIMILARITY.
CC FT NON_TER 129 129
CC SQ SEQUENCE 129 AA; 13833 MW; E4BB73072DC6BE4 CRC64;
OY 1 SASSSV--SYMH 10
Db 46 SASSSVSSSYLH 57
Query Match 70.8%; Score 34; DB 1; Length 129;
Best Local Similarity 75.0%; Pred. No. 3.3;
Matches 9; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
RESULT 14
ALYS_BPRIT STANDARD; PRT; 270 AA.
ID Alys_BPRIT
AC Q38135;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28).
OS Bacteriophage rlt.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=43685;
```

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96332669; PubMed=8730875;  
RA Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.,  
RA Venema G., Nauta A.;  
RT "Sequence analysis and molecular characterization of the temperate  
RT lactococcal bacteriophage  $\phi$ lt.";  
RL Mol. Microbiol. 19:1343-1355(1996).  
CC -1- CATALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl  
CC residues and L-amino acid residues in certain bacterial cell-wall  
CC glycopeptides.  
CC -1- SIMILARITY: BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE  
CC FAMILY 2.  
CC -----  
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CC -----  
DR EMBL; U38906; AAB18724.1; -.  
DR InterPro; IPR002502; Amidase\_2.  
DR Pfam; PF01510; Amidase\_2; 1.  
DR SMART; SM00644; Ami\_2; 1.  
KW Hydrolyase; Cell wall.  
SQ SEQUENCE 270 AA; 30214 MW; 80A5E38F7F2A6675 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 270;  
Best Local Similarity 60.0%; Pred. No. 7.4;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SASSSVSYMH 10  
Db 40 SATNEASVYMH 49

## RESULT 15

BGAL\_MALDO STANDARD; PRT; 731 AA.  
AC P48981;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Beta-galactosidase precursor (EC 3.2.1.23) (lactase) (Acid beta-  
DE galactosidase) (Exo-(1->4)-beta-D-galactanase).  
OS Malus domestica (Apple) (Malus sylvestris).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosid I; Rosales; Rosaceae; Maloideae; Malus.  
OX NCBI\_TaxID=3750;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC STRAIN=cv. Granny Smith; TISSUE=Fruit cortical tissue;  
RX MEDLINE=95083752; PubMed=7991682;  
RA Ross G.S., Wegryzn T., Macrae E.A., Redgwell R.J.;  
RT "Apple beta-galactosidase. Activity against cell wall polysaccharides  
RT and characterization of a related cDNA clone."  
RL Plant Physiol. 106:521-528(1994).  
CC -1- FUNCTION: Involved in cell wall degradation. Degrades  
CC polysaccharides containing beta-(1->4)-linked galactans, acting  
CC as an exo-(1->4)-beta-D-galactanase.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-  
CC galactose residues in beta-D-galactosides.  
CC -1- SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES.

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CC -----  
DR EMBL; L29451; AAA62324.1; -.  
DR PIR; T17002; T17002.  
DR InterPro; IPR001944; Glyco\_hydro\_35.  
DR Pfam; PF01301; Glyco\_hydro\_35; 1.  
DR PRINTS; PR00742; GLHYDRLASE35.  
DR PROSITE; PS01182; GLYCOSYL\_HYDROL\_F35; 1.  
KW Hydrolyase; Glycosidase; Signal.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 731 BETA-GALACTOSIDASE.  
FT ACT\_SITE 182 182 PROTON DONOR (POTENTIAL).  
FT ACT\_SITE 251 251 NUCLEOPHILE (POTENTIAL).  
SQ SEQUENCE 731 AA; 80995 MW; FAB65D24A0D30BD4 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 731;  
Best Local Similarity 70.0%; Pred. No. 23;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SASSSVSYMH 10  
Db 21 AASASVSYDH 30

Search completed: July 30, 2003, 09:45:03  
Job time : 2.56146 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 7.74086 Seconds  
(without alignments)  
333.364 Million cell updates/sec

Title: US-09-865-198-4  
Perfect score: 48  
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	112	11	Q8K1F0	Q8K1F0 mus musculu
2	47	97.9	134	11	Q8VDD0	Q8VDD0 mus musculu
3	45	93.8	112	11	Q8K1F2	Q8K1F2 mus musculu
4	44	91.7	97	11	Q9J176	Q9J176 mus musculu
5	43	89.6	235	11	Q91W12	Q91W12 mus musculu
6	42	87.5	112	11	Q8K1F3	Q8K1F3 mus musculu
7	38	79.2	106	5	Q9U410	Q9U410 schistosoma
8	37	77.1	547	2	Q59117	Q59117 archrobacte
9	37	77.1	858	5	Q9V429	Q9V429 drosophila
10	36	75.0	981	5	Q9V1F5	Q9V1F5 drosophila
11	35	72.9	200	3	Q08003	Q08003 saccharomyc
12	35	72.9	689	5	Q8T6L8	Q8T6L8 drosophila
13	35	72.9	1004	16	Q84646	Q84646 chlamydia t
14	35	72.9	1313	5	Q8T6L9	Q8T6L9 drosophila
15	34	70.8	518	5	Q8I3Q2	Q8I3Q2 plasmodium
16	34	70.8	537	16	Q98LI5	Q98LI5 rhizobium 1

17	34	70.8	731	10	Q9AYS1	Q9AYS1 pyrus pyrif
18	34	70.8	1095	10	Q9C7S5	Q9C7S5 arabidopsis
19	34	70.8	1430	5	Q9W0B0	Q9W0B0 drosophila
20	34	70.8	1501	10	Q94LS3	Q94LS3 oryza sativ
21	34	70.8	2136	10	Q9SL97	Q9SL97 arabidopsis
22	33	68.8	101	11	Q9JL78	Q9JL78 mus musculu
23	33	68.8	184	10	Q8LF58	Q8LF58 arabidopsis
24	33	68.8	234	3	Q94664	Q94664 schistosach
25	33	68.8	347	8	Q9MW74	Q9MW74 acanthodact
26	33	68.8	382	2	Q9AMN1	Q9AMN1 clostridium
27	33	68.8	463	11	Q99LC4	Q99LC4 mus musculu
28	33	68.8	477	16	Q97TF8	Q97TF8 clostridium
29	33	68.8	669	10	Q9SLC7	Q9SLC7 arabidopsis
30	33	68.8	677	5	Q17720	Q17720 caenorhabdi
31	33	68.8	841	5	Q9VC32	Q9VC32 drosophila
32	33	68.8	944	5	Q18137	Q18137 caenorhabdi
33	33	68.8	1148	5	Q95ZY7	Q95ZY7 caenorhabdi
34	33	68.8	1439	5	Q8MQC7	Q8MQC7 caenorhabdi
35	33	68.8	1480	5	Q18138	Q18138 caenorhabdi
36	32	66.7	95	10	Q9M3C7	Q9M3C7 arabidopsis
37	32	66.7	136	10	Q8LJN1	Q8LJN1 oryza sativ
38	32	66.7	158	10	Q9SIH6	Q9SIH6 arabidopsis
39	32	66.7	206	5	Q9VK13	Q9VK13 drosophila
40	32	66.7	219	16	Q9KBL2	Q9KBL2 bacillus ha
41	32	66.7	240	16	Q9KRV9	Q9KRV9 vibrio chol
42	32	66.7	244	10	Q8GYJ2	Q8GYJ2 arabidopsis
43	32	66.7	264	5	Q97455	Q97455 caenorhabdi
44	32	66.7	266	5	Q19536	Q19536 caenorhabdi
45	32	66.7	273	10	Q9SA31	Q9SA31 arabidopsis

ALIGNMENTS

RESULT 1	Q8K1F0	PRELIMINARY;	PRT;	112 AA.
ID	Q8K1F0			
AC	Q8K1F0;			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Anti-VIPase light chain variable region (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;			
RA	Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;			
RT	"Inmate proteolytic antibodies: Failed D-VIPase response to the D-			
RT	entantlomer of VIP and identification of L-VIPase VL domains.";			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF516285; AAM64203.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; IG_1.			
DR	SMART; SM00409; IG_1.			
DR	SMART; SM00406; IGv_1.			
DR	PROSITE; PSS0835; IG-LIKE; 1.			
FT	NON_TER	1		
FT	NON_TER	112		
SO	SEQUENCE	112 AA;	11901 MW;	F6644663201AA239 CRC64;
Query Match 100.0%; Score 48; DB 11; Length 112;				
Best Local Similarity 100.0%; Pred. No. 0.021;				
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 SASSSVSYMH 10			
Db	24 SASSSVSYMH 33			

RESULT 2  
Q8VDD0  
ID Q8VDD0 PRELIMINARY; PRT; 134 AA.  
AC Q8VDD0;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Anti-MOG Z12 variable light chain (Fragment).  
GN ANTI-MOG KAPPA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Chernaiovsky Y.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Sembi P.;  
RT "Targeting T cells to the CNS."  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ416331; CAC94866.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 134 134  
SQ SEQUENCE 134 AA; 14525 MW; CFPDF8E2236E2D0CF CRC64;  
  
Query Match 97.9%; Score 47; DB 11; Length 134;  
Best Local Similarity 90.0%; Pred. No. 0.041;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SASSSVSVMH 10  
Db 46 SASSSISVMH 55  
  
RESULT 3  
Q8K1F2  
ID Q8K1F2 PRELIMINARY; PRT; 112 AA.  
AC Q8K1F2;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Anti-VIPase light chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;  
RA Zhou Y.-X.; Taguchi H.; Planque S.; Karle S.; Nishiyama Y.; Paul S.;  
RT "Inmate proteolytic antibodies: Failed D-VIPase response to the D-  
entantioner of VIP and identification of L-VIPase VL domains."  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF16283; AAM64201.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
RL PROSITE; PSS0835; IG\_LIKE; 1.

FT NON\_TER 1 1  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 11953 MW; 4716B87FADB543ED CRC64;  
  
Query Match 93.8%; Score 45; DB 11; Length 112;  
Best Local Similarity 90.0%; Pred. No. 0.089;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SASSSVSVMH 10  
Db 24 NASSSVSVMH 33  
  
RESULT 4  
Q9JL76  
ID Q9JL76 PRELIMINARY; PRT; 97 AA.  
AC Q9JL76;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Anti-myosin immunoglobulin light chain variable region  
(Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DBA/2;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Malkiel S.; Liao L.; Cunningham M.W.; Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of  
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
with cardiac myosin."  
RT Infect. Immun. 68:5803-5808 (2000).  
RL EMBL; AF206030; AAF69328.1; -.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1 1  
FT NON\_TER 97 97  
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFE1F49DA1C CRC64;  
  
Query Match 91.7%; Score 44; DB 11; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 ASSSVSYM 10  
Db 15 ASSSVSYM 23  
  
RESULT 5  
Q91W12  
ID Q91W12 PRELIMINARY; PRT; 235 AA.  
AC Q91W12;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Unknown (Protein for MGC:6582).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast tumor;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.



DR EMBL; BC006643; AAH06643.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 89.6%; Score 43; DB 11; Length 235;  
Best Local Similarity 90.0%; Pred. No. 0.52;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSYMH 10  
DB 46 SASSSVSHMH 55

## RESULT 6

ID Q8K1F3 PRELIMINARY; PRT; 112 AA.  
AC Q8K1F3;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Anti-Vipase light chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;  
RC Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
RT "Innate proteolytic antibodies: Failed D-Vipase response to the D-  
entantioner of VIP and identification of L-Vipase VL domains.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF516282; AAM64200.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 112  
SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Query Match 87.5%; Score 42; DB 11; Length 112;  
Best Local Similarity 90.0%; Pred. No. 0.38;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSYMH 10  
DB 24 SASSSVSYMY 33

## RESULT 7

ID Q9U410 PRELIMINARY; PRT; 106 AA.  
AC Q9U410;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Monoclonal anti-Idiotypic antibody NP30 immunoglobulin light chain  
variable region (Fragment).  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
OC Schistosomatoidae; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6182;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;  
RT "Amplification, cloning and sequence analysis of the light chain  
variable region gene of monoclonal anti-idiotypic antibody NP30 of  
Schistosoma japonicum";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF207620; AAF19434.1; -  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 79.2%; Score 38; DB 5; Length 106;  
Best Local Similarity 80.0%; Pred. No. 2.5;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSYMH 10  
DB 24 SASSSVSYVY 33

## RESULT 8

ID Q59117 PRELIMINARY; PRT; 547 AA.  
AC Q59117;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Choline oxidase (EC 1.1.3.17).  
GN CODA.  
OS Arthrobacter globiformis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Micrococcineae; Micrococcaceae; Arthrobacter.  
OX NCBI\_TaxID=1665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96145502; PubMed=8555454;  
RA Deshmum P., Los D.A., Hayashi H., Mustardy L., Murata N.;  
RT "Transformation of *Synechococcus* with a gene for choline oxidase  
enhances tolerance to salt stress.";  
RT Plant Mol. Biol. 29:897-907(1995).  
DR EMBL; X84895; CAA59321.1; -  
DR HSSP; P22637; 3COX.  
DR InterPro; IPR00172; GMC\_oxred.  
DR Pfam; PF00732; GMC\_oxred; 1.  
DR PROSITE; PS00624; GMC\_OXRED\_2; 1.  
KW Oxidoreductase.

SQ SEQUENCE 547 AA; 58865 MW; 589175892034B3BE CRC64;

Query Match 77.1%; Score 37; DB 2; Length 547;  
Best Local Similarity 77.8%; Pred. No. 23;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASSSVSYMH 10  
DB 208 SSSSVSYIH 216

## RESULT 9

ID Q9V429 PRELIMINARY; PRT; 858 AA.  
AC Q9V429;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE CG11770 protein (LINES).

GN LIN OR CG11770.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RA "The genome sequence of Drosophila melanogaster.";  
RA Science 287:2185-2195(2000).  
RL [2]  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20296724; PubMed=10837029;  
RA Hatini V., Bokor P., Goto-Mandeville R., Dinardo S.;  
RA "Tissue- and stage-specific modulation of wingless signaling by the  
RT segment polarity gene lines.";  
RL Genes Dev. 14:1364-1376(2000).  
DR EMBL; AE003835; AAF59024.1; -  
DR EMBL; AF272358; AAF76228.1; -  
DR FlyBase; FBgn0002552; lin.  
SQ SEQUENCE 858 AA; 96291 MW; 95030ED5FE096139 CRC64;

Query Match 77.1%; Score 37; DB 5; Length 858;  
Best Local Similarity 70.0%; Pred. No. 38;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
| : |||||  
Db 366 STEASVSVMH 375

RESULT 10  
Q9VIF5  
ID Q9VIF5 PRELIMINARY; PRT; 981 AA.  
AC Q9VIF5;

DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
DE CG9252 protein.  
GN CG9252.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RA "The genome sequence of Drosophila melanogaster.";  
RA Science 287:2185-2195(2000).  
RL [2]  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,  
RA Gonzalez C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,  
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RA "Sequencing of Drosophila melanogaster genome.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A.  
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,  
 RT "Annotation of Drosophila melanogaster genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003669; AAF53964.2; -.  
 DR FlyBase; FBgn0032920; CG9252.  
 SQ SEQUENCE 981 AA; 110816 MW; 9A825881240BDC1B CRC64;

Query Match 75.0%; Score 36; DB 5; Length 981;  
 Best Local Similarity 70.0%; Pred. No. 71;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
 :|||:|  
 Db 917 NASKSYSVMH 926

## RESULT 11

ID Q08003 PRELIMINARY; PRT; 200 AA.  
 AC Q08003;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Chromosome XII reading frame ORF YLR073C.  
 GN YLR073C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pohl T.M.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RT Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; Z73245; CAA97630.1; -.  
 DR SGD; S0004063; YLR073C.  
 SQ SEQUENCE 200 AA; 22850 MW; 1C93378ED78C41A4 CRC64;

Query Match 72.9%; Score 35; DB 3; Length 200;  
 Best Local Similarity 70.0%; Pred. No. 21;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
 |:|:|:|:|  
 Db 75 SSSSSSYIH 84

## RESULT 12

ID Q8T6L8 PRELIMINARY; PRT; 689 AA.  
 AC Q8T6L8;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
 DE Unconventional myosin 29D short isoform.  
 GN D OR MYO29D OR CG10595.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Oregon R; TISSUE=Ovary;  
 RA Tzolovskiy G., Bowles M., Millo H., Pathirana S., Wood T.;  
 RT "Identification and phylogenetic analysis of Drosophila melanogaster  
 RT myosins."  
 RL Mol. Biol. Evol. 0:0-0(2002).  
 DR EMBL; AF454349; AAL91723.1; -.  
 DR FlyBase; FBgn000410; d.  
 DR InterPro; IPR001609; myosin\_head.  
 DR Pfam; PF00063; myosin\_head; 1.  
 DR ProDom; PD000355; myosin\_head; 1.  
 DR SMART; SM00242; MYSC; 1.  
 SQ SEQUENCE 689 AA; 74009 MW; 9525A3C5B928FD2A CRC64;

Query Match 72.9%; Score 35; DB 5; Length 689;  
 Best Local Similarity 60.0%; Pred. No. 79;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
 :|||:|:|  
 Db 613 AASSAVSFH 622

## RESULT 13

ID O84646 PRELIMINARY; PRT; 1004 AA.  
 AC O84646;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE Exodeoxyribonuclease V, gamma.  
 GN RECC OR CT640.  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D/UW-3/Cx;  
 RX MEDLINE=99000809; PubMed=9784136;  
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,  
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,  
 RA Davis R.W.;  
 RT "Genome sequence of an obligate intracellular pathogen of humans:  
 RT Chlamydia trachomatis."  
 RL Science 282:754-759(1998).  
 DR EMBL; AE001334; AAC68244.1; -.  
 KW Complete proteome.  
 SQ SEQUENCE 1004 AA; 114401 MW; BB89266ED55F1496 CRC64;

Query Match 72.9%; Score 35; DB 16; Length 1004;  
 Best Local Similarity 70.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
 |:|:|:|:|  
 Db 108 SSSSEVSYSH 117

## RESULT 14

ID Q8T6L9 PRELIMINARY; PRT; 1313 AA.  
 AC Q8T6L9;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Unconventional myosin 29D.  
 GN D OR MYO29D OR CG10595.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCB1\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Oregon R; TISSUE=Ovary;  
RA Tzolovsky G., Bowens M., Millo H., Pachirana S., Wood T.;  
RT "Identification and phylogenetic analysis of Drosophila melanogaster  
myosins."  
RL Mol. Biol. Evol. 0:0-0(2002).  
DR EMBL; AF454348; AAL91722.1; -.  
DR FlyBase; FBgn0000410; d.  
DR InterPro; IPR000048; IQ\_region.  
DR InterPro; IPR001609; myosin\_head.  
DR Pfam; PF00612; IQ; 1.  
DR Pfam; PF00063; myosin\_head; 1.  
DR ProDom; PD000355; myosin\_head; 1.  
DR SMART; SM00015; IQ; 1.  
DR SMART; SM00242; MYSC; 1.  
DR PROSITE; PS50096; IQ; 1.  
SQ SEQUENCE 1313 AA; 142708 MW; 1A164E5A073D9450 CRC64;

Query Match 72.9%; Score 35; DB 5; Length 1313;  
Best Local Similarity 60.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
Db 1237 AASSAVSFLH 1246

Best Local Similarity 70.0%; Pred. No. 95;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 113 SSSSSSYKX 122

Search completed: July 30, 2003, 09:42:38  
Job time : 10.852 secs

RESULT 15  
Q8I3Q2 PRELIMINARY; PRT; 518 AA.  
ID Q8I3Q2;  
AC 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN PFE1055C.  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCB1\_TaxID=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,  
RA Hall N., Bowman S., Churcher C., Quail M., Barrell B.;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22255708; PubMed=12368867;  
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,  
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,  
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,  
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,  
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,  
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,  
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,  
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,  
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,  
RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,  
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,  
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,  
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,  
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,  
RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;  
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";  
RL Nature 419:527-531(2002).  
DR EMBL; A929353; CAD51575.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 518 AA; 63009 MW; 8AE81B1DD59638D7 CRC64;

Query Match 70.8%; Score 34; DB 5; Length 518;



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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 3.22259 Seconds  
(without alignments)  
131.295 Million cell updates/sec

Title: US-09-865-198-4  
Perfect score: 48  
Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	48	100.0	10	2	US-08-116-778E-9 Sequence 9, Appli
2	48	100.0	10	2	US-08-438-562-9 Sequence 9, Appli
3	48	100.0	10	2	US-08-483-528B-97 Sequence 97, Appli
4	48	100.0	10	3	US-08-836-561-49 Sequence 49, Appli
5	48	100.0	10	4	US-09-393-385B-108 Sequence 108, App
6	48	100.0	10	4	US-09-434-122-49 Sequence 49, Appli
7	48	100.0	97	3	US-09-280-028-4 Sequence 4, Appli
8	48	100.0	100	2	US-08-308-494A-19 Sequence 19, Appli
9	48	100.0	105	3	US-08-434-000A-12 Sequence 12, Appli
10	48	100.0	105	4	US-09-312-157-12 Sequence 12, Appli
11	48	100.0	110	3	US-08-836-561-33 Sequence 33, Appli
12	48	100.0	110	4	US-09-434-122-33 Sequence 33, Appli
13	48	100.0	129	2	US-08-116-778E-2 Sequence 2, Appli
14	48	100.0	129	2	US-08-438-562-2 Sequence 2, Appli
15	48	100.0	129	2	US-08-483-528B-92 Sequence 92, Appli
16	48	100.0	130	4	US-09-393-385B-111 Sequence 111, App
17	48	100.0	130	4	US-09-393-385B-113 Sequence 113, App
18	48	100.0	133	2	US-08-116-778E-37 Sequence 37, Appli
19	48	100.0	133	2	US-08-438-562-37 Sequence 37, Appli
20	48	100.0	133	2	US-08-483-528B-101 Sequence 101, App
21	48	100.0	144	4	US-09-318-78E-29 Sequence 29, Appli
22	48	100.0	222	2	US-08-190-199A-67 Sequence 67, Appli
23	48	100.0	235	2	US-08-190-199A-61 Sequence 61, Appli
24	48	100.0	270	2	US-08-652-507-2 Sequence 2, Appli
25	48	100.0	553	2	US-08-661-052-16 Sequence 16, Appli
26	48	100.0	553	3	US-09-188-082-16 Sequence 16, Appli
27	48	100.0	553	4	US-09-364-088-16 Sequence 16, Appli

28	48	100.0	553	4	US-09-102-716-16 Sequence 16, Appli
29	47	97.9	106	1	US-07-634-278-1 Sequence 1, Appli
30	47	97.9	106	1	US-07-634-278-7 Sequence 7, Appli
31	47	97.9	106	1	US-07-634-278-8 Sequence 8, Appli
32	47	97.9	106	1	US-07-634-278-16 Sequence 16, Appli
33	47	97.9	106	1	US-08-477-728-1 Sequence 1, Appli
34	47	97.9	106	1	US-08-477-728-7 Sequence 7, Appli
35	47	97.9	106	1	US-08-477-728-8 Sequence 8, Appli
36	47	97.9	106	1	US-08-477-728-16 Sequence 16, Appli
37	47	97.9	106	1	US-08-474-040-1 Sequence 1, Appli
38	47	97.9	106	1	US-08-474-040-7 Sequence 7, Appli
39	47	97.9	106	1	US-08-474-040-8 Sequence 8, Appli
40	47	97.9	106	1	US-08-474-040-16 Sequence 16, Appli
41	47	97.9	106	1	US-08-487-200-1 Sequence 1, Appli
42	47	97.9	106	1	US-08-487-200-7 Sequence 7, Appli
43	47	97.9	106	1	US-08-487-200-8 Sequence 8, Appli
44	47	97.9	106	1	US-08-487-200-16 Sequence 16, Appli
45	47	97.9	106	1	US-08-488-113B-163 Sequence 163, App

ALIGNMENTS

RESULT 1  
US-08-116-778E-9  
; Sequence 9, Application US/08116778E  
; Patent No. 5830470  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KUMANA, YOSHIOHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/116,778E  
; FILING DATE: 07-SEP-93  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 249-59  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-116-778E-9

Query Match 100.0%; Score 48; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSYMH 10  
|||||



Db 1 SASSSVSVMH 10

## RESULT 2

US-08-438-562-9

; Sequence 9, Application US/08438562  
; Patent No. 5874255

## ; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

; APPLICANT: KIWANA, YOSHIHISA

; APPLICANT: HASEGAWA, MAMORU

; TITLE OF INVENTION: HUMANIZED ANTIBODIES

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON &amp; VANDERHAYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/438,562

; FILING DATE: 10-MAY-95

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/116,778

; FILING DATE: 07-SEP-93

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 249-76

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4000

; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-438-562-9

Query Match 100.0%; Score 48; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10

Db 1 SASSSVSVMH 10

## RESULT 3

US-08-483-528B-97

; Sequence 97, Application US/08483528B  
; Patent No. 5939532

## ; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: KOIKE, MASAMICHI

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

; APPLICANT: KIWANA, YOSHIHISA

; APPLICANT: HASEGAWA, MAMORU

; TITLE OF INVENTION: HUMANIZED ANTIBODIES

; NUMBER OF SEQUENCES: 103

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON &amp; VANDERHAYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,528B

; FILING DATE: 07-JUN-95

; CLASSIFICATION: 536

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4000

; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 97:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-483-528B-97

Query Match 100.0%; Score 48; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10

Db 1 SASSSVSVMH 10

## RESULT 4

US-08-836-561-49

; Sequence 49, Application US/08836561  
; Patent No. 6018032

## ; GENERAL INFORMATION:

; APPLICANT: KOIKE, Masamichi

; APPLICANT: FURUYA, Akiko

; APPLICANT: NAKAMURA, Kazuyasu

; APPLICANT: IIDA, Akihito

; APPLICANT: ANAZAWA, Hideharu

; APPLICANT: HANAI, No. 6018032uo

; APPLICANT: TAKATSU, Kiyoshi

; TITLE OF INVENTION: Antibody Against Human Interleukin-5

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie &amp; Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: IBM Compatible

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/836,561

; FILING DATE: 09-MAY-1997

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 232384/95

; FILING DATE: 11-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lawrence, III, Stanton T

; REGISTRATION NUMBER: 25,736

REFERENCE/DOCKET NUMBER: 7005-115-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-836-561-49

Query Match 100.0%; Score 48; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10

RESULT 5  
US-09-393-385B-108  
Sequence 108, Application US/09393385B  
Patent No. 6423511  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUWANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/393,385B  
FILING DATE: 27-JUN-96  
CLASSIFICATION:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-393-385B-108

Query Match 100.0%; Score 48; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10

RESULT 6  
US-09-434-122-49  
Sequence 49, Application US/09434122  
Patent No. 6538111  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Masamichi  
FURUYA, Akiko  
NAKAMURA, Kazuyasu  
IIDA, Akihito  
ANAZAWA, Hideharu  
HANAI, No. 6538111uo  
TAKATSU, Kiyoshi  
TITLE OF INVENTION: Antibody Against Human Interleukin-5  
Receptor Alpha Chain  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/434,122  
FILING DATE: 05-NO. 6538111-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,561  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: JP 232384/95  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, III, Stanton T  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-115-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
US-09-434-122-49

Query Match 100.0%; Score 48; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10

RESULT 7  
US-09-280-028-4  
Sequence 4, Application US/09280028  
Patent No. 6241961  
GENERAL INFORMATION:  
APPLICANT: BENES, IVAN FRIEDRICH  
APPLICANT: BOSSLET, KLAUS  
TITLE OF INVENTION: RADIOIMMUNO CONJUGATES FOR USE IN HUMAN THERAPY AND  
FILE REFERENCE: BENES  
CURRENT APPLICATION NUMBER: US/09/280,028

CURRENT FILING DATE: 1999-03-26  
; EARLIER APPLICATION NUMBER: 199 11 329.7  
; EARLIER FILING DATE: 1999-03-15  
; EARLIER APPLICATION NUMBER: 198 13 687.0  
; EARLIER FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-280-028-4

Query Match 100.0%; Score 48; DB 3; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSYMH 10  
DB 16 SASSSVSYMH 25

RESULT 8  
US-08-308-494A-19  
; Sequence 19, Application US/08308494A  
; Patent No. 5959083  
; GENERAL INFORMATION:  
; APPLICANT: Bosslet, Klaus  
; APPLICANT: Seeman, Gerhard  
; TITLE OF INVENTION: Tetravalent Bispecific Receptors, The  
; TITLE OF INVENTION: Preparation and Use Thereof  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/308,494A  
; FILING DATE: 21-SEP-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/891,739  
; FILING DATE: 01-JUN-1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P4118120.4  
; FILING DATE: 03-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kulik, David J.  
; REGISTRATION NUMBER: 36,576  
; REFERENCE/DOCKET NUMBER: 05552-1186-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 100 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-308-494A-19  
Query Match 100.0%; Score 48; DB 2; Length 100;

Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SASSSVSYMH 10  
DB 21 SASSSVSYMH 30

RESULT 9  
US-08-434-000A-12  
; Sequence 12, Application US/08434000A  
; Patent No. 6046037  
; GENERAL INFORMATION:  
; APPLICANT: ANDREW C. HIATT, JULIAN  
; APPLICANT: K.-C. MA, THOMAS LEHNER  
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
; MEDIUM TYPE: storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/434,000A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; APPLICATION DATA: described below: 1  
; APPLICATION NUMBER: 08/367,395  
; FILING DATE: 12/30/94  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Guise, Jeffrey W.  
; REGISTRATION NUMBER: 34,613  
; REFERENCE/DOCKET NUMBER: 212/127  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 552-8400  
; TELEFAX: (619) 552-0159  
; TELEX: 67-3510  
; TELEX: SEQUENCE LISTING  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 105 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; TOPOLOGY: DESCRIPTION: Guy's 13 Kappa  
US-08-434-000A-12  
Query Match 100.0%; Score 48; DB 3; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SASSSVSYMH 10  
DB 24 SASSSVSYMH 33  
RESULT 10  
US-09-312-157-12  
; Sequence 12, Application US/09312157  
; Patent No. 6303341  
; GENERAL INFORMATION:

APPLICANT: ANDREW C. HIATT, JULIAN  
K.-C. MA, THOMAS LEHNER  
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
PROTEINS IN PLANTS AND THEIR USES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/312,157  
FILING DATE: 14-May-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/434,000  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 212/127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 552-8400  
TELEFAX: (619) 552-0159  
TELEX: 67-351  
SEQUENCE LISTING  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
DESCRIPTION: Guy's 13 Kappa  
US-09-312-157-12  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
Query Match 100.0%; Score 48; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33  
RESULT 11  
US-08-836-561-33  
Sequence 33, Application US/08836561  
Patent No. 6018032  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Masamichi  
APPLICANT: FURUYA, Akiko  
APPLICANT: NAKAMURA, Kazuyasu  
APPLICANT: IIDA, Akihiko  
APPLICANT: ANAZAWA, Hideharu  
APPLICANT: HANAI, No. 6018032uo  
APPLICANT: TAKATSU, Kiyoshi  
TITLE OF INVENTION: Antibody Against Human Interleukin-5  
Receptor Alpha Chain  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York

STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,561  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 232384/95  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, III, Stanton T  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-115-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-836-561-33

Query Match 100.0%; Score 48; DB 3; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.056;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 27 SASSSVSVMH 36

RESULT 12  
US-09-434-122-33  
Sequence 33, Application US/09434122  
Patent No. 6538111  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Masamichi  
APPLICANT: FURUYA, Akiko  
APPLICANT: NAKAMURA, Kazuyasu  
APPLICANT: IIDA, Akihiko  
APPLICANT: ANAZAWA, Hideharu  
APPLICANT: HANAI, No. 6538111uo  
APPLICANT: TAKATSU, Kiyoshi  
TITLE OF INVENTION: Antibody Against Human Interleukin-5  
Receptor Alpha Chain  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/434,122  
FILING DATE: 05-No. 6538111-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,561

FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: JP 232384/95  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, III, Stanton T  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-115-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-434-122-33

Query Match 100.0%; Score 48; DB 4; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.056;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
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DB 27 SASSSVSVMH 36

RESULT 13  
US-08-116-778E-2  
Sequence 2, Application US/08116778E  
Patent No. 5830470  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUMANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/116,778E  
FILING DATE: 07-SEP-93  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 249-59  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:

NAME/KEY: sig\_peptide  
LOCATION: -22...-1  
IDENTIFICATION METHOD: BY SIMILARITY  
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO AN ESTABLISHED  
IDENTIFICATION METHOD: CONSENSUS  
FEATURE:  
NAME/KEY: domain  
LOCATION: 24..33  
IDENTIFICATION METHOD: BY SIMILARITY  
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED  
IDENTIFICATION METHOD: CONSENSUS  
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"  
FEATURE:  
NAME/KEY: domain  
LOCATION: 49..55  
IDENTIFICATION METHOD: BY SIMILARITY  
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED  
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OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"  
FEATURE:  
NAME/KEY: domain  
LOCATION: 88..96  
IDENTIFICATION METHOD: BY SIMILARITY  
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED  
IDENTIFICATION METHOD: CONSENSUS  
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"  
US-08-116-778E-2

Query Match 100.0%; Score 48; DB 2; Length 129;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
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DB 46 SASSSVSVMH 55

RESULT 14  
US-08-438-562-2  
Sequence 2, Application US/08438562  
Patent No. 5874255  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUMANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,562  
FILING DATE: 10-MAY-95  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/116,778  
FILING DATE: 07-SEP-93  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955



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REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -22...-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
FEATURE:
NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-438-562-2

Query Match          100.0%; Score 48; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASSSVSYMH 10
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Db      46 SASSSVSYMH 55

RESULT 15
US-08-483-528B-92
; Sequence 92, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KIWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -22...-1
IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN
IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
FEATURE:
NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88..96
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IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-483-528B-92

Query Match          100.0%; Score 48; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASSSVSYMH 10
        |||||
Db      46 SASSSVSYMH 55
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:42:53 ; Search time 12.2924 Seconds  
(without alignments)  
96.613 Million cell updates/sec

Title: US-09-865-198-4

Perfect score: 48

Sequence: 1 SASSSVSYMH 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

451899

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
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#### SUMMARIES

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3	48	100.0	10	11	US-09-563-222-41
4	48	100.0	10	11	US-09-798-689-4
5	48	100.0	10	15	US-10-195-752-108
6	48	100.0	10	15	US-10-160-232-12
7	48	100.0	10	15	US-10-160-232-18
8	48	100.0	10	15	US-10-283-349-49
9	48	100.0	10	10	US-09-982-107-12
10	48	100.0	10	9	US-09-976-787-24
11	48	100.0	10	10	US-09-865-198-23
12	48	100.0	10	11	US-09-798-689-8
13	48	100.0	10	10	US-09-144-886-76
14	48	100.0	10	10	US-09-144-886-82
15	48	100.0	10	10	US-09-144-886-83

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17	48	100.0	10	9	US-09-976-787-8	Sequence 8, Appli
18	48	100.0	10	10	US-09-865-198-8	Sequence 8, Appli
19	48	100.0	11	15	US-10-283-349-33	Sequence 33, Appli
20	48	100.0	12	15	US-10-160-232-89	Sequence 89, Appli
21	48	100.0	12	15	US-10-160-232-93	Sequence 93, Appli
22	48	100.0	12	15	US-10-160-232-94	Sequence 94, Appli
23	48	100.0	12	15	US-10-160-232-96	Sequence 96, Appli
24	48	100.0	12	15	US-10-160-232-87	Sequence 87, Appli
25	48	100.0	12	15	US-10-160-232-92	Sequence 92, Appli
26	48	100.0	13	15	US-10-195-752-111	Sequence 111, App
27	48	100.0	13	15	US-10-195-752-113	Sequence 113, App
28	48	100.0	23	9	US-09-976-787-29	Sequence 29, Appli
29	48	100.0	23	10	US-09-865-198-28	Sequence 28, Appli
30	48	100.0	23	11	US-09-798-689-21	Sequence 21, Appli
31	48	100.0	24	9	US-09-976-787-28	Sequence 28, Appli
32	48	100.0	24	10	US-09-865-198-27	Sequence 27, Appli
33	48	100.0	24	16	US-10-259-087A-20	Sequence 20, Appli
34	47	97.9	11	9	US-09-808-037-28	Sequence 28, Appli
35	47	97.9	11	15	US-10-162-889-28	Sequence 28, Appli
36	47	97.9	23	9	US-09-808-037-6	Sequence 6, Appli
37	47	97.9	23	15	US-10-162-889-6	Sequence 6, Appli
38	45	93.8	10	10	US-09-910-059-26	Sequence 26, Appli
39	45	93.8	10	15	US-10-232-187-8	Sequence 8, Appli
40	45	93.8	10	15	US-09-910-059-50	Sequence 50, Appli
41	45	93.8	10	10	US-09-910-059-61	Sequence 61, Appli
42	45	93.8	10	10	US-09-910-059-65	Sequence 65, Appli
43	45	93.8	10	10	US-09-910-059-71	Sequence 71, Appli
44	45	93.8	10	15	US-10-232-187-4	Sequence 4, Appli
45	45	93.8	10	10	US-09-910-059-9	Sequence 9, Appli

#### ALIGNMENTS

RESULT 1  
US-09-976-787-4  
; Sequence 4, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-976-787-4

Query Match 100.0%; Score 48; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSYMH 10  
Db 1 SASSSVSYMH 10

RESULT 2  
US-09-865-198-4  
; Sequence 4, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping

;; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho  
;; FILE OF INVENTION: Production  
;; FILE REFERENCE: 11245/47102  
;; CURRENT APPLICATION NUMBER: US/09/865,198  
;; CURRENT FILING DATE: 2001-05-24  
;; PRIOR APPLICATION NUMBER: US 60/206,749  
;; PRIOR FILING DATE: 2000-05-24  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: WordPerfect 8.0 for Windows  
;; SEQ ID NO 4  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Mouse  
US-09-865-198-4

Query Match 100.0%; Score 48; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10

RESULT 3  
US-09-563-222-41  
; Sequence 41, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-41

Query Match 100.0%; Score 48; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10

RESULT 4  
US-09-798-689-4  
; Sequence 4, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07

;; PRIOR APPLICATION NUMBER: 08/326,552  
;; PRIOR FILING DATE: 1994-10-20  
;; PRIOR APPLICATION NUMBER: 08/196,041  
;; PRIOR FILING DATE: 1994-02-10  
;; NUMBER OF SEQ ID NOS: 41  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 4  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Mouse  
US-09-798-689-4

Query Match 100.0%; Score 48; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10

RESULT 5  
US-10-195-752-108  
; Sequence 108, Application US/10195752  
; Publication No. US2003007276A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KIWANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHAYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/195,752  
; FILING DATE: 16-Jul-2002  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/393,385B  
; FILING DATE: 27-JUN-96  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 108:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-10-195-752-108

Query Match 100.0%; Score 48; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10

RESULT 6  
US-10-160-232-12  
; Sequence 12, Application US/10160232  
; Publication No. US20030088075A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: ITO, MIKITO  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KAWADA, YOKO  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: SHIBUYA, MASABUMI  
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY  
; FILE REFERENCE: 249-107  
; CURRENT APPLICATION NUMBER: US/10/160,232  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US/09/453,718  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: 09/315,051  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/119,014  
; PRIOR FILING DATE: 1998-07-20  
; PRIOR APPLICATION NUMBER: PCT/JP97/04259  
; PRIOR FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-160-232-12  
Query Match 100.0%; Score 48; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10

RESULT 7  
US-10-160-232-18  
; Sequence 18, Application US/10160232  
; Publication No. US20030088075A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: ITO, MIKITO  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KAWADA, YOKO  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: SHIBUYA, MASABUMI  
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY  
; FILE REFERENCE: 249-107  
; CURRENT APPLICATION NUMBER: US/10/160,232  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US/09/453,718  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: 09/315,051  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/119,014  
; PRIOR FILING DATE: 1998-07-20  
; PRIOR APPLICATION NUMBER: PCT/JP97/04259  
; PRIOR FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-160-232-18  
Query Match 100.0%; Score 48; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10  
Db 1 SASSSVSVMH 10

RESULT 8  
US-10-283-349-49  
; Sequence 49, Application US/10283349  
; Publication No. US20030096977A1  
; GENERAL INFORMATION:  
; APPLICANT: KOIKE, Masamichi  
; FURUYA, Akiko  
; NAKAMURA, Kazuyasu  
; IIDA, Akihiko  
; ANAZAWA, Hideharu  
; HANAI, No. US20030096977A1uo  
; TAKATSU, Kiyoshi  
; TITLE OF INVENTION: Antibody Against Human Interleukin-5 Receptor Alpha Chain  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/283,349  
; FILING DATE: 29-Oct-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,561  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: JP 232384/95  
; FILING DATE: 11-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lawrence, III, Stanton T  
; REGISTRATION NUMBER: 25,736  
; REFERENCE/DOCKET NUMBER: 7005-115-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
US-10-283-349-49  
Query Match 100.0%; Score 48; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASSSVSVMH 10



Db 1 SASSSVSVMH 10

## RESULT 9

US-09-982-107-12  
; Sequence 12, Application US/09982107  
; Patent No. US20020159958A1  
; GENERAL INFORMATION:  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING  
; PROTECTION PROTEINS IN PLANTS AND THEIR USE  
; FILE REFERENCE: EPI3002E  
; CURRENT APPLICATION NUMBER: US/09/982,107  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa  
US-09-982-107-12

Query Match 100.0%; Score 48; DB 10; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33

## RESULT 10

US-09-976-787-24  
; Sequence 24, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 24  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-24

Query Match 100.0%; Score 48; DB 9; Length 106;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33

## RESULT 11

US-09-865-198-23  
; Sequence 23, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods

; TITLE OF INVENTION: Production

; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 23  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-23

Query Match 100.0%; Score 48; DB 10; Length 106;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33

## RESULT 12

US-09-798-689-8  
; Sequence 8, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/326,552  
; PRIOR FILING DATE: 1994-10-20  
; PRIOR APPLICATION NUMBER: 08/196,041  
; PRIOR FILING DATE: 1994-02-10  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-798-689-8

Query Match 100.0%; Score 48; DB 11; Length 106;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASSSVSVMH 10  
Db 24 SASSSVSVMH 33

## RESULT 13

US-09-144-886-76  
; Sequence 76, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; TITLE OF INVENTION: Botulinum Neurotoxins

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; FILE REFERENCE: 2500.117USO
; CURRENT-APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C9 region VL epitope 1
US-09-144-886-76
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Query Match          100.0%; Score 48; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SASSSVSVMH 10
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Db      24 SASSSVSVMH 33
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RESULT 14
US-09-144-886-82
; Sequence 82, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 1B8 region VL epitope 1
US-09-144-886-82
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Query Match          100.0%; Score 48; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SASSSVSVMH 10
      |||||
Db      24 SASSSVSVMH 33
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RESULT 15
US-09-144-886-83
; Sequence 83, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 1G7 region VL epitope 1
US-09-144-886-83
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Query Match          100.0%; Score 48; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SASSSVSVMH 10
      |||||
Db      24 SASSSVSVMH 33
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OM protein - protein search, using sw model

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158.727 Million cell updates/sec

Title: US-09-865-198-5  
Perfect score: 31  
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	18 AAW41383	CDR2 of light chain
2	31	100.0	7	19 AAW73170	CDR2 of light chain
3	31	100.0	7	20 AAY28391	Peptide fragment f
4	31	100.0	7	21 AAY97233	Complementary dete
5	31	100.0	7	21 AAB10005	H. pylori 26 kDa p
6	31	100.0	7	22 AAE13141	Humanised antibody
7	31	100.0	7	22 AAB82707	VEGF antagonist an
8	31	100.0	7	22 AAB81968	Ganglioside GD2 sp
9	31	100.0	7	22 AAB83164	Mouse ganglioside

10	31	100.0	7	22 AAG63992	Complementarity de
11	31	100.0	7	23 AAE25953	Mouse anti-KDR pic
12	31	100.0	7	23 AAU81254	Murine trkC antibo
13	31	100.0	7	23 AAU74410	Light chain comple
14	31	100.0	7	24 ABJ26722	VEGF binding relat
15	31	100.0	8	23 AAG80315	Anti-human TNF- $\alpha$ p
16	31	100.0	55	24 ABUS6871	BONT/A Hc binding
17	31	100.0	55	24 ABUS6882	BONT/A Hc binding
18	31	100.0	60	24 ABUS6883	BONT/A Hc binding
19	31	100.0	92	20 AAW89175	Anti-p53 monoclonal
20	31	100.0	93	23 ABP02151	Human ORFX protein
21	31	100.0	100	11 AAR07319	Monoclonal antibod
22	31	100.0	100	17 AAW14487	Monoclonal antibod
23	31	100.0	100	17 AAR99876	Monoclonal antibod
24	31	100.0	102	22 AAB62264	Light chain constr
25	31	100.0	102	24 ABG72734	Mouse U16 recombin
26	31	100.0	105	17 AAW03182	Guy's 13 anti-Stre
27	31	100.0	106	22 AAE13144	Humanised antibody
28	31	100.0	106	23 AAU74418	Antigen-binding pr
29	31	100.0	106	24 ABJ26730	VEGF binding relat
30	31	100.0	107	18 AAW41397	Anti-CEA antibody
31	31	100.0	107	18 AAW41400	Humanised antibody
32	31	100.0	107	18 AAW41401	Humanised antibody
33	31	100.0	107	18 AAW41390	Anti-CEA antibody
34	31	100.0	107	22 AAB83159	Mouse ganglioside
35	31	100.0	107	22 AAB83167	Ganglioside GM2 an
36	31	100.0	107	22 AAG63987	Amino acid sequenc
37	31	100.0	108	13 AAR21294	Murine VL kappa gr
38	31	100.0	108	13 AAR21290	Murine VL kappa gr
39	31	100.0	108	16 AAR79884	Anti-EGFR antibody
40	31	100.0	108	18 AAW41388	Anti-CEA antibody
41	31	100.0	108	21 AAY97236	Variable light cha
42	31	100.0	108	21 AAB10021	H. pylori 26 kDa p
43	31	100.0	108	21 AAY90815	33f8 hybridoma VL
44	31	100.0	108	21 AAY53591	Light chain from a
45	31	100.0	108	21 AAY59306	DC8 light chain va

ALIGNMENTS

RESULT 1	
AAW41383	
ID AAW41383 standard; peptide; 7 AA.	
XX	
AC AAW41383;	
XX	
DT 02-JUN-1998 (first entry)	
XX	
DE CDR2 of light chain of anti-CEA antibody.	
XX	
KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;	
KW cancer diagnosis; complementarity determining region; light chain.	
XX	
OS Synthetic.	
XX	
PN W09742329-A1.	
XX	
PD 13-NOV-1997.	
XX	
PF 29-APR-1997; 97WO-GB01165.	
XX	
PR 14-FEB-1997; 97GB-0003103.	
PR 04-MAY-1996; 96GB-0009405.	
XX	
PA (ZENEC ) ZENECA LTD.	
XX	
PI Copley CG, Edge MD, Emery SC;	
XX	
DR WPI; 1997-558987/51.	
XX	
PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for	
PT diagnosis and therapy of cancer	

XX Claim 1; Page 196; 208pp; English.  
PS  
XX  
CC This sequence represents a complementarity determining region (CDR) of  
CC the light chain of the antibody of the invention. The antibody is an  
CC anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or  
CC transgenic organisms transformed with DNA encoding the antibody, are used  
CC to make the antibody or conjugate. The conjugate is used in a medicament  
CC suitable for intravenous administration. The conjugate can be used for  
CC cancer therapy, selectively killing tumour cells. The antibody can be  
CC used for in vivo or in vitro diagnosis of cancer.  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 18; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
|||  
Db 1 STSNLAS 7

RESULT 2  
AAW73170  
ID AAW73170 standard; peptide; 7 AA.

AC AAW73170;

DT 22-JAN-1999 (first entry)

DE CDR2 of light chain of ganglioside GM2 targeting antibody.

KW Ganglioside GM2; antibody; complementarity determining region; cancer;  
anti-tumour agent.

OS Homo sapiens.

PN JP10257893-A.

PD 29-SEP-1998.

PF 19-MAR-1997; 97JP-0066981.

PR 19-MAR-1997; 97JP-0066981.

PA (XYOW ) KYOWA HAKKO KOGYO KK.

DR WPI; 1998-575904/49.

PT A human type complementarity determining region transplanted  
PT antibody against ganglioside GM2 - useful as an anti-tumour agent  
PT and as a diagnostic for related cancers  
PS Claim 1; Page 29; 66pp; Japanese.

CC This sequence represents a complementarity determining region (CDR) from  
CC the heavy chain of the antibody of the invention. The antibody of the  
CC invention is a human CDR transplanted antibody that reacts specifically  
CC with ganglioside GM2. DNA encoding the antibody, and vectors and  
CC transformants containing it, can be used for the recombinant production  
CC of the antibody. The antibody itself can be used as an anti-tumour agent  
CC or as a diagnostic tool for related cancers. The antibody has antitumour  
CC activity against ganglioside GM2 positive cells.  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
|||  
Db 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 3  
AAV28391  
ID AAV28391 standard; Protein; 7 AA.

AC AAV28391;

DT 04-NOV-1999 (first entry)

DE Peptide fragment from the human anti-GM2 light chain in RRI.

KW antibody; RRI; complementarity determining region; CDR;  
chimeric; light chain; heavy chain.

OS Homo sapiens.

PN US5939532-A.

PD 17-AUG-1999.

PF 07-JUN-1995; 95US-0483528.

PR 07-JUN-1995; 95US-0483528.

PR 07-SEP-1993; 93US-0116778.

PA (XYOW ) KYOWA HAKKO KOGYO KK.

PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;  
Shitara K;

DR WPI; 1999-468416/39.

PT Chimeric human antibody expression vectors

PS Example 2; Column 157; 188pp; English.

CC The sequences AAY28390 to AAY28392 replace the CDR regions of the NEMM  
CC DNA and they produce AAY28394, the hKW796L human anti-GM2 antibody light  
CC chain.

CC Chimeric human antibodies of the invention are useful in the treatment  
CC of cancer, especially that which is of neural ectodermal origin.

CC In contrast to prior art constructs based on mouse monoclonal  
CC antibodies, the chimeric human antibodies do not cause anti-mouse  
CC immunoglobulin production.

CC The chimeric human antibodies have a prolonged half-life and a reduced  
CC frequency of adverse effects when compared to mouse monoclonal  
CC antibodies.  
XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
|||  
Db 1 STSNLAS 7

RESULT 4  
AAV97233  
ID AAV97233 standard; Protein; 7 AA.

AC AAV97233;

DT 19-DEC-2000 (first entry)

DE Complementary determining region (CDR2) of anti-SI(KDR) antibody.

KW Immunoglobulin; antibody; complementary determining region; CDR;  
VEGF; vascular endothelial growth factor; KDR;



KW kinase:insert domain containing receptor; multivalent; monovalent;  
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;  
KW glioblastoma multiforme; hemangioblastoma; AIDS;  
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;  
KW acquired immune deficiency syndrome; AIDS; human.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200044777-A1.  
XX  
PD 03-AUG-2000.  
XX  
PF 28-JAN-2000; 2000WO-US02180.  
XX  
PR 29-JAN-1999; 99US-0117726.  
PR 29-JAN-1999; 99US-0240736.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z, Witte L;  
XX  
DR WPI; 2000-505966/45.  
DR N-PSDB; AAA53765.  
XX  
PT Novel immunoglobulin molecules binding kinase insert domain-containing  
PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growth  
XX  
PS Claim 3; Page 50; 55pp; English.  
XX  
CC New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Kaposi's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulins of the invention.  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 31; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 STSNLAS 7  
Db 1 STSNLAS 7  
RESULT 5  
AAB10005  
ID AAB10005 standard; Protein; 7 AA.  
XX  
AC AAB10005;  
XX  
DT 01-NOV-2000 (first entry)  
XX  
DE H. pylori 26 kDa protein-binding antibody light chain CDR2 peptide.  
XX  
KW Acid-resistant microorganism; detection; faecal; intestine; infection;  
KW monoclonal antibody; light chain; complementarity determining region;  
XX  
OS Unidentified.

XX  
PN WO200026671-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 29-OCT-1999; 99WO-EP08212.  
XX  
PR 29-OCT-1998; 98EP-0120517.  
PR 06-NOV-1998; 98EP-0120687.  
XX  
PA (CONN-) CONNEX GMBH.  
XX  
PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;  
PI Ringeis A;  
XX  
DR WPI; 2000-365747/31.  
DR N-PSDB; AAA40161.  
XX  
PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter  
PT pylori, comprises reacting a faecal sample with two binding reagents for  
PT antigens that survive intestinal passage  
XX  
PS Claim 24; Page 21; 84pp; German.  
XX  
CC This invention describes a novel method for the detection of a mammalian  
CC infection by an acid-resistant microorganism (A) by treating a faecal  
CC sample with at least two different monoclonal antibodies (Mab) (or their  
CC fragments or derivatives) or aptamers (collectively (I)) and detecting  
CC formation of a complex (C) between (I) and the corresponding antigen of  
CC (A). The first and second (I) bind to epitopes of different antigens  
CC (Ag). These epitopes are present, after passage through the intestines,  
CC in at least some mammals, and have either: (i) their native structure;  
CC or (ii) a structure against which an antibody is produced by an animal  
CC infected or immunized with (A), or its extract, lysate, derived protein  
CC or fragment, or with a synthetic peptide. Practically all mammals display  
CC at least one of the specified epitopes. The method is used to detect  
CC infection by acid-fast bacteria, particularly of the genera Helicobacter,  
CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,  
CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used  
CC therapeutically. The method is direct and non-invasive, and provides an  
CC inexpensive and easily standardizable diagnosis, despite possible  
CC degradation of antigens during passage through the intestines. This  
CC sequence represents a fragment of a H. pylori 26 kDa protein-binding  
CC antibody light chain complementarity determining region CDR2 which is  
CC used to illustrate the method of the invention.  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 31; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 STSNLAS 7  
Db 1 STSNLAS 7  
RESULT 6  
AAB13141  
ID AAB13141 standard; peptide; 7 AA.  
XX  
AC AAB13141;  
XX  
DT 28-JAN-2002 (first entry)  
XX  
DE Humanised antibody murine light chain hypervariable region (VL) CDR2.  
XX  
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytostatic; light chain hypervariable region; VL; myelocytic leukaemia;  
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;  
KW Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.  
XX  
OS Mus sp.

XX PN WO200174296-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US10504.  
XX PR 31-MAR-2000; 2000US-0540770.  
XX PA (IMCL-) IMCLONE SYSTEMS INC.  
XX PA (CORR ) CORNELL RES FOUND INC.  
XX PI Witte L, Rafil S;  
XX DR WPI; 2001-662942/76.  
XX DR N-PSDB; AAD21667.  
XX PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
XX PT tumors such as leukemias or multiple myeloma comprises treatment with  
XX PT an antagonist of a vascular endothelial growth factor receptor -  
XX PS Claim 8; Page 15; 68pp; English.  
XX CC The invention relates to a method for inhibiting the growth of non-solid  
XX CC tumour cells that are stimulated by a ligand of vascular endothelial  
XX CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
XX CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
XX CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
XX CC variable region joined to human constant region, where the humanised  
XX CC mouse variable region contains mouse complementarity determining region  
XX CC (CDR) grafted into human variable region. The method is useful for  
XX CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
XX CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
XX CC multiple myelomas and lymphoid cells, particularly those related to  
XX CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised  
XX CC antibody murine light chain hypervariable region (VL) CDR-2 used in the  
XX CC exemplification of the invention.  
XX SQ Sequence 7 AA:  
Query Match 100.0%; Score 31; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 STSNLAS 7  
Db 1 STSNLAS 7  
RESULT 7  
AAB82707  
ID AAB82707 standard; Peptide; 7 AA.  
XX AC AAB82707;  
XX DT 15-OCT-2001 (first entry)  
XX DE VEGF antagonist antibody IMC-1C11 VL CDR-2.  
XX KM IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
XX KM vascular endothelial growth factor; angiogenesis; antiangiogenic;  
XX KM antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
XX KM tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
XX KM colon carcinoma; ovarian carcinoma; neuroblastoma;  
XX KM glioblastoma multiforme; melanoma; therapy; light chain; CDR;  
XX KM complementarity determining region.  
XX OS Chimeric - Mus sp.  
XX OS Chimeric - Homo sapiens.  
XX PN WO200154723-A1.  
XX PD 02-AUG-2001.

XX PF 29-JAN-2001; 2001WO-US02839.  
XX XX 28-JAN-2000; 2000US-0178791.  
XX PR 31-MAR-2000; 2000US-0539692.  
XX XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
XX PA (IMCL-) IMCLONE SYSTEMS INC.  
XX PI Kerbel R;  
XX DR WPI; 2001-514531/56.  
XX PT Treating or controlling an angiogenic dependent condition (e.g. a  
XX PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
XX PT administering a combination of an antiangiogenic molecule and a  
XX PT chemotherapeutic agent -  
XX PS Disclosure; Page 37; 42pp; English.  
XX CC The present sequence is that of complementarity determining region  
XX CC 2 of the light chain variable region (see also AAB82702) of  
XX CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
XX CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
XX CC or a fragment of it, can be used as an anti-angiogenic molecule,  
XX CC together with a chemotherapeutic acid, for the treatment of an  
XX CC angiogenic dependent condition in a mammal, especially a human.  
XX CC The invention relates generally to a method of treating or  
XX CC controlling an angiogenic dependent condition by administering an  
XX CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
XX CC regression or arrest of the condition while minimising or  
XX CC preventing significant toxicity of the chemotherapeutic agent.  
XX CC The anti-angiogenic molecule inhibits or blocks the action of a  
XX CC vascular endothelium survival factor such as VEGF or its receptor,  
XX CC and is especially IMC-1C11. Conditions that can be treated include  
XX CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
XX CC especially a solid tumour, including breast carcinoma, lung  
XX CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
XX CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
XX CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX SQ Sequence 7 AA:  
Query Match 100.0%; Score 31; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 STSNLAS 7  
Db 1 STSNLAS 7  
RESULT 8  
AAB81968  
ID AAB81968 standard; Peptide; 7 AA.  
XX AC AAB81968;  
XX DT 03-JUL-2001 (first entry)  
XX DE Ganglioside GD2 specific antibody related peptide SEQ ID NO: 7.  
XX KM Ganglioside; GD2; complementation determining region; CDR; antibody;  
XX KM mouse; cancer.  
XX KM Mus musculus.  
XX OS Mus musculus.  
XX PN WO200123573-A1.  
XX PD 05-APR-2001.  
XX PF 29-SEP-2000; 2000WO-JP06773.  
XX XX

PR 30-SEP-1999; 99JP-0278290.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266163/27.  
XX  
PT Human type complementation-determining domain transplanted antibody and  
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of  
PT e.g. tumours, has low antigenicity, little side effects but potent  
PT activity in cancer -  
XX  
PS Claim 6; Page 100; 123pp; Japanese.  
XX  
CC The present invention describes an antibody, which can react specifically  
CC with ganglioside GD2, and is transplanted with a human type  
CC complementation-determining domain (CDR), or its fragments. The antibody  
CC and its derivatives are useful in diagnosis and therapy of tumours,  
CC particularly cancer diagnosis. The present sequence is a peptide  
CC used in the exemplification of the invention.  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
|||  
Db 1 STSNLAS 7

RESULT 9  
AAB83164  
ID AAB83164 standard; peptide; 7 AA.  
XX  
AC AAB83164;  
XX  
DT 02-JUL-2001 (first entry)  
XX  
DE Mouse ganglioside GM2 antibody light chain variable region CDR2.  
XX  
KW Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer;  
KW complementarity determining region; CDR.  
XX  
OS Mus sp.  
XX  
PN WO200123431-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP06775.  
XX  
PR 30-SEP-1999; 99JP-0278292.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266142/27.  
XX  
PT Monoclonal antibodies against ganglioside GM2 combined with drugs,  
PT radioisotopes or proteins for treatment and diagnosis of cancer -  
XX  
PS Claim 4; Page 72; 80pp; Japanese.  
XX  
CC The present invention relates to derivatives of an antibody against  
CC ganglioside GM2. The antibody may be a monoclonal antibody or its  
CC fragments. The antibody is combined with a radioactive isotope,  
CC protein or small drug in the treatment and diagnosis of cancer.  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
|||  
Db 1 STSNLAS 7

RESULT 10  
AAG63992  
ID AAG63992 standard; peptide; 7 AA.  
XX  
AC AAG63992;  
XX

DT 26-NOV-2001 (first entry)  
XX  
DE Complementary determining region of light chain of antibody 2C4.  
XX  
KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;  
KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;  
KW leukemia; eosinophil.  
XX  
OS Mus sp.  
XX

PN WO200166126-A1.  
XX  
PD 13-SEP-2001.  
XX  
PF 05-MAR-2001; 2001WO-US07193.  
XX  
PR 07-MAR-2000; 2000US-0187595.  
XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX

PI Abrahamson JA, Bochner B, Erickson-Miller CL, Kirkly KK;  
PI Schleimer R;  
XX  
DR WPI; 2001-570749/64.  
XX

PT Novel monoclonal antibody specific for human sialoadhesin factor-2 for  
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases  
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal -  
XX  
PS Claim 10; Page 34; 35pp; English.  
XX

CC AAG63991-93 represent the complementarity determining regions (CDRs)  
CC of the light chain variable region of murine monoclonal antibody 2C4.  
CC This antibody binds to human sialoadhesin factor-2 (SAF-2). The  
CC antibody is useful for treating or preventing allergic rhinitis,  
CC allergies, asthma, anemia, eczema or diseases such as lymphoma,  
CC leukemia or systemic mastocytosis in a mammal. It is also useful for  
CC detecting the presence of a cell, especially eosinophil in a sample,  
CC by detecting binding of the antibody to SAF-2. The antibody can be  
CC coupled to toxins, antiproliferative drugs or radionuclides to  
CC kill cells in areas of excessive SAF-2 expression.  
XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
|||  
Db 1 STSNLAS 7

RESULT 11  
AAE25953

ID AAE25953 standard; peptide; 7 AA.  
XX  
AC AAE25953;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Mouse anti-KDR pIC11 scFv antibody CDR12 peptide.  
XX  
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; light chain complementarity determining region 2;  
KW CDR12; angiogenesis; pIC11; scFv antibody.  
XX  
OS Mus musculus.  
XX  
PN US2002064528-A1.  
XX  
PD 30-MAY-2002.  
XX  
PF 12-OCT-2001; 2001US-0976787.  
XX  
PR 28-JAN-2000; 2000US-0493539.  
XX  
PA (ZHUZ/) ZHU Z.  
PA (WITT/) WITTE L.  
XX  
PI Zhu Z, Witte E;  
XX  
DR WPI; 2002-589175/63.  
DR N-PSDB; AAD42818.  
XX  
PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR  
XX  
PS Claim 3; Page 11; 34pp; English.  
XX  
CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR pIC11 scFv antibody  
CC light chain complementarity determining region 2 (CDR12).  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 31; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 STSNLAS 7  
Db 1 STSNLAS 7  
RESULT 12  
AAU81254  
ID AAU81254 standard; Peptide; 7 AA.  
XX  
AC AAU81254;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Murine trkC antibody light chain CDR2 of variable region #2.  
XX  
KW Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;  
KW trkA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;  
KW peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;  
KW large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;  
KW nerve cell injury; blood cell disorder; leukopaenia; eosinopaenia; wound;  
XX

KW basopaenia; lymphopaenia; monocytopenia; neutropaenia; cancer; ulcer;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;  
KW sickle cell disease; cardiac ischaemia; cerebrovascular disorder;  
KW cellular degeneration; gene therapy.  
XX  
OS Mus sp.  
XX  
PN WO200198361-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 22-JUN-2001; 2001WO-US20153.  
XX  
PR 22-JUN-2000; 2000US-213141P.  
PR 05-OCT-2000; 2000US-238319P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Devaux B, Hongo JS, Presta LG, Shelton DL;  
XX  
DR WPI; 2002-130790/17.  
XX  
PT Novel anti-trkC agonist monoclonal antibody useful for treating  
PT neurodegenerative disease, shows no significant cross-reactivity with  
PT trkA/trkB, and recognizes epitope in domain 5 of trkC  
XX  
PS Claim 13; Fig 11; 121pp; English.  
XX  
CC The invention relates to an anti-trkC agonist monoclonal antibody which  
CC shows no significant cross-reactivity with trkA or trkB, and recognizes  
CC an epitope in domain 5 of trkC. The antibodies of the invention are  
CC effective in the treatment of cisplatin- or pyridoxine-induced  
CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre  
CC sensory neuropathy, neurodegenerative disease including amyotrophic  
CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood  
CC cells such as leukopaenia including eosinopaenia, basopaenia,  
CC lymphopaenia, monocytopenia, neutropaenia, Alzheimer's disease,  
CC Parkinson's disease, Huntington's disease and tumours. The sequences are  
CC also useful for inducing angiogenesis for treating wounds, ulcers and  
CC diabetic complications of sickle cell disease, for treating cardiac  
CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases  
CC involving cellular degeneration. Sequences AAU81229-AAU81284 represent  
CC human and mouse anti-trkC agonist monoclonal antibodies and antibody  
CC fragments of the invention.  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 31; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 STSNLAS 7  
Db 1 STSNLAS 7  
RESULT 13  
AAU74410  
ID AAU74410 standard; peptide; 7 AA.  
XX  
AC AAU74410;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Light chain complementarity determining region L2 (CDR12).  
XX  
KW Complementarity determining region; CDR; CDR12; antigen; cytostatic;  
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;  
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;  
KW antibody light chain variable domain.  
XX  
OS Mus sp.  
XX



PN WO200190192-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US16924.  
XX  
PR 24-MAY-2000; 2000US-206749P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2002-106189/14.  
DR N-PSDB; AAS20281.  
XX  
PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides  
XX  
PS Claim 55; Page 57; 64pp; English.  
XX  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (CL domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This peptide sequence represents the light chain variable domain  
CC complementarity determining region L2 (CDRL2) incorporated into an  
CC antigen-binding protein described in the method of the invention.  
XX  
SQ Sequence 7 AA;  
OY  
Query Match 100.0%; Score 31; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 STSNLAS 7  
OY 1 STSNLAS 7  
Db 1 STSNLAS 7  
RESULT 14  
ABJ26722  
ID ABJ26722 standard; Peptide; 7 AA.  
XX  
AC ABJ26722;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE VEGF binding related peptide SEQ ID No 5.  
XX  
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.  
XX  
OS Mus sp.  
XX  
PN WO2003002144-A1.  
XX

PD 09-JAN-2003.  
XX  
PF 26-JUN-2002; 2002WO-US20332.  
XX  
PR 26-JUN-2001; 2001US-301299P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2003-201468/19.  
DR N-PSDB; ABT23300.  
XX  
PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -  
XX  
PS Claim 6; Page 49; 98pp; English.  
XX  
CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse peptide relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX  
SQ Sequence 7 AA;  
OY  
Query Match 100.0%; Score 31; DB 24; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 STSNLAS 7  
OY 1 STSNLAS 7  
Db 1 STSNLAS 7  
RESULT 15  
AAG80315  
ID AAG80315 standard; peptide; 8 AA.  
XX  
AC AAG80315;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Anti-human TNF-alpha CDR-L2 peptide.  
XX  
KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;  
KW heavy chain; light chain; complementarity determining region; vasotropic;  
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;  
KW rheumatoid arthritis; malaria; multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200179298-A1.  
XX  
PD 25-OCT-2001.  
XX  
PF 18-APR-2001; 2001WO-JP03308.  
XX  
PR 19-APR-2000; 2000JP-0117394.  
XX  
PA (SUNR ) SUNTORY LTD.  
XX  
PI Fukuda Y, Nagahira K, Nakanishi T;  
XX  
DR WPI; 2002-066345/09.  
XX



PT Novel heavy and light-chain polypeptides of chimeric and humanised  
PT antibodies against human tumour necrosis factor alpha for  
PT low-immunogenicity treatment of TNF-related diseases such as toxic  
PT shock syndrome

PS Claim 3b; Page 26; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides  
CC or their fragments of a recombinant antibody to human TNF-alpha which  
CC contain complementarity determining region (CDR) sequences. The products  
CC of the invention have vasotropic, antiarthritic, neuroprotective and  
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in  
CC vivo. The antibodies are used for producing chimeric and humanised  
CC antibodies that may be used for the treatment and prevention of TNF-alpha  
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,  
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in  
CC humans. This sequence represents the anti-human tumour necrosis  
CC factor-alpha (TNF-alpha) light chain CDR1 designated CDR-L2.

XX Sequence 8 AA;

Query Match 100.0%; Score 31; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STSNLAS 7  
Db 2 STSNLAS 8

Search completed: July 30, 2003, 09:36:47  
Job time : 8 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 2.06977 Seconds  
(without alignments)  
325.245 Million cell updates/sec

Title: US-09-865-198-5  
Perfect score: 31  
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	31	100.0	91	2 S17626	Ig kappa chain V r
2	31	100.0	91	2 S17630	Ig kappa chain V r
3	31	100.0	93	2 S17623	Ig kappa chain V r
4	31	100.0	93	2 S17640	Ig kappa chain V r
5	31	100.0	93	2 S17641	Ig kappa chain V r
6	31	100.0	93	2 S17642	Ig kappa chain V r
7	31	100.0	96	2 C33730	Ig kappa chain V r
8	31	100.0	99	2 D38601	Ig kappa chain V r
9	31	100.0	99	2 PH1058	Ig kappa chain V r
10	31	100.0	99	2 PH1059	Ig light chain V r
11	31	100.0	99	2 PH1060	Ig light chain V r
12	31	100.0	109	2 PT0404	Ig light chain V r
13	31	100.0	109	2 PT0405	Ig light chain V r
14	31	100.0	130	2 A32513	Ig kappa chain pre
15	31	100.0	140	2 PL0013	Ig kappa chain pre
16	31	100.0	265	2 AH3513	channel protein vi
17	31	100.0	753	2 S35371	finger protein neu
18	31	100.0	1107	2 S61667	probable membrane
19	28	90.3	86	2 S20651	Ig heavy chain V r
20	28	90.3	106	2 PL0082	Ig kappa chain V r
21	28	90.3	107	2 A42848	Ig light chain V r
22	28	90.3	204	2 S48376	probable membrane
23	28	90.3	531	1 P1W1MS	major capsid prote
24	28	90.3	531	2 AG1812	hypothetical prote
25	28	90.3	567	2 T11653	hypothetical prote
26	28	90.3	597	2 B82881	hypothetical prote
27	28	90.3	601	2 T37738	hypothetical prote
28	28	90.3	707	2 S57157	hypothetical prote
29	28	90.3	963	2 B70524	probable PPE prote

30	28	90.3	1333	2 S38635	blastopia polyprot
31	27	87.1	67	2 S24216	Ig kappa chain - m
32	27	87.1	68	2 S26474	Ig kappa chain V r
33	27	87.1	84	2 S68152	hypothetical prote
34	27	87.1	86	2 S26459	Ig kappa chain V r
35	27	87.1	86	2 S20649	Ig heavy chain V r
36	27	87.1	86	2 S29587	Ig kappa chain V r
37	27	87.1	90	2 S26339	Ig kappa chain V r
38	27	87.1	93	2 S17624	Ig kappa chain V r
39	27	87.1	93	2 S17625	Ig kappa chain V r
40	27	87.1	93	2 S17631	Ig kappa chain V r
41	27	87.1	93	2 S17632	Ig kappa chain V r
42	27	87.1	93	2 S17633	Ig kappa chain V r
43	27	87.1	93	2 S17634	Ig kappa chain V r
44	27	87.1	93	2 S17635	Ig kappa chain V r
45	27	87.1	93	2 S17636	Ig kappa chain V r

## ALIGNMENTS

RESULT 1  
S17626  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S17626  
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A/Title: Making antibody fragments using phage display libraries.  
A/Reference number: S17230; MUID:91326098; PMID:1907718  
A/Accession: S17626  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-91 <CLA>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 41 STSNLAS 47

RESULT 2  
S17630  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S17630  
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A/Title: Making antibody fragments using phage display libraries.  
A/Reference number: S17230; MUID:91326098; PMID:1907718  
A/Accession: S17630  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-91 <CLA>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 41 STSNLAS 47

## RESULT 3

S17623  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C;Accession: S17623  
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A;Title: Making antibody fragments using phage display libraries.  
A;Reference number: S17230; MUID:91326098; PMID:1907718  
A;Accession: S17623  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-93 <CLA>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
|||||  
Db 43 STSNLAS 49

## RESULT 4

S17640  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C;Accession: S17640  
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A;Title: Making antibody fragments using phage display libraries.  
A;Reference number: S17230; MUID:91326098; PMID:1907718  
A;Accession: S17640  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-93 <CLA>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
|||||  
Db 43 STSNLAS 49

## RESULT 5

S17641  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C;Accession: S17641  
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A;Title: Making antibody fragments using phage display libraries.  
A;Reference number: S17230; MUID:91326098; PMID:1907718  
A;Accession: S17641  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-93 <CLA>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
|||||  
Db 43 STSNLAS 49

## RESULT 6

S17642  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C;Accession: S17642  
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A;Title: Making antibody fragments using phage display libraries.  
A;Reference number: S17230; MUID:91326098; PMID:1907718  
A;Accession: S17642  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-93 <CLA>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
|||||  
Db 43 STSNLAS 49

## RESULT 7

C33730  
Ig kappa chain V region (4.68) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Mar-1990 #sequence\_revision 18-Sep-1992 #text\_change 21-Jan-2000  
C;Accession: C33730  
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.  
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989  
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, until  
A;Reference number: A33730; MUID:89367325; PMID:2505260  
A;Accession: C33730  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-96 <LAW>  
A;Cross-references: GB:M25999; NID:g197117; PIDN:AAA38915.1; PID:g197118  
A;Note: the authors translated the codon TTG for residue 34 as Phe  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
|||||  
Db 51 STSNLAS 57

## RESULT 8

D38601  
Ig kappa chain V region (6A7) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 21-Jan-2000  
C;Accession: D38601  
R;Goshorn, S.C.; Retzel, E.; Jemerson, R.

J. Biol. Chem. 266, 2134-2142, 1991  
A;Title: Common structural features among monoclonal antibodies binding the same antigen  
A;Reference number: A38601; MUID:91115823; PMID:1703527  
A;Accession: D38601

A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-99 <GOS>

A;Cross-references: GB:M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
|||||  
Db 41 STSNLAS 47

## RESULT 9

PH1058

Ig light chain V region (clone 163.72) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C;Accession: PH1058

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1058

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-99 <TIL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
|||||  
Db 51 STSNLAS 57

## RESULT 10

PH1059

Ig light chain V region (clone 17s-cl) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C;Accession: PH1059

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1059

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-99 <TIL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7

Db 51 STSNLAS 57  
|||||

## RESULT 11

PH1060

Ig light chain V region (clone 74-cl) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C;Accession: PH1060

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both Igm and Igg anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1060

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-99 <TIL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
|||||  
Db 51 STSNLAS 57

## RESULT 12

PT0404

Ig light chain V region (S107/VH11 group 3-23) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999

C;Accession: PT0404

R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.

J. Exp. Med. 173, 731-741, 1991

A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi

A;Reference number: PT0376; MUID:91147903; PMID:1900082

A;Accession: PT0404

A;Molecule type: DNA

A;Residues: 1-109 <BEH>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
|||||  
Db 51 STSNLAS 57

## RESULT 13

PT0405

Ig light chain V region (S107/VH11 group 3-38) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999

C;Accession: PT0405

R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.

J. Exp. Med. 173, 731-741, 1991

A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi

A;Reference number: PT0376; MUID:91147903; PMID:1900082

A;Accession: PT0405

A;Molecule type: DNA

A;Residues: 1-109 <BEH>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Job time : 3.06977 secs

## Query Match

100.0%; Score 31; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 2.8; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 51 STSNLAS 57

## RESULT 14

A32513

Ig kappa chain precursor V region (MRL22) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000

C;Accession: A32513

R;Kofler, R.; Strohhal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;

J. Clin. Invest. 82, 852-860, 1988

A;Title: Immunoglobulin kappa light chain variable region gene complex organization and

A;Reference number: A94689; MUID:88331394; PMID:3138286

A;Accession: A32513

A;Molecule type: DNA

A;Residues: 1-130 <KOF>

A;Cross-references: GB:M20834; NID:G196943; PIDN:AAA38846.1; PID:G196944

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;38-113/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 73 STSNLAS 79

## RESULT 15

PL0013

Ig kappa chain precursor V region (4C11) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000

C;Accession: PL0013

R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.

Mol. Immunol. 25, 33-40, 1988

A;Title: Structural basis of stimulatory anti-idiotypic antibodies.

A;Reference number: PL0011; MUID:88142863; PMID:3125424

A;Accession: PL0013

A;Molecule type: mRNA

A;Residues: 1-140 <CHE>

A;Experimental source: cell line 4C11

C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>

F;38-111/Domain: immunoglobulin homology <IMM>

F;46-55/Region: complementarity-determining 1

F;71-77/Region: complementarity-determining 2

F;110-118/Region: complementarity-determining 3

F;130-140/Domain: constant region (fragment) #status predicted <COR>

## Query Match

100.0%; Score 31; DB 2; Length 140;

Best Local Similarity 100.0%; Pred. No. 3.7; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7

Db 71 STSNLAS 77

Search completed: July 30, 2003, 09:44:08



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:35 ; Search time 1.09302 Seconds  
(without alignments)  
301.171 Million cell updates/sec

Title: US-09-865-198-5  
Perfect score: 31  
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	90.3	204	1 YIP8_YEAST	P40451 saccharomyc
2	28	90.3	531	1 VLI_HPV16	P03101 human papil
3	28	90.3	567	1 RST2_SCHPO	P78871 schizosacch
4	28	90.3	601	1 YFK5_SCHPO	P87132 schizosacch
5	28	90.3	707	1 YJ9C_YEAST	P47166 saccharomyc
6	27	87.1	108	1 KV6K_MOUSE	P04945 mus musculu
7	27	87.1	126	1 YRP2_IRV6	P18306 chilo tride
8	27	87.1	129	1 KV4A_MOUSE	P01680 mus musculu
9	27	87.1	219	1 TR23_YEAST	P03784 saccharomyc
10	27	87.1	255	1 YFCA_HAEIN	P46490 haemophilus
11	27	87.1	720	1 GTSE_HUMAN	P09ny23 homo sapien
12	27	87.1	919	1 YBO3_YEAST	P38073 saccharomyc
13	27	87.1	1477	1 KELC_DROME	P04652 drosophila
14	26	83.9	87	1 IM08_YEAST	P57744 saccharomyc
15	26	83.9	173	1 SP12_YEAST	P17123 saccharomyc
16	26	83.9	334	1 E13B_HORVU	P15737 hordeum vul
17	26	83.9	348	1 YK51_YEAST	P36152 saccharomyc
18	26	83.9	352	1 NP11_ASPO	P46076 aspergillus
19	26	83.9	382	1 YAE8_SCHPO	P09848 schizosacch
20	26	83.9	469	1 VLA2_BPVI	P03109 bovine papi
21	26	83.9	614	1 TUJ1_SCHPO	P09715 schizosacch
22	26	83.9	687	1 YBG0_YEAST	P34225 saccharomyc
23	26	83.9	816	1 HDA7_CAEEL	P17323 caenorhabdi
24	26	83.9	1050	1 ULK1_HUMAN	P07385 homo sapien
25	26	83.9	1398	1 MHP1_YEAST	P43638 saccharomyc
26	26	83.9	2504	1 FAS_HUMAN	P49327 homo sapien
27	26	83.9	2895	1 HYD_DROME	P51592 drosophila
28	25	80.6	209	1 V281_ARATH	P09897 arabidopsis
29	25	80.6	310	1 YC63_SYNY3	P74068 synechocyst
30	25	80.6	371	1 RLPA_ANASP	P08ys24 anabaena sp
31	25	80.6	444	1 NT4M_LOCOMI	P036424 locusta mig
32	25	80.6	604	1 SP20_YEAST	P50875 saccharomyc
33	25	80.6	735	1 T2FA_YEAST	P41895 saccharomyc

34	25	80.6	838	1 FAS_MOUSE	P19096 mus musculu
35	25	80.6	932	1 HIR1_SCHPO	P87314 schizosacch
36	25	80.6	1060	1 YN18_YEAST	P53836 saccharomyc
37	25	80.6	1090	1 CYA2_RAT	P26769 rattus norv
38	25	80.6	1177	1 JAK_DROME	P24592 drosophila
39	25	80.6	1275	1 RGA2_SCHPO	P10164 schizosacch
40	25	80.6	1356	1 ROM2_YEAST	P51862 saccharomyc
41	25	80.6	1489	1 YGP0_YEAST	P53115 saccharomyc
42	25	80.6	1569	1 GLI3_XENLA	P91660 xenopus lae
43	25	80.6	1571	1 C3G_DROME	P77086 drosophila
44	25	80.6	2505	1 FAS_RAT	P12785 rattus norv
45	24	77.4	103	1 YA40_MYCPN	P75074 mycoplasma

ALIGNMENTS

RESULT 1  
YIP8\_YEAST  
ID YIP8\_YEAST STANDARD; PRT; 204 AA.  
AC P40451;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Hypothetical 22.8 kDa protein in FOX3-UBP7 intergenic region.  
GN YIL158W.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288c / AB972;  
RX PubMed=9169870;  
RA Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,  
RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,  
RA Harris D.E., Hornslell T., Hunt S., Jagels K., Jones M., Lye G.,  
RA Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,  
RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;  
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";  
RL Nature 387:84-87(1997).  
CC -!- SIMILARITY: TO YEAST YKR100C.  
CC  
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CC  
CC -----  
CC DR EMBL; Z38059; CAA86120.1; -.  
CC DR PIR; S48376; S48376.  
CC DR SGD; S0001420; YIL158W.  
CC KM Hypothetical protein; Transmembrane.  
CC FT TRANSMEM 6 POTENTIAL.  
CC SQ SEQUENCE 204 AA; 22840 MW; 7B86FA9F125F19BF CRC64;  
  
Query Match 90.3%; Score 28; DB 1; Length 204;  
Best Local Similarity 85.7%; Pred. No. 11;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 STSNLAS 7  
Db 160 STSNLSS 166  
  
RESULT 2  
VLI\_HPV16 STANDARD; PRT; 531 AA.  
ID VLI\_HPV16  
AC P03101;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)

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DT 01-OCT-1996 (Rel. 34, last annotation update)
DE Major capsid protein L1.
GN L1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP SEQUENCE OF 328-371 FROM N.A.
RX MEDLINE=92407963; PubMed=1326639;
RA Chan S.Y., Bernard H.U., Ong C.K., Chan S.P., Birgit H., Delius H.;
RT "Phylogenetic analysis of 48 papillomavirus types and 28 subtypes and
RT variants: a showcase for the molecular evolution of DNA viruses.";
RL J. Virol. 66:5714-5725(1992).
CC -1- MISCELLANEOUS: HPV16, IN COMPARISON TO HPV TYPES 6 AND 11, IS MORE
CC OFTEN ASSOCIATED WITH MALIGNANT GENITAL CANCERS IN HUMANS.
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CC -----
DR EMBL; K02718; AAA46943.1; -.
DR EMBL; M96285; AAA47024.1; -.
DR EMBL; A06331; CAA00546.1; -.
DR PIR; A03640; P1WLHS.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPV_CAPSID_L1.
DR ProDom; PD000544; PV_capsid_L1; 1.
DR K02718; late_protein.
DR SEQUENCE 531 AA; 59554 MW; 5B3402587093B380 CRC64;
SQ
Query Match 90.3%; Score 28; DB 1; Length 531;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 STSNLAS 7
Db 308 STANLAS 314

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris P., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Welljens I., Vanstreels B., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN [3]
RP SEQUENCE OF 90-567 FROM N.A.
RC STRAIN=PR745;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshiooka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT "Identification of open reading frames in Schizosaccharomyces pombe
RT cDNAs.";
RL DNA Res. 4:363-369(1997).
RN [4]
RP SEQUENCE OF 148-364 FROM N.A.
RC STRAIN=968 h90;
RX MEDLINE=20223868; PubMed=10759889;
RA Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
RA Hiraoaka Y.;
RT "Large-scale screening of intracellular protein localization in living
RT fission yeast cells by the use of a GFP-fusion genomic DNA library.";
RL Genes Cells 5:169-190(2000).
CC -1- FUNCTION: Key transcription factor for sexual development.
CC Activates the transcription of ste11. Binds to a stress response
CC element-like (SRE) region in the ste11 promoter.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Contains 2 C2H2-type zinc fingers.
CC -----
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CC -----
DR EMBL; AB025941; BAA89273.1; -.
DR EMBL; Z98533; CAB11086.1; -.
DR EMBL; D89221; BAA13882.1; -.
DR EMBL; AB027851; BAA87155.1; -.
DR PIR; T11653; T11653.
DR HSSP; P07248; 1ARD.
DR GeneDB SPombe; SPAC6F12.02; -.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 2.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 2.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

```

DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
KW DNA-binding; Nuclear protein; Zinc-finger; Metal-binding; Repeat;  
KW Activator; Transcription regulation.  
FT ZN\_FING 70 92 C2H2-TYPE 1.  
FT ZN\_FING 98 128 C2H2-TYPE 2.  
FT CONFLICT 156 156 T -> P (IN REF. 4).  
SQ SEQUENCE 567 AA; 62559 MW; 1B5CF026E5FAEF5F CRC64;

Query Match 90.3%; Score 28; DB 1; Length 567;  
Best Local Similarity 85.7%; Pred. No. 36;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
||:||||  
Db 154 STTNLAS 160

## RESULT 4

YFK5\_SCHPO STANDARD; PRT; 601 AA.  
AC P87132;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein C167.05 in chromosome 1.  
GN SPAC167.05 OR SPAC57A7.01.  
OS Schizosaccharomyces pombe (fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu S., Dreano S., Gloux S., Leclaire V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
RT "The genome sequence of Schizosaccharomyces pombe.";  
RL Nature 415:871-880(2002).

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DR EMBL; AL035248; CAA22850.1; -.  
DR EMBL; Z95396; CAB08759.1; -.  
DR PIR; T37738; T37738.

DR GenedB Spombe; SPAC167.05; -.  
DR InterPro; IPR006015; USP.  
DR InterPro; IPR006016; USP\_dom.  
DR Pfam; PF00582; USP; 1.  
DR PRINTS; PR01438; UNVRSLSTRESS.  
KW Hypothetical protein.  
SQ SEQUENCE 601 AA; 65947 MW; 13FAACABDCE14239 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 601;  
Best Local Similarity 85.7%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
||:||||  
Db 143 STSNLAS 149

## RESULT 5

YJ9C\_YEAST STANDARD; PRT; 707 AA.  
AC P47166;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Hypothetical 81.2 kDa protein in NMDS-HOM6 intergenic region.  
GN YJR134C OR J2120.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rose M., Koetter P., Entian K.D.;  
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: SOME, TO PARAMYOSINS AND MYOSINS.

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CC -----

DR EMBL; Z49634; CAA89665.1; -.  
DR EMBL; Z49635; CAA89667.1; -.  
DR PIR; S57157; S57157.  
DR SGD; S0003895; SGM1.  
KW Hypothetical protein; Coiled coil.  
FT DOMAIN 122 473 COILED COIL (POTENTIAL).  
FT DOMAIN 594 706 COILED COIL (POTENTIAL).  
SQ SEQUENCE 707 AA; 81171 MW; BA47D1A7265BF3D9 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 707;  
Best Local Similarity 85.7%; Pred. No. 47;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
||:||||  
Db 25 STSNLAS 31

## RESULT 6

KV6K\_MOUSE STANDARD; PRT; 108 AA.  
ID KV6K\_MOUSE  
AC P04945;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-VI region NQ2-6.1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83271467; PubMed=6877353;  
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;  
RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone and its early diversification.";  
RL Nature 304:320-324(1983).  
CC -----  
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CC -----  
DR EMBL; K00746; AAA38691.1; -.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR Immunoglobulin V region; Hybridoma.  
KW DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 34 48 FRAMEWORK-2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 56 87 FRAMEWORK-3.  
FT DOMAIN 88 98 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 99 108 FRAMEWORK-4.  
FT DISULFID 23 87 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;  
  
Query Match 87.1%; Score 27; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 TSNTLAS 7  
Db 50 TSNTLAS 55  
  
RESULT 7  
YRP2\_IRV6 STANDARD; PRT; 126 AA.  
ID YRP2\_IRV6  
AC P18306;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Repetitive protein ORF2.  
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).  
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.  
OX NCBI\_TaxID=10488;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89073753; PubMed=3201751;  
RA Fischer M., Scholtz J., Roesen-Wolff A., Delius H.,  
RA Darai G.;  
RT "DNA nucleotide sequence analysis of the Pvull DNA fragment I of the  
RT genome of insect iridescent virus type 6 reveals a complex cluster of  
RT multiple tandem, overlapping, and interdigitated repetitive DNA  
RT elements.";  
RL Virology 167:497-506(1988).  
CC -1- SIMILARITY: A CONSENSUS SEQUENCE MANIX(6) IGSSSTX(6) LX(1)  
CC LGSX(1) LOISGX(2) LX(1) VN WAS FOUND IN ALL FIVE ORFS.  
CC -----  
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CC -----  
DR EMBL; M23625; AAA66587.1; -.  
DR PIR; B31828; RPKFJ.  
KW Hypothetical protein.  
SQ SEQUENCE 126 AA; 13371 MW; 2C927A1D41C41471 CRC64;  
  
Query Match 87.1%; Score 27; DB 1; Length 126;  
Best Local Similarity 85.7%; Pred. No. 11;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 STSNTLAS 7  
Db 15 STSNTLAS 21  
  
RESULT 8  
KV4A\_MOUSE STANDARD; PRT; 129 AA.  
ID KV4A\_MOUSE  
AC P01680;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-IV region S107B precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82115300; PubMed=6799208;  
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharf M.D.;  
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";  
RL Cell 26:57-66(1981).  
CC -1- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO  
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS  
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE  
CC NORMAL KAPPA CHAIN S107.  
CC -----  
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CC -----  
DR EMBL; J00577; AAA38780.1; -.  
DR EMBL; V00780; CAA24157.1; -.  
DR PIR; A01943; KVM57B.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-IV REGION S107B  
FT DOMAIN 23 45 FRAMEWORK-1.  
FT DOMAIN 46 57 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 58 72 FRAMEWORK-2.  
FT DOMAIN 73 79 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 80 111 FRAMEWORK-3.  
FT DOMAIN 112 118 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 119 128 FRAMEWORK-4.  
FT DISULFID 45 111 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 13833 MW; E4BB73072DC6F6BE4 CRC64;



Query Match 87.1%; Score 27; DB 1; Length 129;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TSNTLAS 7  
Db 74 TSNTLAS 79

## RESULT 9

TR23\_YEAST STANDARD; PRT; 219 AA.  
ID TR23\_YEAST  
AC Q03784;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Transport protein particle 23 kDa subunit (TRAPP 23 kDa subunit).  
GN TRS23 OR YDR246W OR YD8419.13.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C / AB972;  
RA Oliver K., Harris D., Barrell B.G., Rajandream M.A.;  
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP IDENTIFICATION IN TRAPP COMPLEX.  
RX MEDLINE=21664186; PubMed=11805826;

RA Gavin A.C., Bosche M., Krause R., Grandi P., Marzioch M., Bauer A.,  
RA Schultz J., Rick J.M., Michon A.M., Cruciat C.M., Remor M., Hofert C.,  
RA Scheider M., Brajenovic M., Ruffner H., Merino A., Klein K., Hudak M.,  
RA Dickson D., Rudi T., Gnan V., Bauch A., Bastuck S., Huhse B.,  
RA Leutwein C., Heurtier M.A., Copley R.R., Edelmann A., Querfurth E.,  
RA Rybin V., Drewes G., Raida M., Bouwmeester T., Bork P., Seraphin B.,  
RA Kuster B., Neubauer G., Superti-Furga G.;  
RT "Functional organization of the yeast proteome by systematic analysis  
of protein complexes";  
RL Nature 415:141-147(2002).  
CC -1- FUNCTION: TRAPP plays a key role in the late stages of endoplasmic  
reticulum to Golgi traffic.  
CC -1- SUBUNIT: Part of multisubunit complex composed of BET3, BET5,  
TRS30, TRS23, TRS31, TRS33, TRS65, TRS85, TRS120 and TRS130.  
CC -1- SIMILARITY: BELONGS TO THE TRAPP SMALL SUBUNITS FAMILY.  
CC TRS23 SUBFAMILY.

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CC -----  
CC EMBL; 249701; CAA89732.1; -.  
DR PIR; S54542; S54542.  
DR SGD; S0002654; TRS23.  
DR GO; GO:0030008; C:TRAPP; IDA.  
DR GO; GO:0006888; P:ER to Golgi transport; IMP.  
DR Pfam; PF04099; Sybindin; 1.  
KW Transport; Endoplasmic reticulum; Golgi stack.  
SQ SEQUENCE 219 AA; 24863 MW; 8B32BID5FE3846ED CRC64;

Query Match 87.1%; Score 27; DB 1; Length 219;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLA 6  
Db 166 STSNLA 171

RESULT 10  
YFCA\_HAEIN STANDARD; PRT; 255 AA.  
ID YFCA\_HAEIN  
AC P46490;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein HI0198.  
GN HI0198.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Rd / KM20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
Rd";  
RL Science 269:496-512(1995).  
RN [2]  
RP REVISIONS.  
RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;  
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- SIMILARITY: STRONG, TO E.COLI YFCA.  
CC -1- SIMILARITY: TO M.LEPRAE U1177B.

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CC -----  
CC EMBL; U32705; AAC21867.1; -.  
DR TIGR; HI0198; -.  
DR InterPro; IPR002781; DUF81.  
DR Pfam; PF01925; DUF81; 1.  
KW Hypothetical protein; Transmembrane; Complete proteome.

FT TRANSMEM 27 POTENTIAL.  
FT TRANSMEM 28 48 POTENTIAL.  
FT TRANSMEM 76 96 POTENTIAL.  
FT TRANSMEM 99 119 POTENTIAL.  
FT TRANSMEM 132 152 POTENTIAL.  
FT TRANSMEM 153 173 POTENTIAL.  
FT TRANSMEM 191 211 POTENTIAL.  
FT TRANSMEM 235 255 POTENTIAL.  
SQ SEQUENCE 255 AA; 27608 MW; 7C0936C07FB58F5 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 255;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TSNTLAS 7  
Db 185 TSNTLAS 190

RESULT 11  
GTSE\_HUMAN STANDARD; PRT; 720 AA.  
ID GTSE\_HUMAN



AC Q9NYZ3; Q9BRE0; Q9UGZ9; Q9Y557;  
AT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE G2 and S phase expressed protein 1 (B99 homolog).  
GN GTSE1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=20432105; PubMed=10974554;  
RA Monte M., Collavyn L., Lazarevic D., Utrera R., Dragani T.A.,  
RA Schneider C.;  
RT "Cloning, chromosome mapping and functional characterization of a  
RT human homologue of murine Gtse-1 (B99) gene.";  
RL Gene 254:229-236(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20057165; PubMed=10591208;  
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,  
RA Clamp M., Smitk L.J., Ainscough R., Almeida J.P., Babbage A.K.,  
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,  
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,  
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
RA Gilbert J.G.R., Goward M.E., Grahm D.V., Griffiths M.N.D., Hall C.,  
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,  
RA Laird G.K., Langford C.F., Levertha M.A., Lloyd C., Lloyd D.M.,  
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,  
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,  
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,  
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,  
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,  
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,  
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,  
RA Zhang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,  
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,  
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,  
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,  
RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,  
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,  
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,  
RA Serousi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,  
RA Wilkison P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,  
RA Tilahun Y., Wright H.;  
RT "The DNA sequence of human chromosome 22.";  
RL Nature 402:489-495(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: May be involved in p53-induced cell cycle arrest in G2/M  
CC phase by interfering with microtubule rearrangements that are  
CC required to enter mitosis. Overexpression delays G2/M phase  
CC progression.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Associated with microtubules.  
CC -!- DEVELOPMENTAL STAGE: Expressed in G2/M phase. Not detected in  
CC quiescent cells.  
CC -!- PTM: Phosphorylated in mitosis (By similarity).  
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CC -----  
DR EMBL: AF223408; AAF31459.1; -;  
DR EMBL: AL031588; CAB38415.1; -;  
DR EMBL: BC006325; AAH06325.1; -;  
DR Genew; HGNC:13698; GTSE1.  
DR GK; Q9NYZ3; -;  
DR MIM; 607477; -;  
DR GO; GO:0005881; C:cytoplasmic microtubule; NAS.  
DR GO; GO:0006977; P:DNA damage response, induction of cell arre. . .; NAS.  
DR GO; GO:0000085; P:G2 phase of mitotic cell cycle; NAS.  
DR GO; GO:0007017; P:microtubule-based process; NAS.  
KW Microtubules; Phosphorylation.  
KW DOMAIN  
FT 22  
FT CONFLICT 259 259 V -> I (IN REF. 1).  
FT CONFLICT 506 506 R -> W (IN REF. 2; CAB38415).  
SQ SEQUENCE 720 AA; 76614 MW; ACD91CCDD008A89C CRC64;

Query Match 87.1%; Score 27; DB 1; Length 720;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLA 6  
Db 303 STSNLA 308

RESULT 12  
YB03\_YEAST  
ID YB03\_YEAST STANDARD; PRT; 919 AA.  
AC P38073;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Putative 103.4 kDa transcriptional regulatory protein in RPL4A-HMT1  
DE intergenic region.  
DE YBR033W OR YBR0318.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA MEDLINE=94378725; PubMed=8091864;
RT "The complete sequence of a 33 kb fragment on the right arm of
RT chromosome II from Saccharomyces cerevisiae reveals 16 open reading
RT frames, including ten new open reading frames, five previously
RT identified genes and a homologue of the SCO1 gene."
RL Yeast 10:S75-S80(1994).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
CC domain.
-----
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-----
DR EMBL; X76078; CAA53688.1; -
DR EMBL; Z35902; CAA84975.1; -
DR PIR; S45889; S45889.
DR SGD; S0000237; YBR033W.
DR InterPro; IPR001138; Fungi_Trn.
DR Pfam; PF00172; Zn_clus; 1.
DR SMART; SM00066; GAL4; 1.
DR PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.
DR PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.
KW Hypothetical protein; Transcription regulation; DNA-binding;
KW Nuclear protein; Zinc; Metal-binding.
FT DNA_BIND 56 85 ZN(2)-CYS(6), FUNGAL-TYPE.
SQ SEQUENCE 919 AA; 103396 MW; 18DD2E37A042E246 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 919;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSNLAS 7
Db 756 TSNLAS 761

RESULT 13
KELC_DROME STANDARD; PRT; 1477 AA.
ID KELC_DROME STANDARD; PRT; 1477 AA.
AC Q04652; Q04653; Q9VJA2;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ring canal kelch protein [Contains: Kelch short protein].
GN KEL OR CG7210.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=93201592; PubMed=8453663;
RA Xue F., Cooley L.;
RT "Kelch encodes a component of intercellular bridges in Drosophila egg
RT chambers."
RL Cell 72:681-693(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Picman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [3]
RP CHARACTERIZATION.
RC TISSUE=Embryo;
RX MEDLINE=97236487; PubMed=9118811;
RA Robinson D.N., Cooley L.;
RT "Examination of the function of two kelch proteins generated by stop
RT codon suppression."
RL Development 124:1405-1417(1997).
CC -1- FUNCTION: COMPONENT OF RING CANALS THAT REGULATES THE FLOW OF
CC CYTOPLASM BETWEEN CELLS. MAY BE INVOLVED IN THE REGULATION OF
CC CYTOPLASM FLOW FROM NURSE CELLS TO THE OOCYTE DURING OOGENESIS.
CC BINDS ACTIN.
CC -1- SUBCELLULAR LOCATION: INNER SURFACE OF CYTOPLASMIC BRIDGES OR RING
CC CANALS PRESENT IN EGG CHAMBERS. SUBCORTICALLY IN IMAGINAL DISK
CC EPITHELIA.
CC -1- TISSUE SPECIFICITY: BOTH PROTEINS ARE EXPRESSED IN OVARIES, MALE
CC TESTIS, OVARECTOMIZED FEMALES, CUTICLE, SALIVARY GLAND AND
CC IMAGINAL DISKS. KELCH ORP1 IS THE PREDOMINANT PROTEIN AND IS ALSO
CC EXPRESSED IN FAT BODIES. ON ENTRY INTO METAMORPHOSIS LEVELS OF
CC FULL LENGTH PROTEIN INCREASE IN TESTIS AND IMAGINAL DISKS.
CC -1- DEVELOPMENTAL STAGE: LARVAE, PUPAE AND ADULTS.
CC -1- SIMILARITY: Contains 1 BTB/POZ domain.
CC -1- SIMILARITY: Contains 6 kelch repeats.
CC -1- CAUTION: REF.3 BELIEVES RESIDUE 690 IS A SELENOCYSTEINE.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
-----
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DR EMBL; L08483; AAAS3471.1; -
DR EMBL; L08483; AAAS3472.2; -
DR EMBL; AE003657; AAF53651.1; ALT_SEQ.

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DR HSSP; Q05516; 1CS3.
DR FlyBase; FBgn0001301; kel.
DR GO; GO:0007292; P:oogenesis; IMP.
DR GO; GO:0007301; P:ring canal formation; IDA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR006651; Kelch.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00612; Kelch; 6.
DR PROSITE; PS50097; BTB; 1.
KW Cytoskeleton; Actin-binding; Selenium; Selenocysteine; Kelch repeat;
KW Repeat.
FT CHAIN 1 1477 KELCH PROTEIN.
FT CHAIN 1 689 KELCH SHORT PROTEIN.
FT DOMAIN 157 223 BTB.
FT REPEAT 404 449 KELCH 1.
FT REPEAT 450 496 KELCH 2.
FT REPEAT 498 543 KELCH 3.
FT REPEAT 545 592 KELCH 4.
FT REPEAT 594 639 KELCH 5.
FT REPEAT 641 687 KELCH 6.
FT DOMAIN 18 28 ASN-RICH.
FT DOMAIN 29 36 GLN-RICH.
FT DOMAIN 29 36 POLY-GLN.
FT SE_CYS 690 690 PROBABLE.
FT CONFLICT 493 493 V -> A (IN REF. 1).
FT CONFLICT 596 596 A -> R (IN REF. 1).
FT CONFLICT 824 824 P -> L (IN REF. 1).
FT CONFLICT 858 858 G -> D (IN REF. 1).
FT CONFLICT 1083 1083 A -> R (IN REF. 1).
FT CONFLICT 1086 1086 A -> G (IN REF. 1).
SQ SEQUENCE 1477 AA; 160086 MW; 4851EEAE9D9DBA47 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 1477;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSNNLAS 7
Db 650 TSNNLAS 655

RESULT 14
IM08_YEAST STANDARD; PRT; 87 AA.
AC P57744;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit TIM8.
GN TIM8 OR YJR135W-A OR YJR135BW.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rose M., Koetter P., Entian K.D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in mitochondrial carrier import.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
similarity).
CC -!- SIMILARITY: Belongs to the Tim8/Tim10 family.
CC -----
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CC -----
DR EMBL; Z49636; -, NOT_ANNOTATED_CDS.
DR PIR; S78075; S78075.
DR SGD; S0007348; TIM8.
DR GO; GO:0005758; C:mitochondrial intermembrane space; IDA.
DR GO; GO:0006628; P:mitochondrial translocation; IMP.
DR InterPro; IPR004217; Znf_Tim10/DDP.
DR Pfam; PF02953; zf-Tim10/DDP; 1.
KW Transport; Protein transport; Translocation; Mitochondrion;
KW Inner membrane.
SQ SEQUENCE 87 AA; 9764 MW; B91D1DD41707EA24 CRC64;

Query Match 83.9%; Score 26; DB 1; Length 87;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 5 STSNLAS 11

RESULT 15
SP12_YEAST STANDARD; PRT; 173 AA.
ID SP12_YEAST
AC P17123;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Sporulation protein SPO12.
GN SPO12 OR YHR152W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Malvaasic M.J., Elder R.T.;
RL MEDLINE=90258869; PubMed=2188099;
RT "Complementary transcripts from two genes necessary for normal
meiosis in the yeast Saccharomyces cerevisiae.";
RL Mol. Cell. Biol. 10:2809-2819(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Moyer L.,
RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
VIII.";
RL Science 265:2077-2082(1994).
CC -!- FUNCTION: IT IS REQUIRED FOR MEIOSIS I CHROMOSOME DIVISION DURING
SPORULATION.
CC -!- MISCELLANEOUS: ITS NEGATIVE TAIL IS FUNCTIONALLY IMPORTANT.
CC -!- SIMILARITY: TO YEAST G8558.
CC -----
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CC -----
DR EMBL; M32653; AAA35076.1; -.
DR EMBL; U10397; AAB68979.1; -.
DR PIR; B36321; B36321.

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DR SGD; S0001195; SP012.  
DR GO; GO:0005730; C:nucleolus; IDA.  
DR GO; GO:0007096; P:exit from mitosis; IGI.  
DR GO; GO:0007127; P:meiosis I; IMP.  
DR GO; GO:0000278; P:mitotic cell cycle; IMP.  
DR Pfam; PF05032; Sp012; 1.  
KW Sporulation; Meiosis.  
FT DOMAIN 159 173 NEGATIVE-CHARGED TAIL.  
SQ SEQUENCE 173 AA; 19912 MW; E114394516451F60 CRC64;

Query Match 83.9%; Score 26; DB 1; Length 173;  
Best Local Similarity 85.7%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
| | | | |  
Db 78 STSNLKS 84

Search completed: July 30, 2003, 09:45:06  
Job time : 4.09302 secs

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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:42:53 ; Search time 8.60465 Seconds  
(without alignments)  
96.613 Million cell updates/sec

Title: US-09-865-198-5  
Perfect score: 31  
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	9	US-09-976-787-5 Sequence 5, Appli
2	31	100.0	7	10	US-09-865-198-5 Sequence 5, Appli
3	31	100.0	7	10	US-09-910-059-27 Sequence 27, Appli
4	31	100.0	7	11	US-09-798-689-5 Sequence 5, Appli
5	31	100.0	7	15	US-10-195-752-109 Sequence 109, App
6	31	100.0	7	15	US-10-232-187-9 Sequence 9, Appli
7	31	100.0	9	14	US-10-032-482-4 Sequence 4, Appli
8	31	100.0	10	10	US-09-982-107-12 Sequence 12, Appli
9	31	100.0	9	9	US-09-976-787-24 Sequence 24, Appli
10	31	100.0	10	10	US-09-865-198-23 Sequence 23, Appli
11	31	100.0	10	11	US-09-798-689-8 Sequence 8, Appli
12	31	100.0	10	10	US-09-910-059-50 Sequence 50, Appli
13	31	100.0	10	10	US-09-910-059-61 Sequence 61, Appli
14	31	100.0	10	10	US-09-910-059-65 Sequence 65, Appli
15	31	100.0	10	10	US-09-910-059-71 Sequence 71, Appli

16	31	100.0	10	10	US-09-144-886-76 Sequence 76, Appli
17	31	100.0	10	10	US-09-144-886-88 Sequence 88, Appli
18	31	100.0	10	15	US-10-232-187-4 Sequence 4, Appli
19	31	100.0	10	9	US-09-976-787-8 Sequence 8, Appli
20	31	100.0	10	10	US-09-865-198-8 Sequence 8, Appli
21	31	100.0	10	10	US-09-910-059-9 Sequence 9, Appli
22	31	100.0	11	10	US-09-144-886-89 Sequence 89, Appli
23	31	100.0	13	15	US-10-195-752-111 Sequence 111, App
24	31	100.0	13	15	US-10-195-752-113 Sequence 113, App
25	31	100.0	23	10	US-09-910-059-17 Sequence 17, Appli
26	31	100.0	23	10	US-09-910-059-52 Sequence 52, Appli
27	31	100.0	23	10	US-09-910-059-97 Sequence 97, Appli
28	31	100.0	23	10	US-09-910-059-99 Sequence 99, Appli
29	31	100.0	23	9	US-09-976-787-29 Sequence 29, Appli
30	31	100.0	23	10	US-09-865-198-28 Sequence 28, Appli
31	31	100.0	23	11	US-09-798-689-21 Sequence 21, Appli
32	31	100.0	24	9	US-09-976-787-28 Sequence 28, Appli
33	31	100.0	24	10	US-09-865-198-27 Sequence 27, Appli
34	31	100.0	25	15	US-10-247-488-2 Sequence 2, Appli
35	31	100.0	25	15	US-10-247-488-4 Sequence 4, Appli
36	31	100.0	6	10	US-09-807-721-2 Sequence 13, Appli
37	28	90.3	7	10	US-09-965-099-13 Sequence 13, Appli
38	28	90.3	7	14	US-10-051-852-13 Sequence 13, Appli
39	28	90.3	8	10	US-09-169-048-16 Sequence 16, Appli
40	28	90.3	8	10	US-09-169-048-28 Sequence 28, Appli
41	28	90.3	8	11	US-09-997-209-16 Sequence 16, Appli
42	28	90.3	8	11	US-09-997-209-28 Sequence 28, Appli
43	28	90.3	27	10	US-09-965-099-55 Sequence 55, Appli
44	28	90.3	27	14	US-10-051-852-55 Sequence 55, Appli
45	28	90.3	9	10	US-09-965-099-35 Sequence 35, Appli

## ALIGNMENTS

RESULT 1  
US-09-976-787-5  
; Sequence 5, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-976-787-5

Query Match 100.0%; Score 31; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 1 STSNLAS 7

RESULT 2  
US-09-865-198-5  
; Sequence 5, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping

;; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods  
;; FILE OF INVENTION: Production  
;; FILE REFERENCE: 11245/47102  
;; CURRENT APPLICATION NUMBER: US/09/865,198  
;; CURRENT FILING DATE: 2001-05-24  
;; PRIOR APPLICATION NUMBER: US 60/206,749  
;; PRIOR FILING DATE: 2000-05-24  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: WordPerfect 8.0 for Windows  
;; SEQ ID NO 5  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Mouse  
US-09-865-198-5

Query Match 100.0%; Score 31; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
Db 1 STSNLAS 7

RESULT 3  
US-09-910-059-27  
; Sequence 27, Application US/09910059  
; Patent No. US20020142359A1  
; GENERAL INFORMATION:  
; APPLICANT: Copley, Clive G  
; APPLICANT: Edge, Michael Derek  
; APPLICANT: Emery, Stephen Charles  
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,  
; TITLE OF INVENTION: Their Therapeutic use in an Adept System  
; FILE REFERENCE: 1991-209  
; CURRENT APPLICATION NUMBER: US/09/910,059  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 09/171,945  
; PRIOR FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: PCT/GB97/01165  
; PRIOR FILING DATE: 1997-04-29  
; PRIOR APPLICATION NUMBER: GB 9703103.3  
; PRIOR FILING DATE: 1997-02-14  
; PRIOR APPLICATION NUMBER: GB9609405.7  
; PRIOR FILING DATE: 1996-05-04  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-910-059-27

Query Match 100.0%; Score 31; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
Db 1 STSNLAS 7

RESULT 4  
US-09-798-689-5  
; Sequence 5, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; TITLE OF INVENTION: Combined With Radiation and Chemotherapy  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
; CURRENT APPLICATION NUMBER: US/09/798,689

;; CURRENT FILING DATE: 2001-03-02  
;; PRIOR APPLICATION NUMBER: 09/401,163  
;; PRIOR FILING DATE: 1999-09-22  
;; PRIOR APPLICATION NUMBER: 08/967,113  
;; PRIOR FILING DATE: 1997-11-10  
;; PRIOR APPLICATION NUMBER: 08/706,804  
;; PRIOR FILING DATE: 1996-09-03  
;; PRIOR APPLICATION NUMBER: 08/476,533  
;; PRIOR FILING DATE: 1995-06-07  
;; PRIOR APPLICATION NUMBER: 08/326,552  
;; PRIOR FILING DATE: 1994-10-20  
;; PRIOR APPLICATION NUMBER: 08/196,041  
;; PRIOR FILING DATE: 1994-02-10  
;; NUMBER OF SEQ ID NOS: 41  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 5  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Mouse  
US-09-798-689-5

Query Match 100.0%; Score 31; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
Db 1 STSNLAS 7

RESULT 5  
US-10-195-752-109  
; Sequence 109, Application US/10195752  
; Publication No. US2003007276A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KUMANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHAYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/195,752  
; FILING DATE: 16-Jul-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/393,385B  
; FILING DATE: 27-JUN-96  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:

US-10-195-752-109

Query Match 100.0%; Score 31; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
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Db 1 STSNLAS 7

RESULT 6

US-10-232-187-9

; Sequence 9, Application US/10232187  
; Publication No. US20030092091A1  
; GENERAL INFORMATION:  
; APPLICANT: Abrahamson, Julie A.  
; APPLICANT: Bochner, Bruce  
; APPLICANT: Erickson-Miller, Connie L.  
; APPLICANT: Kikly, Kristine K.  
; APPLICANT: Schleimer, Robert  
; APPLICANT: Nulku, Turkan E.  
; TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies  
; FILE REFERENCE: GH50042-1  
; CURRENT APPLICATION NUMBER: US/10/232,187  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/187,595  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: PCT/US01/07193  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/315,943  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/349,830  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: 60/394,741  
; PRIOR FILING DATE: 2002-07-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-232-187-9

Query Match 100.0%; Score 31; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
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Db 1 STSNLAS 7

RESULT 7

US-10-032-482-4

; Sequence 4, Application US/10032482  
; Publication No. US20020197270A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Irun  
; APPLICANT: ROTTER, Varda  
; APPLICANT: Wolkowicz, Roland  
; APPLICANT: RUIZ, Pedro  
; APPLICANT: EREZ-ALON, Neta  
; APPLICANT: HERKEL, Johannes  
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR  
; TITLE OF INVENTION: IMMUNITY  
; FILE REFERENCE: COHEN42  
; CURRENT APPLICATION NUMBER: US/10/032,482  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: US/09/445,602  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: PCT/IL98/00266  
; PRIOR FILING DATE: 1999-12-09

; PRIOR APPLICATION NUMBER: IL 121041  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 92

; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (53)..(53)  
; OTHER INFORMATION: Xaa is any amino acid.  
; NAME/KEY: misc\_feature  
; LOCATION: (86)..(86)  
; OTHER INFORMATION: Xaa is any amino acid  
; NAME/KEY: misc\_feature  
; LOCATION: (90)..(90)  
; OTHER INFORMATION: Xaa is any amino acid  
US-10-032-482-4

Query Match 100.0%; Score 31; DB 14; Length 92;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
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Db 32 STSNLAS 38

RESULT 8

US-09-982-107-12

; Sequence 12, Application US/09982107  
; Patent No. US2002015958A1  
; GENERAL INFORMATION:  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICHAEL B.  
; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING  
; TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE  
; FILE REFERENCE: EPI3002E  
; CURRENT APPLICATION NUMBER: US/09/982,107  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa  
US-09-982-107-12

Query Match 100.0%; Score 31; DB 10; Length 105;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
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Db 49 STSNLAS 55

RESULT 9

US-09-976-787-24

; Sequence 24, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 24  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-24

Query Match 100.0%; Score 31; DB 9; Length 106;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 49 STSNLAS 55

RESULT 10  
US-09-865-198-23  
; Sequence 23, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Znu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; PRIOR FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Wordperfect 8.0 for Windows  
; SEQ ID NO 23  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-23

Query Match 100.0%; Score 31; DB 10; Length 106;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 49 STSNLAS 55

RESULT 11  
US-09-798-689-8  
; Sequence 8, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; TITLE OF INVENTION: Combined With Radiation and Chemotherapy  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/326,552  
; PRIOR FILING DATE: 1994-10-20  
; PRIOR APPLICATION NUMBER: 08/196,041  
; PRIOR FILING DATE: 1994-02-10

; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-798-689-8

Query Match 100.0%; Score 31; DB 11; Length 106;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 49 STSNLAS 55

RESULT 12  
US-09-910-059-50  
; Sequence 50, Application US/09910059  
; Patent No. US20020142359A1  
; GENERAL INFORMATION:  
; APPLICANT: Copley, Clive G  
; APPLICANT: Edge, Michael Derek  
; APPLICANT: Emery, Stephen Charles  
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,  
; FILE REFERENCE: 1991-209  
; CURRENT APPLICATION NUMBER: US/09/910,059  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 09/171,945  
; PRIOR FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: PCT/GB97/01165  
; PRIOR FILING DATE: 1997-04-29  
; PRIOR APPLICATION NUMBER: GB 9703103.3  
; PRIOR FILING DATE: 1997-02-14  
; PRIOR APPLICATION NUMBER: GB9609405.7  
; PRIOR FILING DATE: 1996-05-04  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 50  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized light chain variable region  
US-09-910-059-50

Query Match 100.0%; Score 31; DB 10; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 49 STSNLAS 55

RESULT 13  
US-09-910-059-61  
; Sequence 61, Application US/09910059  
; Patent No. US20020142359A1  
; GENERAL INFORMATION:  
; APPLICANT: Copley, Clive G  
; APPLICANT: Edge, Michael Derek  
; APPLICANT: Emery, Stephen Charles  
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,  
; FILE REFERENCE: 1991-209  
; CURRENT APPLICATION NUMBER: US/09/910,059  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 09/171,945  
; PRIOR FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: PCT/GB97/01165

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; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain variable region variant
US-09-910-059-61
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Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 STSNLAS 7
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Db      49 STSNLAS 55
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RESULT 14
US-09-910-059-65:
; Sequence 65, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain variable region variant
US-09-910-059-65
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Query Match      100.0%; Score 31; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 STSNLAS 7
         |||||
Db      49 STSNLAS 55
```

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RESULT 15
US-09-910-059-71
; Sequence 71, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
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; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain variable region variant
US-09-910-059-71
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Query Match      100.0%; Score 31; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 STSNLAS 7
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Db      49 STSNLAS 55
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 5.4186 Seconds

(without alignments)  
333.364 Million cell updates/sec

Title: US-09-865-198-5

Perfect score: 31

Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	100.0	112	11	Q8K1F2	Q8K1F2 mus musculu
2	31	100.0	114	11	Q8K1F1	Q8K1F1 mus musculu
3	31	100.0	265	16	Q8YDZ0	Q8YDZ0 bruceella me
4	31	100.0	388	2	Q9KIS6	Q9KIS6 bruceella ab
5	31	100.0	391	2	Q9RPX5	Q9RPX5 bruceella su
6	31	100.0	391	16	Q8FXK6	Q8FXK6 bruceella su
7	31	100.0	595	9	Q37901	Q37901 bacterioph
8	31	100.0	753	5	Q26306	Q26306 drosophila
9	31	100.0	1107	3	Q12271	Q12271 saccharomyc
10	28	90.3	97	11	Q9J176	Q9J176 mus musculu
11	28	90.3	187	10	Q9C5K8	Q9C5K8 arabidopsis
12	28	90.3	208	12	Q8JMU6	Q8JMU6 human papil
13	28	90.3	211	12	Q8JMU9	Q8JMU9 human papil
14	28	90.3	221	12	Q8JMU5	Q8JMU5 human papil
15	28	90.3	253	5	Q8IC42	Q8IC42 plasmodium
16	28	90.3	401	3	Q8X084	Q8X084 neurospora

17	28	90.3	419	12	Q8JQW4	Q8JQW4 human papil
18	28	90.3	494	12	Q8I010	Q8I010 human papil
19	28	90.3	494	12	Q8I002	Q8I002 human papil
20	28	90.3	494	12	Q8I006	Q8I006 human papil
21	28	90.3	494	12	Q8I011	Q8I011 human papil
22	28	90.3	494	12	Q8I005	Q8I005 human papil
23	28	90.3	494	12	Q80998	Q80998 human papil
24	28	90.3	494	12	Q8I004	Q8I004 human papil
25	28	90.3	494	12	Q8I007	Q8I007 human papil
26	28	90.3	494	12	Q80996	Q80996 human papil
27	28	90.3	494	12	Q80997	Q80997 human papil
28	28	90.3	494	12	Q8I008	Q8I008 human papil
29	28	90.3	494	12	Q80999	Q80999 human papil
30	28	90.3	494	12	Q8I009	Q8I009 human papil
31	28	90.3	494	12	Q8I012	Q8I012 human papil
32	28	90.3	494	12	Q8I001	Q8I001 human papil
33	28	90.3	494	12	Q90204	Q90204 human papil
34	28	90.3	494	12	Q8I000	Q8I000 human papil
35	28	90.3	495	12	Q12343	Q12343 human papil
36	28	90.3	505	12	Q9WLO6	Q9WLO6 human papil
37	28	90.3	505	12	Q9WLO5	Q9WLO5 human papil
38	28	90.3	505	12	Q9WHS6	Q9WHS6 human papil
39	28	90.3	505	12	Q9WPH4	Q9WPH4 human papil
40	28	90.3	505	12	Q92282	Q92282 human papil
41	28	90.3	505	12	Q9WHS5	Q9WHS5 human papil
42	28	90.3	522	3	Q96VF4	Q96VF4 uromyces fa
43	28	90.3	531	12	Q00530	Q00530 human papil
44	28	90.3	531	12	Q8B5N9	Q8B5N9 human papil
45	28	90.3	531	16	Q8Z0P3	Q8Z0P3 anabaena sp

ALIGNMENTS

RESULT 1	Q8K1F2	PRELIMINARY;	PRT;	112 AA.
ID	Q8K1F2			
AC	Q8K1F2;			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Anti-VIPase light chain variable region (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;			
RA	Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;			
RT	"Innate proteolytic antibodies: Failed D-VIPase response to the D-			
RT	enantiomer of VIP and identification of L-VIPase VL domains.";			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF516283; AAM64201.1; -			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; IG; 1.			
DR	SMART; SM00409; IG; 1.			
DR	SMART; SM00406; IGv; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
FT	NON_TER	1		
FT	NON_TER	112		
SO	SEQUENCE	112 AA; 11953 MW; 4716B87FADB543ED CRC64;		
Query Match				
Best Local Similarity 100.0%; Score 31; DB 11; Length 112;				
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 STSNLAS 7			
Db	49 STSNLAS 55			

## RESULT 2

Q8K1F1 PRELIMINARY; PRT; 114 AA.

ID Q8K1F1  
AC Q8K1F1;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Anti-VIPase light chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;  
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
RT "Innate proteolytic antibodies: Failed D-VIPase response to the D-  
entantlomer of VIP and identification of L-VIPase VL domains.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF516284; AAM64202.1; -.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 31; DB 11; Length 114;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 51 STSNLAS 57

RESULT 3

Q8YDZ0 PRELIMINARY; PRT; 265 AA.

ID Q8YDZ0  
AC Q8YDZ0;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Channel protein VIRB10 homolog.  
GN BMEI10034.  
OS Brucella melitensis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29459;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=16M / ATCC 23456 / Biotype 1;  
RX MEDLINE=20020109; PubMed=11756688;  
RA Delvecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,  
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,  
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,  
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
Haselkorn R., Kyrpides N., Overbeek R.;  
RT "The genome sequence of the facultative intracellular pathogen  
Brucella melitensis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).  
DR EMBL; AE009642; AL53275.1; -.  
DR InterPro; IPR005498; TrbI.  
DR Pfam; PF03743; TrbI; 1.  
KW Complete proteome.  
SQ SEQUENCE 265 AA; 28204 MW; 042033AA2FD5EC73 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 31; DB 16; Length 265;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 219 STSNLAS 225

## RESULT 4

Q9KIS6 PRELIMINARY; PRT; 388 AA.

ID Q9KIS6  
AC Q9KIS6;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE VIRB10.  
GN VIRB10.  
OS Brucella abortus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=235;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2308;  
RX MEDLINE=20398168; PubMed=10940027;  
RA Sieira R., Comerzi D.J., Sanchez D.O., Ugalde R.A.;  
RT "A Homologue of an Operon Required for DNA Transfer in Agrobacterium  
Is Required in Brucella abortus for Virulence and Intracellular  
Multiplication.";  
RL J. Bacteriol. 182:4849-4855(2000).  
DR EMBL; AF226278; AAF73903.1; -.  
DR InterPro; IPR005498; TrbI.  
DR Pfam; PF03743; TrbI; 1.  
SQ SEQUENCE 388 AA; 41193 MW; D8A63372B267E7F3 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 31; DB 2; Length 388;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 342 STSNLAS 348

## RESULT 5

Q9RPX5 PRELIMINARY; PRT; 391 AA.

ID Q9RPX5  
AC Q9RPX5;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE VIRB10.  
GN VIRB10.  
OS Brucella suis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29461;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1330;  
RX MEDLINE=99440171; PubMed=10510235;  
RA O'Callaghan D., Cazeville C., Allardet-Servent A., Boschiroli M.L.,  
Bourg G., Foulongue V., Frutos P., Kulakov Y., Ramuz M.;  
RT "A homologue of the Agrobacterium tumefaciens VirB and Bordetella  
pertussis Ptl type IV secretion systems is essential for intracellular  
survival of Brucella suis.";  
RL Mol. Microbiol. 33:1210-1220(1999).  
DR EMBL; AF141604; AAD56620.1; -.  
DR InterPro; IPR005498; TrbI.  
DR Pfam; PF03743; TrbI; 1.  
SQ SEQUENCE 391 AA; 41453 MW; A6DCA4C9AFBB490D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
 |||||  
 Db 345 STSNLAS 351

## RESULT 6

Q8FXK6 PRELIMINARY; PRT; 391 AA.  
 AC Q8FXK6;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Type IV secretion system protein VirB10.  
 GN BRA0060.  
 OS Brucella suis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OK NCBI\_TaxID=29461;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1330 / Biovar 1;  
 RX MEDLINE=22247741; PubMed=12271122;  
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,  
 RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,  
 RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,  
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,  
 RT "The Brucella suis genome reveals fundamental similarities between  
 animal and plant pathogens and symbionts."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).  
 DR EMBL; AE014510; AAN33272.1; -.  
 DR TIGR; BRA0060; -.  
 KW Complete proteome.  
 SQ SEQUENCE 391 AA; 41484 MW; A7720A28B30194B6 CRC64;

Query Match 100.0%; Score 31; DB 16; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
 |||||  
 Db 345 STSNLAS 351

## RESULT 7

Q37901 PRELIMINARY; PRT; 595 AA.  
 AC Q37901;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Tail protein.  
 GN HRS.  
 OS Bacteriophage BF23.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 OC T5-like viruses.  
 OK NCBI\_TaxID=10707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96204568; PubMed=8623528;  
 RA Mondigler M., Holz T., Heller K.J.,  
 RT "Identification of the receptor-binding regions of pbs proteins of  
 RT bacteriophages T5 and BF23."  
 RL Virology 219:19-28 (1996).  
 DR EMBL; L42820; AAB05216.1; -.  
 SQ SEQUENCE 595 AA; 63909 MW; E79B717F88EA2099 CRC64;

Query Match 100.0%; Score 31; DB 9; Length 595;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
 |||||  
 Db 264 STSNLAS 270

## RESULT 8

Q26306 PRELIMINARY; PRT; 753 AA.  
 AC Q26306;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE NEU-NEURALIZED.  
 GN NEUR OR NEU OR CG11988.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OK NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93285130; PubMed=8508781;  
 RA Boulianne G.L., la Concha A., Campos-Ortega J.A., Jan L.Y., Jan Y.N.,  
 RT "The Drosophila neurogenic gene neuralized encodes a novel protein and  
 is expressed in precursors of larval and adult neurons."  
 RL EMBO J. 12:2586-2586 (1993).  
 CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL; S62597; AAB27151.1; -.  
 DR FlyBase; FBgn0002932; neur.  
 DR InterPro; IPR006573; Neu\_Z.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00588; NEUZ; 2.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 DR Metal-binding; Zinc; Zinc-finger.  
 KW Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 753 AA; 82307 MW; 45056A93EDDA7B41 CRC64;

Query Match 100.0%; Score 31; DB 5; Length 753;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7  
 |||||  
 Db 585 STSNLAS 591

## RESULT 9

Q12271 PRELIMINARY; PRT; 1107 AA.  
 AC Q12271;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE YOR3231W from chromosome XV.  
 GN INP53 OR YOR3231W OR YOR109W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OK NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Benes V., Andrade M.A., Rechmann S., Teodoru C., Banrevi A.,  
 RA Sander C., Valencía A., Ansoerge W., Voss H.,  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Voss H., Benes V., Rechmann S., Teodoru C., Schwager C., Paces V.,  
 RA Ansoerge W.,

```
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X94335; CAA64029.1; -.
DR EMBL; Z75017; CAA99307.1; -.
DR SGD; S0005635; INP53.
DR InterPro; IPR005135; Exo_endo_phos.
DR InterPro; IPR000300; IPPC.
DR InterPro; IPR002013; Syja_N.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR Pfam; PF02383; Syja_N; 1.
DR SMART; SM00128; IPPC; 1.
DR PROSITE; PS50275; SAC; 1.
SQ SEQUENCE 1107 AA; 124576 MW; 1E024F15085261EA CRC64;

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 1107;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 1029 STSNLAS 1035

RESULT 10
Q9JL76 PRELIMINARY; PRT; 97 AA.
AC Q9JL76;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206030; AAF69328.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFE1F49DA1C CRC64;

Query Match
Best Local Similarity 90.3%; Score 28; DB 11; Length 97;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 39 ATSNLAS 45

RESULT 11
Q9C5K8 PRELIMINARY; PRT; 187 AA.
AC Q9C5K8;
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DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical 19.9 kDa protein.
GN F22D1.70/AT5G20900.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene F22D1.70/AT5G20900."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene F22D1.70/AT5G20900."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF360184; AAK25894.1; -.
DR EMBL; AY051013; AAK93690.1; -.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
KM Hypothetical protein.
SQ SEQUENCE 187 AA; 19933 MW; 4F0C66DECBB4F0E1 CRC64;

Query Match
Best Local Similarity 90.3%; Score 28; DB 10; Length 187;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7
Db 112 STSNVAS 118

RESULT 12
Q8JMU6 PRELIMINARY; PRT; 208 AA.
AC Q8JMU6;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Major capsid protein L1 (Fragment).
GN L1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bsb-102;
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RT "Human papillomavirus type 16 variants in Central Brazil."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY098925; AAM29173.1; -.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late protein L1; 1.
DR PRINTS; PR00865; HPVCAPSIDL1.
```



DR ProDom; PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 1  
FT NON\_TER 208  
SQ SEQUENCE 208 AA; 23455 MW; 936AA0DDA7EDE483 CRC64;

Query Match  
Best Local Similarity 90.3%; Score 28; DB 12; Length 208;  
Matches 6; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 24 STANLAS 30

## RESULT 13

Q8JMU9 PRELIMINARY; PRT; 211 AA.

AC Q8JMU9;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Major capsid protein L1 (Fragment).  
GN L1.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;

RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=Bsb-178;  
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,  
RA Martins C.R.F.;  
RT "Human papillomavirus type 16 variants in Central Brazil."  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY098921; AAM29169.1; -  
DR InterPro; IPR002210; PV\_capsid\_L1.  
DR Pfam; PF00500; late\_protein\_L1; 1.  
DR PRINTS; PR00865; HPVcapsidL1.  
DR ProDom; PD000544; PV\_capsid\_L1; 1.

FT NON\_TER 1  
FT NON\_TER 211  
SQ SEQUENCE 211 AA; 23840 MW; 28134419632A1E9D CRC64;

Query Match  
Best Local Similarity 90.3%; Score 28; DB 12; Length 211;  
Matches 6; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 27 STANLAS 33

## RESULT 14

Q8JMU5 PRELIMINARY; PRT; 221 AA.

AC Q8JMU5;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Major capsid protein L1 (Fragment).  
GN L1.

OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bsb-14;  
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,  
RA Martins C.R.F.;

RT "Human papillomavirus type 16 variants in Central Brazil."  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY098926; AAM29174.1; -.

DR InterPro; IPR002210; PV\_capsid\_L1.  
DR Pfam; PF00500; late\_protein\_L1; 1.  
DR PRINTS; PR00865; HPVcapsidL1.  
DR ProDom; PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 1  
FT NON\_TER 221  
SQ SEQUENCE 221 AA; 25004 MW; 9C29F33B4E4BD218 CRC64;

Query Match  
Best Local Similarity 90.3%; Score 28; DB 12; Length 221;  
Matches 6; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 30 STANLAS 36

## RESULT 15

Q8IC42 PRELIMINARY; PRT; 253 AA.

AC Q8IC42;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN PF07\_0008.  
OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,  
RA Quail M., Barrell B.;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL844506; CAD50798.1; -  
DR KW Hypothetical protein.  
SQ SEQUENCE 253 AA; 27673 MW; 0488837CF18651D9 CRC64;

Query Match  
Best Local Similarity 90.3%; Score 28; DB 5; Length 253;  
Matches 6; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 229 NTSNLAS 235

Search completed: July 30, 2003, 09:42:42  
Job time : 9.52972 secs

**THIS PAGE BLANK (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 2.25581 Seconds  
(without alignments)  
131.295 Million cell updates/sec

Title: US-09-865-198-5  
Perfect score: 31  
Sequence: 1 STSNLAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	2 US-08-116-778E-10	Sequence 10, Appl
2	31	100.0	7	2 US-08-438-562-10	Sequence 10, Appl
3	31	100.0	7	2 US-08-483-528B-98	Sequence 98, Appl
4	31	100.0	7	3 US-09-171-945-27	Sequence 27, Appl
5	31	100.0	7	4 US-09-393-385B-109	Sequence 109, App
6	31	100.0	100	2 US-08-308-494A-15	Sequence 15, Appl
7	31	100.0	105	3 US-08-434-000A-12	Sequence 12, Appl
8	31	100.0	105	4 US-09-312-157-12	Sequence 12, Appl
9	31	100.0	107	3 US-09-171-945-50	Sequence 50, Appl
10	31	100.0	107	3 US-09-171-945-61	Sequence 61, Appl
11	31	100.0	107	3 US-09-171-945-65	Sequence 65, Appl
12	31	100.0	107	3 US-09-171-945-71	Sequence 71, Appl
13	31	100.0	108	3 US-08-483-749A-8	Sequence 8, Appl
14	31	100.0	108	3 US-09-171-945-9	Sequence 9, Appl
15	31	100.0	110	4 US-09-343-698-8	Sequence 8, Appl
16	31	100.0	129	2 US-08-116-778E-2	Sequence 2, Appl
17	31	100.0	129	2 US-08-438-562-2	Sequence 92, Appl
18	31	100.0	129	2 US-08-483-528B-92	Sequence 92, Appl
19	31	100.0	130	4 US-09-393-385B-111	Sequence 111, App
20	31	100.0	130	4 US-09-393-385B-113	Sequence 113, App
21	31	100.0	133	2 US-08-116-778E-37	Sequence 37, Appl
22	31	100.0	133	2 US-08-438-562-37	Sequence 37, Appl
23	31	100.0	133	2 US-08-483-528B-101	Sequence 101, App
24	31	100.0	213	3 US-08-630-820-6	Sequence 6, Appl
25	31	100.0	215	6 5455030-3	Patent No. 5455030
26	31	100.0	225	6 5455030-5	Patent No. 5455030
27	31	100.0	235	3 US-09-171-945-17	Sequence 17, Appl

28	31	100.0	235	3	US-09-171-945-52	Sequence 52, Appl
29	31	100.0	235	3	US-09-171-945-97	Sequence 97, Appl
30	31	100.0	235	3	US-09-171-945-99	Sequence 99, Appl
31	31	100.0	236	6	5455030-7	Patent No. 5455030
32	31	100.0	244	1	US-08-230-843-2	Sequence 2, Appl
33	31	100.0	244	2	US-08-636-936-2	Sequence 2, Appl
34	31	100.0	247	6	5455030-9	Patent No. 5455030
35	31	100.0	248	6	5455030-11	Patent No. 5455030
36	31	100.0	270	2	US-08-652-507-2	Sequence 2, Appl
37	31	100.0	281	4	US-09-423-439-44	Sequence 44, Appl
38	31	100.0	553	2	US-08-661-052-16	Sequence 16, Appl
39	31	100.0	553	3	US-09-188-082-16	Sequence 16, Appl
40	31	100.0	553	4	US-09-364-088-16	Sequence 16, Appl
41	31	100.0	553	4	US-09-102-716-16	Sequence 16, Appl
42	31	100.0	666	4	US-09-423-439-51	Sequence 51, Appl
43	28	90.3	7	3	US-08-783-853A-13	Sequence 13, Appl
44	28	90.3	7	3	US-09-280-028-14	Sequence 14, Appl
45	28	90.3	7	4	US-09-344-050-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-08-116-778E-10  
; Sequence 10, Application US/08116778E  
; Patent No. 5830470  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KUMANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHAYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/116,778E  
; FILING DATE: 07-SEP-93  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 249-59  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-116-778E-10

Query Match 100.0%; Score 31; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
|||||||

Db 1 STSNLAS 7

## RESULT 2

US-08-438-562-10

; Sequence 10, Application US/08438562  
; Patent No. 5874255

## ; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: KOIKE, MASAMICHI

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

; APPLICANT: KUMAWA, YOSHIHISA

; APPLICANT: HASEGAWA, MAMORU

; TITLE OF INVENTION: HUMANIZED ANTIBODIES

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON &amp; VANDERHAYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/438,562

; FILING DATE: 10-MAY-95

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/116,778

; FILING DATE: 07-SEP-93

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 249-76

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4000

; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-438-562-10

Query Match 100.0%; Score 31; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7

Db 1 STSNLAS 7

## RESULT 3

US-08-483-528B-98

; Sequence 98, Application US/08483528B

; Patent No. 5939532

## ; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: KOIKE, MASAMICHI

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

; APPLICANT: KUMAWA, YOSHIHISA

; APPLICANT: HASEGAWA, MAMORU

; TITLE OF INVENTION: HUMANIZED ANTIBODIES

; NUMBER OF SEQUENCES: 103

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON &amp; VANDERHAYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,528B

; FILING DATE: 07-JUN-95

; CLASSIFICATION: 536

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4000

; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 98:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-483-528B-98

Query Match 100.0%; Score 31; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7

Db 1 STSNLAS 7

## RESULT 4

US-09-171-945-27

; Sequence 27, Application US/09171945

; Patent No. 6277599

## ; GENERAL INFORMATION:

; APPLICANT: Emery, Stephen

; APPLICANT: Copley, Clive Graham

; APPLICANT: Edge, Michael Derek

; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said

; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System

; FILE REFERENCE: Monoclonal Antibody to CEA

; CURRENT APPLICATION NUMBER: US/09/171,945

; CURRENT FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: GB9703103.3

; PRIOR FILING DATE: 1997-02-14

; PRIOR APPLICATION NUMBER: GB9609405.7

; PRIOR FILING DATE: 1996-05-04

; PRIOR APPLICATION NUMBER: PCT/GB97/01165

; PRIOR FILING DATE: 1997-04-29

; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 27

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: humanized

; US-09-171-945-27

Query Match 100.0%; Score 31; DB 3; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSNLAS 7

Db 1 STSNLAS 7

RESULT 5  
US-09-393-385B-109  
; Sequence 109, Application US/09393385B  
; Patent No. 6423511  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KIWANA, YOSHIOHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/393,385B  
; FILING DATE: 27-JUN-96  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-393-385B-109

Query Match 100.0%; Score 31; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 1 STSNLAS 7

RESULT 6  
US-08-308-494A-15  
; Sequence 15, Application US/08308494A  
; Patent No. 5959083  
; GENERAL INFORMATION:  
; APPLICANT: Bosslet, Klaus  
; APPLICANT: Seeman, Gerhard  
; TITLE OF INVENTION: Tetravalent Bispecific Receptors, The  
; TITLE OF INVENTION: Preparation and Use Thereof  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/308,494A  
; FILING DATE: 21-SEP-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/891,739  
; FILING DATE: 01-JUN-1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P4118120.4  
; FILING DATE: 03-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kulik, David J.  
; REGISTRATION NUMBER: 36,576  
; REFERENCE/DOCKET NUMBER: 05552-1186-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 100 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-308-494A-15

Query Match 100.0%; Score 31; DB 2; Length 100;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 46 STSNLAS 52

RESULT 7  
US-08-434-000A-12  
; Sequence 12, Application US/08434000A  
; Patent No. 6046037  
; GENERAL INFORMATION:  
; APPLICANT: ANDREW C. HIATT, JULIAN  
; APPLICANT: K.-C. MA, THOMAS LEHNER  
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: Storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/434,000A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 08/367,395  
; FILING DATE: 12/30/94  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Guise, Jeffrey W.  
; REGISTRATION NUMBER: 34,613



REFERENCE/DOCKET NUMBER: 212/127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 552-8400  
TELEFAX: (619) 552-0159  
TELEX: 67-3510  
TELEX: SEQUENCE LISTING  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-434-000A-12  
Guy's 13 Kappa

Query Match 100.0%; Score 31; DB 3; Length 105;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 49 STSNLAS 55

RESULT 8  
US-09-312-157-12  
Sequence 12, Application US/09312157  
Patent No. 6303341  
GENERAL INFORMATION:  
APPLICANT: ANDREW C. HIATT, JULIAN  
K.-C. MA, THOMAS LEHNER  
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
PROTEINS IN PLANTS AND THEIR USES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/312,157  
FILING DATE: 14-May-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/434,000  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 212/127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 552-8400  
TELEFAX: (619) 552-0159  
TELEX: 67-351  
SEQUENCE LISTING  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
DESCRIPTION: Guy's 13 Kappa  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-312-157-12

Query Match 100.0%; Score 31; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 49 STSNLAS 55

RESULT 9  
US-09-171-945-50  
Sequence 50, Application US/09171945  
Patent No. 6277599  
GENERAL INFORMATION:  
APPLICANT: Emery, Stephen  
APPLICANT: Copley, Clive Graham  
APPLICANT: Edge, Michael Derek  
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said  
Antibody, and Their Therapeutic Use in an Adept System  
FILE REFERENCE: Monoclonal Antibody to CEA  
CURRENT APPLICATION NUMBER: US/09/171,945  
CURRENT FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: GB9703103.3  
PRIOR FILING DATE: 1997-02-14  
PRIOR APPLICATION NUMBER: GB9609405.7  
PRIOR FILING DATE: 1996-05-04  
PRIOR APPLICATION NUMBER: PCT/GB97/01165  
PRIOR FILING DATE: 1997-04-29  
NUMBER OF SEQ ID NOS: 131  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 61  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial Sequence  
OTHER INFORMATION: Description of Artificial Sequence: humanized  
US-09-171-945-50

Query Match 100.0%; Score 31; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
Db 49 STSNLAS 55

RESULT 10  
US-09-171-945-61  
Sequence 61, Application US/09171945  
Patent No. 6277599  
GENERAL INFORMATION:  
APPLICANT: Emery, Stephen  
APPLICANT: Copley, Clive Graham  
APPLICANT: Edge, Michael Derek  
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said  
Antibody, and Their Therapeutic Use in an Adept System  
FILE REFERENCE: Monoclonal Antibody to CEA  
CURRENT APPLICATION NUMBER: US/09/171,945  
CURRENT FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: GB9703103.3  
PRIOR FILING DATE: 1997-02-14  
PRIOR APPLICATION NUMBER: GB9609405.7  
PRIOR FILING DATE: 1996-05-04  
PRIOR APPLICATION NUMBER: PCT/GB97/01165  
PRIOR FILING DATE: 1997-04-29  
NUMBER OF SEQ ID NOS: 131  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 61  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-61

Query Match      100.0%; Score 31; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 STSNLAS 7
        |||||
Db      49 STSNLAS 55

RESULT 11
US-09-171-945-65
; Sequence 65, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-65

Query Match      100.0%; Score 31; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 STSNLAS 7
        |||||
Db      49 STSNLAS 55

RESULT 12
US-09-171-945-71
; Sequence 71, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 71
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; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-71

Query Match      100.0%; Score 31; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 STSNLAS 7
        |||||
Db      49 STSNLAS 55

RESULT 13
US-08-483-749A-8
; Sequence 8, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; FILE REFERENCE: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-749A-8

Query Match      100.0%; Score 31; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 STSNLAS 7
        |||||
Db      51 STSNLAS 57

RESULT 14
US-09-171-945-9
; Sequence 9, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
```

; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said  
; FILE REFERENCE: Antibody, and Their Therapeutic Use in an Adept System  
; CURRENT APPLICATION NUMBER: US/09/171,945  
; CURRENT FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: GB9703103.3  
; PRIOR FILING DATE: 1997-02-14  
; PRIOR APPLICATION NUMBER: GB9609405.7  
; PRIOR FILING DATE: 1996-05-04  
; PRIOR APPLICATION NUMBER: PCT/GB97/01165  
; PRIOR FILING DATE: 1997-04-29  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: humanized  
US-09-171-945-9

Query Match 100.0%; Score 31; DB 3; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
|||||||  
Db 49 STSNLAS 55

## RESULT 15

US-09-343-698-8  
; Sequence 8, Application US/09343698  
; Patent No. 6475486

## GENERAL INFORMATION:

APPLICANT: Seeman, Gerhard

Bosslet, Klaus

Czech, Joerg

Kolar, Cenek

Hoffman, Dieter

Sedlacek, Hans-Harald

TITLE OF INVENTION: Glycosyl-Etoposide Prodrugs, A Process For  
Preparation Thereof And The Use Thereof In Combination With  
Functionalized Tumor-Specific Enzyme Conjugates

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/343,698

FILING DATE: 30-Jun-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/325,955

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Ogden, Stasia L.

REGISTRATION NUMBER: 36,228

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

FAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-343-698-8

Query Match 100.0%; Score 31; DB 4; Length 110;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STSNLAS 7  
|||||||  
Db 53 STSNLAS 59

Search completed: July 30, 2003, 09:38:30  
Job time : 3.25581 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 2.6613 Seconds  
(without alignments)  
325.245 Million cell updates/sec

Title: US-09-865-198-6  
Perfect score: 48  
Sequence: 1 QORSSYPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	132	2	S05268	Ig kappa chain pre
2	42	87.5	93	2	S17641	Ig kappa chain V r
3	42	87.5	106	2	B54378	Ig light chain V r
4	42	87.5	106	2	PS0070	Ig kappa chain V r
5	40	83.3	35	2	E38601	Ig kappa chain V r
6	40	83.3	99	2	D38601	Ig kappa chain V r
7	38	79.2	91	2	S17626	Ig kappa chain V r
8	38	79.2	117	2	S42466	Ig kappa chain V r
9	38	79.2	140	2	PL0013	Ig kappa chain pre
10	37	77.1	106	2	G27887	Ig kappa chain V r
11	37	77.1	130	2	A32513	Ig kappa chain pre
12	37	77.1	132	2	S40334	Ig kappa chain - h
13	37	77.1	1501	1	B29813	Ig kappa chain - h
14	36	75.0	86	2	C28195	Ig kappa chain V r
15	36	75.0	886	2	F83862	penicillin-binding
16	35	72.9	91	2	S17628	Ig kappa chain V r
17	35	72.9	107	2	A28195	Ig kappa chain V r
18	35	72.9	108	1	K1HUBN	Ig kappa chain V-I
19	35	72.9	108	2	PL0204	anti-DNA autoantib
20	35	72.9	111	2	S23628	Ig kappa chain V r
21	35	72.9	129	2	S40369	Ig kappa chain - h
22	35	72.9	133	2	S49632	hypothetical prote
23	34	70.8	98	2	S26342	Ig kappa chain V r
24	34	70.8	102	2	S29584	Ig kappa chain V r
25	34	70.8	106	2	PC4282	Ig kappa chain (an
26	34	70.8	108	1	K2DCGM	Ig kappa chain V r
27	34	70.8	108	2	S29581	Ig kappa chain V r
28	34	70.8	128	2	S40379	Ig kappa chain V-J
29	34	70.8	129	2	D32513	Ig kappa chain pre

30	34	70.8	144	2	PL0106	Ig kappa chain pre
31	34	70.8	275	2	H82106	chemotaxis protein
32	34	70.8	341	1	VHBPEL	major capsid prote
33	34	70.8	341	2	C90833	major capsid prote
34	34	70.8	341	2	P90900	probable major cap
35	34	70.8	341	2	E85690	probable capsid pr
36	34	70.8	343	1	KHDO	cysteine proteinas
37	34	70.8	377	2	T12042	cysteine proteinas
38	34	70.8	380	2	S55923	conserved hypothet
39	34	70.8	397	2	B70048	ABC transporter BH
40	34	70.8	399	2	H84108	probable membrane
41	34	70.8	653	2	S67035	Ig kappa chain V r
42	33	68.8	77	2	D30502	Ig kappa chain V r
43	33	68.8	93	2	S17635	Ig kappa chain V-I
44	33	68.8	108	1	K1HUKU	Ig kappa chain V-I
45	33	68.8	108	2	PS0069	Ig kappa chain V r

## ALIGNMENTS

RESULT 1  
S05268  
Ig kappa chain precursor V-J region (38C13-V1) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text\_change 21-Jan-2000  
C/Accession: S05268; J10062; S03846  
R/Levy, S.  
submitted to the EMBL Data Library, February 1989  
A/Reference number: S05267  
A/Accession: S05268  
A/Molecule type: mRNA  
A/Residues: 1-132 <LEV>  
A/Cross-references: EMBL:X14098; NID:952562; PIDN:CAA32260.1; PID:G736261  
R/Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.  
J. Exp. Med. 168, 1607-1620, 1988  
A/Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explana  
A/Reference number: J10061; MUID:89035985; PMID:3141553  
A/Accession: J10062  
A/Molecule type: mRNA  
A/Residues: 1-120 <CAR>  
A/Cross-references: EMBL:X14098  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/1-14/Domain: signal sequence (fragment) #status predicted <SIG>  
F/15-132/Product: Ig kappa chain (fragment) #status predicted <MAT>  
F/15-108/Domain: V region (V-kappa-1) <VRE>  
F/30-103/Domain: immunoglobulin homology <IMM>  
F/109-132/Domain: J region (J-kappa-4) (fragment) <JRE>

Query Match 100.0%; Score 48; DB 2; Length 132;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
Db 102 QORSSYPFT 110

RESULT 2  
S17641  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S17641  
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A/Title: Making antibody fragments using phage display libraries.  
A/Reference number: S17230; MUID:91326098; PMID:1907718  
A/Accession: S17641  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-93 <CLA>

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;8-83/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 42; DB 2; Length 93;  
Best Local Similarity 88.9%; Pred. No. 0.26;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
|||  
Db 82 QORSSYPFT 90

RESULT 3  
B54378

Ig light chain V region anti-triplex DNA - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: B54378

R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.

J. Biol. Chem. 269, 7019-7023, 1994

A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence  
A;Reference number: A54378; PMID:94165109; PMID:7509814

A;Accession: B54378

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-106 <AGA>

A;Cross-references: GB:S68985; NID:G545746; PIDN:AAB30096.1; PID:G545747

A;Experimental source: spleen and myeloma cell line MOPC 315.43

A;Note: sequence inconsistent with nucleotide translation

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 42; DB 2; Length 106;  
Best Local Similarity 88.9%; Pred. No. 0.29;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
|||  
Db 88 QORSSYPFT 96

RESULT 4  
PS0070

Ig kappa chain V region (38C13.V6.1) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000

C;Accession: PS0070

R;Levy, S.; Campbell, M.J.; Levy, R.

J. Exp. Med. 170, 1-13, 1989

A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement

A;Reference number: A92781; PMID:89310348; PMID:2501443

A;Accession: PS0070

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-106 <LEV>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 42; DB 2; Length 106;  
Best Local Similarity 88.9%; Pred. No. 0.29;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
|||  
Db 88 QORSSYPFT 96

RESULT 5  
E38601

Ig kappa chain V region (14D2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Jul-1999

C;Accession: E38601

R;Goshorn, S.C.; Retzel, E.; Jemerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A;Title: Common structural features among monoclonal antibodies binding the same antigen

A;Reference number: A38601; PMID:91115823; PMID:1703527

A;Accession: E38601

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-35 <GOS>

A;Cross-references: GB:M57982; NID:G196410; PIDN:AAA63363.1; PID:G196411

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 83.3%; Score 40; DB 2; Length 35;  
Best Local Similarity 87.5%; Pred. No. 0.26;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 QRSSYPFT 9  
|||  
Db 24 QRSSYPFT 31

RESULT 6  
D38601

Ig kappa chain V region (6A7) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 21-Jan-2000

C;Accession: D38601

R;Goshorn, S.C.; Retzel, E.; Jemerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A;Title: Common structural features among monoclonal antibodies binding the same antigen

A;Reference number: A38601; PMID:91115823; PMID:1703527

A;Accession: D38601

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-99 <GOS>

A;Cross-references: GB:M57981; NID:G196408; PIDN:AAA63362.1; PID:G196409

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 40; DB 2; Length 99;  
Best Local Similarity 77.8%; Pred. No. 0.7;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
|||  
Db 80 QORSSYPFT 88

RESULT 7  
S17626

Ig kappa chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000

C;Accession: S17626

R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A;Title: Making antibody fragments using phage display libraries.

A;Reference number: S17230; PMID:91326098; PMID:1907718

A;Accession: S17626

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-91 <CIA>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 38; DB 2; Length 91;  
Best Local Similarity 88.9%; Pred. No. 1.6;



Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9

Db 80 QQRSSYPFT 88

## RESULT 8

S42466

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S42466

R/Shiyanov, P.A.; Bespalov, I.A.; Terletskaia, H.N.; Deyev, S.M.

submitted to the EMBL Data Library, March 1994

A/Reference number: S42466

A/Accession: S42466

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-117 <SHI>

A/Cross-references: EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PID:g460825

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;26-100/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 38; DB 2; Length 117;

Best Local Similarity 77.8%; Pred. No. 2.1;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9

Db 99 QQRSSYPFT 107

## RESULT 9

PL0013

Ig kappa chain precursor V region (4C11) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000

C/Accession: PL0013

R/Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.

Mol. Immunol. 25, 33-40, 1988

A/Title: Structural basis of stimulatory anti-idiotypic antibodies.

A/Reference number: PL0011; MUID:88142863; PMID:3125424

A/Accession: PL0013

A/Molecule type: mRNA

A/Residues: 1-140 <CHE>

A/Experimental source: cell line 4C11

C/Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>

F;38-111/Domain: immunoglobulin homology <IMM>

F;46-55/Region: complementarity-determining 1

F;71-77/Region: complementarity-determining 2

F;110-118/Region: complementarity-determining 3

F;130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 79.2%; Score 38; DB 2; Length 140;

Best Local Similarity 88.9%; Pred. No. 2.4;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9

Db 110 QQRSSYPFT 118

## RESULT 10

G27887

Ig kappa chain V region (H18-S415) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 21-Jan-2000

C/Accession: G27887

R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A/Title: Structural and functional implications of a restricted antibody response to a d

A/Reference number: A91043; MUID:86300658; PMID:2427335

A/Accession: G27887

A/Molecule type: DNA

A/Residues: 1-106 <CAT>

A/Experimental source: strain Balb/c

A/Note: this sequence was determined from the germline gene

C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus r

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 37; DB 2; Length 106;

Best Local Similarity 87.5%; Pred. No. 3;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9

Db 89 QRSSYPFT 96

## RESULT 11

A32513

Ig kappa chain precursor V region (MRL22) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000

C/Accession: A32513

R/Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;

J. Clin. Invest. 82, 852-860, 1988

A/Title: Immunoglobulin kappa light chain variable region gene complex organization and

A/Reference number: A94689; MUID:88331394; PMID:3138286

A/Accession: A32513

A/Molecule type: DNA

A/Residues: 1-130 <KOF>

A/Cross-references: GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:g196944

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;38-113/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 37; DB 2; Length 130;

Best Local Similarity 77.8%; Pred. No. 3.6;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9

Db 112 QQRSSYPFT 120

## RESULT 12

S40334

Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C/Accession: S40334

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40334

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-132 <KLE>

A/Cross-references: EMBL:X72444

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;37-111/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 37; DB 2; Length 132;

Best Local Similarity 77.8%; Pred. No. 3.7;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
||:|||||  
Db 110 QOFNSYPFT 118

## RESULT 13

B29813  
174K ninac protein - fruit fly (Drosophila melanogaster)  
N:Contains: protein kinase (EC 2.7.1.-)  
C:Species: Drosophila melanogaster  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001  
R:Montell, C.; Rubin, G.M.  
Cell 52, 757-772, 1988  
A:Title: The Drosophila ninac locus encodes two photoreceptor cell specific proteins with  
A:Reference number: A90898; MUID:88151067; PMID:2449973  
A:Accession: B29813  
A:Molecule type: mRNA  
A:Residues: 1-1501 <MON>  
A:Cross-references: GB:M20230; NID:g157967; PIDN:AAA28721.1; PID:g157968  
C:Genetics:  
A:Gene: FlyBase:ninac  
A:Cross-references: FlyBase:FBgn0002938  
C:Superfamily: ninac protein; myosin motor domain homology; protein kinase homology  
C:Keywords: actin binding; alternative splicing; ATP; nucleotide binding; P-loop; phosph  
F:14-282/Domain: protein kinase homology <KIN>  
F:335-1022/Domain: myosin motor domain homology <MMOT>  
F:425-432/Region: nucleotide-binding motif A (P-loop)  
F:911-936/Region: actin binding #status predicted  
F:1054-1501/Domain: carboxyl-terminal <CBT>  
F:45,60,145/Active site: Lys, Glu, Asp #status predicted  
F:431/Binding site: ATP (Lys) #status predicted

Query Match 77.1%; Score 37; DB 1; Length 1501;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYP 7  
|||||  
Db 1352 QORSSYP 1358

## RESULT 14

C28195  
Ig kappa chain V region (anti-haloperidol antibody C) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-May-1997  
C:Accession: C28195  
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
J. Biol. Chem. 263, 4059-4063, 1988  
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s  
A:Reference number: A28195; MUID:88153717; PMID:3267217  
A:Accession: C28195  
A:Molecule type: mRNA  
A:Residues: 1-86 <SH3>  
A:Cross-references: GB:M19768  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 75.0%; Score 36; DB 2; Length 86;  
Best Local Similarity 66.7%; Pred. No. 3.9;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
||:|||||  
Db 68 QOXNSYPYT 76

## RESULT 15

F83862  
penicillin-binding proteins 1A/1B ponA [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: F83862  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: F83862  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-886 <STO>  
A:Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA805421.1; GSPDB:GN00  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: ponA

Query Match 75.0%; Score 36; DB 2; Length 886;  
Best Local Similarity 75.0%; Pred. No. 36;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QORSSYPF 8  
||:|||||  
Db 282 QERESYPF 289

Search completed: July 30, 2003, 09:44:09  
Job time : 3.66113 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:35 ; Search time 1.40532 Seconds  
(without alignments)  
301.171 Million cell updates/sec

Title: US-09-865-198-6  
Perfect score: 48  
Sequence: 1 QQRSSYPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	77.1	1501	1 NINC_DROME	P10676 drosophila
2	35	72.9	108	1 KVIIV_HUMAN	P04430 homo sapien
3	34	70.8	108	1 KVII_CANFA	P01618 canis famli
4	34	70.8	275	1 CHRI_VIBCH	Q9kg06 vibrio chol
5	34	70.8	341	1 HEAD_LAMBD	P03713 bacterioph
6	34	70.8	343	1 CYS1_DICDI	P04988 dictyosteli
7	33	68.8	108	1 KVIIL_HUMAN	P01604 homo sapien
8	33	68.8	345	1 YDE9_SCHPO	Q10442 schizosacch
9	33	68.8	556	1 PPBD_BACSU	P42251 bacillus su
10	33	68.8	662	1 YLN9_CAEEL	Q09512 caenorhabdi
11	32	66.7	265	1 TF2D_STRPU	P91809 strongyloce
12	32	66.7	446	1 CN7B_MOUSE	Q9qxl1 mus musculu
13	32	66.7	450	1 CN7B_HUMAN	Q9np56 homo sapien
14	32	66.7	872	1 SCDS_YEAST	P34758 saccharomyc
15	32	66.7	1476	1 AT7A_CRIGR	P49015 cricetulus
16	31	64.6	129	1 KVA4_MOUSE	P01680 mus musculu
17	31	64.6	275	1 CHER_VIBAN	Q57508 vibrio angu
18	31	64.6	275	1 CHER_VIBPA	Q9x9k2 vibrio para
19	31	64.6	360	1 CHLI_MESVI	Q9mult3 mesostigma
20	31	64.6	398	1 KYEL_KULUA	P40952 kluyveromyc
21	31	64.6	588	1 CMC2_CAEEL	Q20799 caenorhabdi
22	31	64.6	673	1 FXO3_HUMAN	Q43524 homo sapien
23	31	64.6	750	1 PTP2_YEAST	P29461 saccharomyc
24	31	64.6	891	1 MAZ3_SCHCO	P37937 schizophy11
25	31	64.6	1115	1 DP3A_BACSU	Q34623 bacillus su
26	30	62.5	118	1 YMX2_YEAST	Q04276 saccharomyc
27	30	62.5	268	1 GCH3_METJA	Q57609 methanococc
28	30	62.5	313	1 VU47_HSVJ7	P52525 human herpe
29	30	62.5	317	1 YRC3_CAEEL	Q10042 caenorhabdi
30	30	62.5	329	1 YHO3_YEAST	P14693 saccharomyc
31	30	62.5	376	1 CYS2_DICDI	P04989 dictyosteli
32	30	62.5	380	1 CYB_HUMAN	P00156 homo sapien
33	30	62.5	396	1 REPA_BACSU	P13962 bacillus su

34	30	62.5	396	1 VE2_HP48	Q80923 human papil
35	30	62.5	403	1 IF4A_LEIBR	Q25225 leishmania
36	30	62.5	442	1 CYS4_DICDI	P54639 dictyosteli
37	30	62.5	450	1 YVAB_STRGY	Q8kra0 streptococc
38	30	62.5	478	1 VP26_DROME	Q9w552 drosophila
39	30	62.5	658	1 S282_HUMAN	O43868 homo sapien
40	30	62.5	726	1 YE40_MYCPN	P75338 mycoplasma
41	30	62.5	865	1 FLUG_EMENTI	P38094 emericella
42	30	62.5	928	1 DNL1_CANAL	P52496 candida alb
43	30	62.5	1072	1 SYIC_YEAST	P09436 saccharomyc
44	30	62.5	1106	1 ACILY_CAEEL	P53585 caenorhabdi
45	30	62.5	1487	1 MDS3_YEAST	P53094 saccharomyc

ALIGNMENTS

RESULT 1  
NINC\_DROME STANDARD; PRT; 1501 AA.  
AC P10676; P10677; (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neither inactivation nor afterpotential protein C (EC 2.7.1.37).  
GN NINAC.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.  
RX MEDLINE=88151067; PubMed=2449973;  
RA Montell C., Rubin G.M.;  
RT "The Drosophila ninac locus encodes two photoreceptor cell specific  
RT proteins with domains homologous to protein kinases and the myosin  
RT heavy chain head."  
RL Cell 52:757-772(1988).  
CC -!- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL FUNCTION. THE NINAC  
CC PROTEINS JOIN PUTATIVE SERINE/THREONINE-PROTEIN KINASE AND MYOSIN  
CC ACTIVITIES.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SUBCELLULAR LOCATION: CYTOSKELETON.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=P10676-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=P10676-2; Sequence=VSP\_004940, VSP\_004941;  
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SER/THR  
CC FAMILY OF PROTEIN KINASES.  
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE MYOSIN  
CC SUPERFAMILY.  
CC -!- SIMILARITY: Contains 1 IQ domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC EMBL; J03131; AAA28718.1; -;  
CC EMBL; J03131; AAA28719.1; -;  
CC EMBL; M20230; AAA28721.1; -;  
CC EMBL; M20231; AAA28720.1; -;  
CC PIR; B29813; B29813.  
CC HSSP; P08799; 1MND.  
CC FlyBase; FBgn0002938; ninac.  
CC GO; GO:0042385; C:myosin III; NAS.  
CC GO; GO:0016028; C:rhabdomere; IDA.

DR GO; GO:0005516; F:calmodulin binding activity; IMP.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.  
DR GO; GO:0016062; P:adaptation of rhodopsin mediated signaling; IMP.  
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IMP.  
DR GO; GO:0016059; P:deactivation of rhodopsin mediated signaling; IMP.  
DR GO; GO:0007603; P:phototransduction, visible light; IMP.  
DR GO; GO:0008104; P:protein localization; IMP.  
DR InterPro; IPR000048; IQ\_region.  
DR InterPro; IPR001609; myosin head.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR Pfam; PF00612; IQ; 2.  
DR Pfam; PF00063; myosin head; 1.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00193; MYOSINHEAVY.  
DR ProDom; PD000355; myosin head; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00015; IQ; 2.  
DR SMART; SM00242; MYSC; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS50096; IQ; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
DR PROSITE; PS00109; PROTEIN KINASE\_TYR; 1.  
DR PROSITE; PS50011; PROTEIN KINASE\_DOM; 1.  
KW Cytoskeleton; Actin-binding; ATP-binding; Myosin; Transferase; Vision;  
KW Serine/threonine-protein kinase; Alternative splicing.  
FT DOMAIN 16 282 PROTEIN KINASE.  
FT DOMAIN 335 1035 MYOSIN.  
FT DOMAIN 1036 1065 IQ.  
FT DOMAIN 1066 1501 NON ALPHA-HELICAL, C-TERMINAL DOMAIN.  
FT NP\_BIND 22 30 ATP (BY SIMILARITY).  
FT BINDING 45 45 ATP (BY SIMILARITY).  
FT ACT\_SITE 145 145 BY SIMILARITY.  
FT DOMAIN 913 934 ACTIN-BINDING (BY SIMILARITY).  
FT VARSPLIC 1082 1135 AFRGRDPVRLPLVNEKSGOLNENTADFRPEAKKWRKES  
IFQVLHYRAARF -> GKKTQVRLREYDEEHIDISSTPS  
EAEEMFLAEAMDEALAAVRIAKIEQASAE (in  
isoform short).  
/FTID=VSP\_004940.  
Missing (in isoform short).  
FT VARSPLIC 1136 1501  
FT CONFLICT 253 253 /FTID=VSP\_004941.  
FT CONFLICT 1089 1089 K -> Q (IN REF. 1; AAA28720/AAA28721).  
FT CONFLICT 1089 1089 P -> R (IN REF. 1; AAA28721).  
SQ SEQUENCE 1501 AA; 174269 MW; D167EABC82A3933A CRC64;  
Query Match 77.1%; Score 37; DB 1; Length 1501;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QQRSSYP 7  
DB 1352 QQRSSYP 1358  
RESULT 2  
KV1V\_HUMAN STANDARD; PRT; 108 AA.  
AC P04430;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region BAN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86174817; PubMed=3083240;  
RA Dwulet F.E., O'Connor T.P., Benson M.D.;  
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";  
RL Mol. Immunol. 23:73-78(1986).

DR PIR; A01878; KIHUBN.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR Immunoglobulin V region; Amyloid.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;  
Query Match 72.9%; Score 35; DB 1; Length 108;  
Best Local Similarity 66.7%; Pred. No. 2.3;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QQRSSYPFT 9  
DB 89 QQRSSYPFT 97  
RESULT 3  
KV1\_CANFA STANDARD; PRT; 108 AA.  
AC P01618;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V region GOM.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79026193; PubMed=100411;  
RA Wasserman R.L., Capra J.D.;  
RT "The amino acid sequence of the light chain variable region of a  
canine myeloma immunoglobulin: evidence that the VK subgroups  
RT predicated mammalian speciation.";  
RL Immunochimistry 15:303-305(1978).  
CC -I- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA  
CHAINS.  
CC -I- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF  
THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.  
DR PIR; A01907; K2DGM.  
DR HSSP; P01607; 1REI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.



FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match  
Best Local Similarity 70.8%; Score 34; DB 1; Length 108;  
Matches 6; Conservativity 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 RSSYPT 9  
Db 90 QRSFYPY 97

## RESULT 4

CHRI\_VIBCH STANDARD; PRT; 275 AA.  
ID CHRI\_VIBCH  
AC Q9K06; O9XCL5;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Chemotaxis protein methyltransferase 1 (EC 2.1.1.80).  
GN CHRI OR CHER OR VC2201.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=666;

## [1]

SEQUENCE FROM N.A.  
RP STRAIN=El Tor N16961 / Serotype O1;  
RX MEDLINE=20406833; PubMed=10952301;  
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,  
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
McDonald L., Uetebach T., Fleischmann R.D., Nierman W.C., White O.,  
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
Fraser C.M.;  
RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
cholerae.";  
RT Nature 406:477-483(2000).  
RL  
RN [2]

RP SEQUENCE OF 10-266 FROM N.A.  
RC STRAIN=CVD110;  
RX MEDLINE=99328977; PubMed=10400589;  
RA O'Toole R., Lundberg S., Fredriksson S.A., Jansson A., Nilsson B.,  
Wolf-Watz H.;  
RA "The chemotactic response of Vibrio anguillarum to fish intestinal  
mucus is mediated by a combination of multiple mucus components.";  
RT J. Bacteriol. 181:4308-4317(1999).  
RL  
CC -1- FUNCTION: METHYLATION OF THE MEMBRANE-BOUND METHYL-ACCEPTING  
CHEMOTAXIS PROTEINS (MCP) TO FORM GAMMA-GLUTAMYL METHYL ESTER  
RESIDUES IN MCP (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + protein L-glutamate  
= S-adenosyl-L-homocysteine + protein L-glutamate methyl ester.  
CC -1- SIMILARITY: Contains 1 cher-type methyltransferase domain.  
CC  
CC  
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CC  
CC

DR EMBL; AE004291; AAF95346.1; -.  
DR EMBL; AF139167; AAD45254.1; -.  
DR PIR; H82106; H82106.  
DR HSSP; P07801; 1AF7.  
DR TIGR; VC2201; -.  
DR InterPro; IPR000780; CHER\_Metranf.  
DR InterPro; IPR001601; Methyltransf.  
DR Pfam; PF01739; CHER; 1.  
DR Pfam; PF03705; CHER\_N; 1.  
DR PRINTS; PR00996; CHERMTFRASE.

DR SMART; SMO0138; Metrc; 1.  
DR PROSITE; PS50123; CHER; 1.  
KW Transferase; Methyltransferase; Complete proteome.  
FT DOMAIN 1 275 CHER-TYPE METHYLTRANSFERASE.  
SQ SEQUENCE 275 AA; 30871 MW; F008ADCBFA46A921 CRC64;

Query Match  
Best Local Similarity 70.8%; Score 34; DB 1; Length 275;  
Matches 6; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 RSSYPT 9  
Db 82 RDSYPT 88

## RESULT 5

HEAD\_LAMB  
ID HEAD\_LAMB STANDARD; PRT; 341 AA.  
AC P03713;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE Major head protein (GPE) (Major coat protein).  
GN E.  
OS Bacteriophage lambda.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC Lambda-like viruses.  
OX NCBI\_TaxID=10710;

## [1]

SEQUENCE FROM N.A.  
RX MEDLINE=83189071; PubMed=6221115;  
RA Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;  
RT "Nucleotide sequence of bacteriophage lambda DNA.";  
RL J. Mol. Biol. 162:729-773(1982).  
CC -1- FUNCTION: GENE E PROTEIN IS A MAJOR COMPONENT OF THE PHAGE HEAD.  
CC THERE ARE ABOUT 420 COPIES OF PROTEIN E PER MATURE PHAGE. SOME OF  
CC THE E PROTEIN IS COVALENTLY LINKED WITH AN EQUI-MOLAR AMOUNT OF  
CC PROTEIN C AND CLEAVED TO YIELD MINOR CAPSID PROTEINS X1 AND X2.  
CC -1- SIMILARITY: STRONG, TO MAJOR HEAD PROTEIN OF PHI-80 AND P21.  
CC

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CC  
CC

DR EMBL; J02459; AAA96540.1; -.  
DR PIR; H04333; VHBPEL.  
DR InterPro; IPR005564; Phage\_cap\_E.  
DR Pfam; PF03864; Phage\_cap\_E; 1.  
KW Coat protein.  
SQ SEQUENCE 341 AA; 38188 MW; 31C50E4B38DA44A9 CRC64;

Query Match  
Best Local Similarity 70.8%; Score 34; DB 1; Length 341;  
Matches 6; Conservativity 85.7%; Pred. No. 13;  
Matches 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 RSSYPT 9  
Db 29 RDSYPT 35

## RESULT 6

CYS1\_DICDI STANDARD; PRT; 343 AA.  
ID CYS1\_DICDI  
AC P04988;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cysteine proteinase 1 precursor (EC 3.4.22.-).  
GN CPRA OR CPL.



OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85257519; PubMed=2990918;  
 RA Williams J.G., North M.J., Mahubani H.M.;  
 RT "A developmentally regulated cysteine proteinase in Dictyostelium discoideum.";  
 RL EMBL J. 4:999-1006(1985).  
 RN [2]  
 RP STRUCTURE OF CARBOHYDRATES.  
 RX MEDLINE=96210028; PubMed=8631906;  
 RA Mehta D.P., Ichikawa M., Salimath P.V., Etchison J.R., Haak R., Manzi A., Freeze H.H.;  
 RT "A lysosomal cysteine proteinase from Dictyostelium discoideum contains N-acetylglucosamine-1-phosphate bound to serine but not mannose-6-phosphate on N-linked oligosaccharides.";  
 RL J. Biol. Chem. 271:10897-10903(1996).  
 CC -1- FUNCTION: CYSTEINE PROTEINASES 1 AND 2 ARE BELIEVED TO PARTICIPATE IN THE BREAKDOWN OF PROTEIN DURING DIFFERENTIATION OF DICTYOSTELIUM AS A RESPONSE TO STARVATION.  
 CC -1- SUBCELLULAR LOCATION: Lysosomal.  
 CC -1- PTM: PHOSPHOGLYCOSYLATED, CONTAINS GLCNAC-ALPHA-1-P-SER RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 CC -----  
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 CC -----  
 DR EMBL; X02407; CAA26255.1; -.  
 DR PIR; A22827; KHDO.  
 DR HSSP; P25779; LAIM.  
 DR MEROPS; C01.UPA; -.  
 DR GlycosuitedB; P04988; -.  
 DR SWISS-2DPAGE; P04988; DICTY.  
 DR DictyDb; DD02003; cpra.  
 DR InterPro; IPR000668; Peptidase\_C1.  
 DR InterPro; IPR000169; SHprot\_acsite.  
 DR Pfam; PF00112; Peptidase\_C1; 1.  
 DR PRINTS; PR00705; PAPAIN.  
 DR ProDom; PD000158; Peptidase\_C1; 1.  
 DR SMART; SM00645; Pept\_C1; 1.  
 DR PROSITE; PS00139; THIOL\_PROTEASE\_CYS; 1.  
 DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; 1.  
 DR PROSITE; PS00640; THIOL\_PROTEASE\_ASN; 1.  
 KW Hydrolyase; Thiol protease; Lysosome; Zymogen; Glycoprotein; Phosphorylation; Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 117 ACTIVATION PEPTIDE.  
 FT CHAIN 118 343 CYSTEINE PROTEINASE 1.  
 FT ACT\_SITE 142 142 BY SIMILARITY.  
 FT ACT\_SITE 286 286 BY SIMILARITY.  
 FT ACT\_SITE 311 311 BY SIMILARITY.  
 FT DISULFID 139 190 BY SIMILARITY.  
 FT DISULFID 173 224 BY SIMILARITY.  
 FT DISULFID 279 332 BY SIMILARITY.  
 SQ SEQUENCE 343 AA; 38495 MW; 71804C15F2B361E2 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 343;  
 Best Local Similarity 66.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9  
 Db 209 QTESSYPYT 217

RESULT 7

KVIL\_HUMAN  
 ID KVIL\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01604;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, last sequence update)  
 DT 15-JUL-1999 (Rel. 38, last annotation update)  
 DE Ig kappa chain V-I region Kue.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79237924; PubMed=112021;  
 RA Eulitz M., Kley H.-P., Zeitler H.-J.;  
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01870; KIHUKU.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 FRAMEWORK-3.  
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 108;  
 Best Local Similarity 66.7%; Pred. No. 6;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9  
 Db 89 QQYSRYPYT 97

RESULT 8  
 YDE9\_SCHPO  
 ID YDE9\_SCHPO STANDARD; PRT; 345 AA.  
 AC Q10442;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, last sequence update)  
 DT 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Putative mitochondrial carrier C12B10.09.  
 GN SPAC12B10.09.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckie E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Murgall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,  
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakowski G.V., Usery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of *Schizosaccharomyces pombe*.";  
 RL Nature 415:871-880(2002).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (Potential).  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
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 CC -----  
 DR EMBL: Z70721; CA94699.1; -.  
 DR PIR: T37576; T37576.  
 DR GeneDB: SPombe; SPAC12B10.09; -.  
 DR InterPro: IPR002067; Mit\_carrier.  
 DR InterPro: IPR001993; Mitoch\_carrier.  
 DR Pfam: PF00153; mito\_carr; 3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PROSITE: PS00215; MITOCH\_CARRIER; 2.  
 KW Hypothetical protein; Mitochondrion; Inner membrane; Repeat;  
 KW Transmembrane; Transport.  
 FT TRANSMEM 1 21 POTENTIAL.  
 FT TRANSMEM 83 103 POTENTIAL.  
 FT TRANSMEM 128 148 POTENTIAL.  
 FT TRANSMEM 220 240 POTENTIAL.  
 FT TRANSMEM 262 282 POTENTIAL.  
 FT TRANSMEM 296 316 POTENTIAL.  
 FT TRANSMEM 319 339 POTENTIAL.  
 SQ SEQUENCE 345 AA; 38451 MW; 39081A6AAC984B2C CRC64;

Query Match 68.8%; Score 33; DB 1; Length 345;  
 Best Local Similarity 77.8%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
 ||| |||  
 Db 290 QORLSYVFT 298

RESULT 9  
 PPBD\_BACSU STANDARD; PRT; 556 AA.  
 AC P42251;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Alkaline phosphatase D precursor (EC 3.1.3.1) (APased).  
 GN PHOD.

OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 57-76.  
 RC STRAIN=168 / JH642;  
 RX MEDLINE=96349109; PubMed=8760916;  
 RA Eder S., Shi L., Jensen K., Yamane K., Hulet F.M.;  
 RT "A *Bacillus subtilis* secreted phosphodiesterase/alkaline phosphatase  
 RT is the product of a *pho* regulon gene, *phod*.";  
 RL Microbiology 142:2041-2047(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bercero M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Ertian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,  
 RA Gilm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
 RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsteppel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivoita C., Rocha E., Roche B., Rose M., Sadaie Y.,  
 RA Sato T., Scanlan B., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;  
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*  
 RT *subtilis*.";  
 RL Nature 390:249-256(1997).  
 RN [3]  
 RP SEQUENCE OF 95-556 FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=95219079; PubMed=7704254;  
 RA Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;  
 RT "Determination of a 21548 bp nucleotide sequence around the 24  
 RT degrees region of the *Bacillus subtilis* chromosome.";  
 RL Microbiology 141:269-275(1995).  
 RN [4]  
 RP CHARACTERIZATION.  
 RC STRAIN=6060-BC6;  
 RX MEDLINE=78171419; PubMed=25878;  
 RA Yamane K., Maruo B.;  
 RT "Purification and characterization of extracellular soluble and  
 RT membrane-bound insoluble alkaline phosphatases possessing  
 RT phosphodiesterase activities in *Bacillus subtilis*.";  
 RL J. Bacteriol. 134:100-107(1978).  
 CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an  
 CC alcohol + phosphate.  
 CC -1- INDUCTION: By phosphate starvation.  
 CC -----  
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CC -----
DR EMBL; U49060; AAB47803.1; -.
DR EMBL; Z99105; CAB12056.1; -.
DR EMBL; D30808; BAA06483.1; -.
DR PIR; D69676; D69676.
DR Subtilisin; BG11174; phoD.
DR InterPro; IPR001952; Alk_phosphatase.
DR InterPro; IPR006311; Tat.
DR Pfam; PF00245; alk_phosphatase; 1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Hydrolase; Signal; Complete proteome.
FT SIGNAL 1 56
FT CHAIN 57 556 ALKALINE PHOSPHATASE D.
FT VARIANT 59 59 N -> K.
SQ SEQUENCE 556 AA; 62829 MW; 125F7FDDA08817E3 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSSYPT 9
Db 61 SSSYPT 66

RESULT 10
YLN9_CAEEL STANDARD; PRT; 662 AA.
ID YLN9_CAEEL
AC Q09512;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 76.7 kDa protein D2013.9 in chromosome II.
GN D2013.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Mortimore B.; Matthews P.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 SET domain.
CC -1- SIMILARITY: Contains 1 TTL domain.
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CC -----
DR EMBL; Z47808; CAA87778.1; -.
DR EMBL; Z47809; CAA87778.1; JOINED.
DR EMBL; Z47809; CAA87783.1; -.
DR EMBL; Z47808; CAA87783.1; JOINED.
DR PIR; T20343; T20343.
DR WormPep; D2013.9; CE01535.
DR InterPro; IPR001214; SET.
DR InterPro; IPR004344; Tub_cyr_lygase.
DR Pfam; PF03133; TTL; 1.
DR PROSITE; PS50280; SET; 1.
KW Hypothetical protein.
FT DOMAIN 136 260 SET.
FT DOMAIN 370 662 TTL.
SQ SEQUENCE 662 AA; 76750 MW; 5044C76422145698 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 662;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 1 QORSSYPT 9
Db 3 EDRSAYPFS 11

RESULT 11
TF2D_STRPU STANDARD; PRT; 265 AA.
ID TF2D_STRPU
AC P91809;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription initiation factor TFIID (TATA-box factor)
DE (TATA sequence-binding protein) (TBP).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Rybacki L.; Childs G.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
CC OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIID BINDS
CC SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO
CC THE POSITION OF TRANSCRIPTION INITIATION.
CC -1- SUBUNIT: Binds DNA as a monomer.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE TBP FAMILY.
CC -----
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CC -----
DR EMBL; U86586; AAB47272.1; -.
DR HSSP; P20226; 1TGH.
DR InterPro; IPR00814; TFIID.
DR Pfam; PF00352; TBP; 2.
DR PRINTS; PR00686; TIFACTORIID.
DR PROSITE; PS00351; TFIID; 2.
KW Transcription regulation; DNA-binding; Nuclear protein; Repeat.
FT REPEAT 91 167 1.
FT REPEAT 181 258 2.
SQ SEQUENCE 265 AA; 29107 MW; 53AED314D2D98926 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 265;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPT 7
Db 23 QORSHYP 29

RESULT 12
CN7B_MOUSE STANDARD; PRT; 446 AA.
ID CN7B_MOUSE
AC Q9QXQ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN PDE7B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087273; PubMed=10618442;
RA Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
RT "Cloning and characterization of PDE7B, a CAMP-specific
RT phosphodiesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20329226; PubMed=10872825;
RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT "Cloning and characterisation of the human and mouse PDE7B, a novel
RT CAMP-specific nucleotide phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC -1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate.
CC -1- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
CC -1- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.
CC -1- INSENSITIVE TO ZAPRINAST, ROLIPRAM, AND MILRINONE.
CC -1- PATHWAY: Cyclic nucleotide metabolism.
CC -1- TISSUE SPECIFICITY: Highly expressed in brain.
CC -1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF190639; AAF25195.1; -
CC EMBL; AJ251859; CAB92530.1; -
CC MGD; MGI:1352752; Pde7b.
CC GO; GO:0004115; F:CAMP-specific phosphodiesterase activity; IDA.
CC InterPro; IPR003607; Met_phosphohydro.
CC InterPro; IPR002073; PDEase.
CC Pfam; PF00233; PDEase; 1.
CC PRINTS; PR00387; PDIESTERASE1.
CC SMART; SM00471; HDC; 1.
CC PROSITE; PS00126; PDEASE_I; 1.
CC KMW Domain; CAMP.
CC FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
CC SQ SEQUENCE 446 AA; 51337 MW; 7C052664B693A5A8 CRC64;
CC -----
CC Query Match 66.7%; Score 32; DB 1; Length 446;
CC Best Local Similarity 62.5%; Pred. No. 45;
CC Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC -----
QY 1 QORSSYYPF 8
Db 41 ERRGSYYPF 48
CN7B_HUMAN STANDARD; PRT; 450 AA.
AC Q9NP56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN PDE7B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OK NCBI_TaxID=9606;
```

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20275458; PubMed=10814504;
RA Sasaki T., Kotera J., Yuasa K., Omori K.;
RT "Identification of human PDE7B, a CAMP-specific phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 271:575-583(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=20329226; PubMed=10872825;
RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT "Cloning and characterisation of the human and mouse PDE7B, a novel
RT CAMP-specific nucleotide phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC -1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate.
CC -1- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
CC -1- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.
CC -1- INSENSITIVE TO ZAPRINAST, ROLIPRAM, AND MILRINONE.
CC -1- PATHWAY: Cyclic nucleotide metabolism.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN. ALSO EXPRESSED IN
CC HEART, LIVER, SKELETAL MUSCLE AND PANCREAS.
CC -1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB038040; BAA96537.1; -
CC EMBL; AJ251860; CAB92441.1; -
CC PIR; JC7266; JC7266.
CC PDB; 1LXW; 26-JUN-02.
CC Genew; HGNC:8792; PDE7B.
CC MIM; 604645; -
CC GO; GO:0004115; F:CAMP-specific phosphodiesterase activity; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC GO; GO:0007268; P:synaptic transmission; TAS.
CC InterPro; IPR003607; Met_phosphohydro.
CC InterPro; IPR002073; PDEase.
CC Pfam; PF00233; PDEase; 1.
CC PRINTS; PR00387; PDIESTERASE1.
CC SMART; SM00471; HDC; 1.
CC PROSITE; PS00126; PDEASE_I; 1.
CC KMW Domain; CAMP; 3D-structure.
CC FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
CC SQ SEQUENCE 450 AA; 51835 MW; EC142BF3E28D0028 CRC64;
CC -----
CC Query Match 66.7%; Score 32; DB 1; Length 450;
CC Best Local Similarity 62.5%; Pred. No. 45;
CC Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC -----
QY 1 QORSSYYPF 8
Db 41 ERRGSYYPF 48
SCD5_YEAST STANDARD; PRT; 872 AA.
AC P34758;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
```



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DE SCD5 protein (FTBI protein).
GN SCD5 OR FTBI OR YOR329C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RX MEDLINE=96228684; PubMed=8688556;
RA Nelson K.K., Holmer M., Lemmon S.K.;
RT "SCD5, a suppressor of clathrin deficiency, encodes a novel protein
RT with a late secretory function in yeast.";
RL Mol. Biol. Cell 7:245-260(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RA Wang W., Zheng L., Chan C.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=GRF88;
RA Song J.M., Cheung E., Rabinowitz J.C.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051586; PubMed=8896263;
RA Parle-McDermott A.G., Hand N.J., Goulding S.G., Wolfe K.H.;
RT "Sequence of 29 kb around the PDRI0 locus on the right arm of
RT Saccharomyces cerevisiae chromosome XV: similarity to part of
RT chromosome I.";
RL Yeast 12:999-1004(1996).
CC -!- FUNCTION: Involved in vesicular transport at a late stage of the
CC secretory pathway.
CC -!- SUBUNIT: PUTATIVE 10-FORMYL-TETRAHYDROFOLATE BINDING PROTEIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U03492; AAB09719.1; -
DR EMBL; U42227; AAA85443.1; -
DR EMBL; Z49821; CAA89976.1; -
DR EMBL; Z75237; CAA99650.1; -
DR PIR; S62061; S62061.
DR SGD; S0005856; SCD5.
DR GO; GO:0000300; C:peripheral membrane protein of membrane fra. .; IDA.
DR GO; GO:0009306; P:protein secretion; IGI.
KW Transport; Protein transport; Membrane; Repeat.
FT DOMAIN 405 448 3 X 20 AA APPROXIMATE REPEATS.
FT REPEAT 405 424 1-1.
FT REPEAT 439 458 1-2.
FT REPEAT 479 498 1-3.
FT DOMAIN 534 728 9 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 534 545 2-1.
FT REPEAT 564 575 2-2.
FT REPEAT 593 604 2-3.
FT REPEAT 608 619 2-4.
FT REPEAT 623 634 2-5.
FT REPEAT 636 647 2-5.
FT REPEAT 650 661 2-7.
FT REPEAT 683 694 2-8.
FT REPEAT 717 728 2-9.
SQ SEQUENCE 872 AA; 97305 MW; C60F5BE8808E1D31 CRC64;
Query Match 66.7%; Score 32; DB 1; Length 872;
Best Local Similarity 55.6%; Pred. No. 92;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 1 QORSSYPFT 9
Db 831 QQQQQFPFT 839
RESULT 15
AT7A_CRIGR STANDARD; PRT; 1476 AA.
AC P49015;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Copper-transporting ATPase 1 (EC 3.6.3.4) (Copper pump 1)
DE (Fragment).
GN ATP7A.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=96154683; PubMed=8589689;
RA Camakaris J., Petris M.J., Bailey L., Shen P., Lockhart P.,
RA Glover T.W., Barcroft C., Patton J., Mercer J.F.;
RT "Gene amplification of the Menkes (MNK; ATP7A) P-type ATPase gene of
RT CHO cells is associated with copper resistance and enhanced copper
RT efflux.";
RL Hum. Mol. Genet. 4:2117-2123(1995).
CC -!- FUNCTION: MAY FUNCTION IN THE EXPORT OF COPPER FROM THE CYTOPLASM
CC TO AN INTRACELLULAR ORGANELLE. IT MAY SERVE AS WELL FOR THE EXPORT
CC OF OTHER METALS.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + Cu(2+) (In) = ADP + phosphate +
CC Cu(2+) (Out).
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: FOUNDS IN MOST TISSUES EXCEPT LIVER.
CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type
CC ATPases).
CC -!- SIMILARITY: Contains 6 HMA domains.
CC -----
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CC -----
DR EMBL; U29946; AAB39918.1; -
DR HSSP; Q04656; IAWO.
DR InterPro; IPR006403; ATPase-IB1_Cu.
DR InterPro; IPR006416; ATPase-IB_hvy.
DR InterPro; IPR001757; ATPase_B1-E2.
DR InterPro; IPR001877; Cu_ATPase1.
DR InterPro; IPR006122; Cu_bind_dom.
DR InterPro; IPR006121; HeavyMe_transpt.
DR InterPro; IPR005834; Hydrolase.
DR InterPro; IPR006191; Metal_bind.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00403; HMA; 6.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00942; CUATPASI.
DR TIGRFAMS; TIGR01511; ATPase-IB1_Cu; 1.
DR TIGRFAMS; TIGR01525; ATPase-IB_hvy; 1.
DR TIGRFAMS; TIGR01494; ATPase_P-type; 3.
DR TIGRFAMS; TIGR00003; TIGR00003; 6.
DR PROSITE; PS00154; ATPASE_B1_E2; 1.
DR PROSITE; PS01047; HMA_1; 5.
DR PROSITE; PS0846; HMA_2; 6.

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KW Hydrolase; Copper transport; Transmembrane; Phosphorylation;  
KW ATP-binding; Metal-binding; Copper; Repeat.  
FT DOMAIN 1 642 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 643 665 POTENTIAL.  
FT TRANSMEM 695 717 POTENTIAL.  
FT TRANSMEM 736 760 POTENTIAL.  
FT TRANSMEM 770 788 POTENTIAL.  
FT TRANSMEM 930 952 POTENTIAL.  
FT TRANSMEM 978 998 POTENTIAL.  
FT TRANSMEM 1347 1373 POTENTIAL.  
FT TRANSMEM 1379 1397 POTENTIAL.  
FT DOMAIN 9 75 HMA 1.  
FT DOMAIN 172 238 HMA 2.  
FT DOMAIN 277 343 HMA 3.  
FT DOMAIN 377 443 HMA 4.  
FT DOMAIN 479 545 HMA 5.  
FT DOMAIN 555 621 HMA 6.  
FT MOD\_RES 1034 1034 PHOSPHORYLATION (PROBABLE).  
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 685 685 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 887 887 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 953 953 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1130 1130 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1134 1134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1448 1448 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT NON\_TER 1476 1476  
SQ SEQUENCE 1476 AA; 160335 MW; 6B36F5A2AC358C0B CRC64;

Query Match 66.7%; Score 32; DB 1; Length 1476;  
Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYP 7  
|||  
Db 267 QQRPSYP 273

Search completed: July 30, 2003, 09:45:08  
Job time : 3.40532 secs

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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 6.96678 Seconds  
(without alignments)  
333.364 Million cell updates/sec

Title: US-09-865-198-6  
Perfect score: 48  
Sequence: 1 QORSSYPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- SPTREMBL\_23:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_virus:\*
  - 16: sp\_bacteriaph:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	87.5	112	11 Q8K1F2	Q8K1F2 mus musculu
2	38	79.2	134	11 Q8VDD0	Q8VDD0 mus musculu
3	37	77.1	106	5 Q9U410	Q9U410 schistosoma
4	37	77.1	269	5 Q18582	Q18582 caenorhabdi
5	37	77.1	289	13 Q8U0Z5	Q8U0Z5 brachydanio
6	37	77.1	489	16 Q8E270	Q8E270 leptospira
7	37	77.1	1501	5 Q9VM23	Q9VM23 drosophila
8	36	75.0	380	16 Q8EXK4	Q8EXK4 leptospira
9	36	75.0	886	16 Q9KC72	Q9KC72 bacillus ha
10	35	72.9	108	11 Q8V1J0	Q8V1J0 mus musculu
11	35	72.9	133	3 Q12744	Q12744 saccharomyc
12	34	70.8	341	16 Q8X6Y8	Q8X6Y8 escherichia
13	34	70.8	341	16 Q8FEW0	Q8FEW0 escherichia
14	34	70.8	363	10 Q9SWC7	Q9SWC7 glycine max
15	34	70.8	377	10 Q24324	Q24324 phaseolus v
16	34	70.8	380	10 Q43448	Q43448 glycine max

17	34	70.8	393	5 Q96635	Q96635 trypanosoma
18	34	70.8	397	16 Q35007	Q35007 bacillus su
19	34	70.8	399	16 Q9K6Q6	Q9K6Q6 bacillus ha
20	34	70.8	478	5 Q96750	Q96750 trypanosoma
21	34	70.8	653	3 Q12171	Q12171 saccharomyc
22	34	70.8	721	16 Q99YL1	Q99YL1 streptococc
23	34	70.8	721	16 Q8K6D6	Q8K6D6 streptococc
24	34	70.8	977	5 Q97357	Q97357 trypanosoma
25	34	70.8	1005	5 Q9VSI2	Q9VSI2 drosophila
26	34	70.8	1005	5 Q8MT33	Q8MT33 drosophila
27	34	70.8	1138	16 Q92XB6	Q92XB6 rhizobium m
28	33	68.8	112	11 Q8K1F3	Q8K1F3 mus musculu
29	33	68.8	169	5 Q8SVY7	Q8SVY7 encephalito
30	33	68.8	234	11 Q8R062	Q8R062 mus musculu
31	33	68.8	246	13 Q9W6E5	Q9W6E5 gallus gall
32	33	68.8	380	3 Q9P8H2	Q9P8H2 cryptococcu
33	33	68.8	434	5 Q94503	Q94503 dictyosteli
34	33	68.8	529	5 Q9V490	Q9V490 drosophila
35	33	68.8	543	5 Q961N4	Q961N4 drosophila
36	33	68.8	543	5 Q9XZC2	Q9XZC2 drosophila
37	33	68.8	580	10 Q9S1Y8	Q9S1Y8 arabidopsis
38	33	68.8	685	16 Q92TJ0	Q92TJ0 rhizobium m
39	33	68.8	733	13 Q91817	Q91817 xenopus lae
40	33	68.8	1108	5 Q8T2E2	Q8T2E2 dictyosteli
41	33	68.8	3232	3 Q94205	Q94205 claviceps p
42	32	66.7	210	5 Q95SL8	Q95SL8 drosophila
43	32	66.7	210	5 Q9W3R3	Q9W3R3 drosophila
44	32	66.7	237	5 Q8SXD8	Q8SXD8 drosophila
45	32	66.7	237	5 Q9VDZ9	Q9VDZ9 drosophila

ALIGNMENTS

RESULT 1	ID	Q8K1F2	PRELIMINARY;	PRT;	112 AA.
AC	Q8K1F2;				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	Anti-VIPase light chain variable region (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;				
RA	Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;				
RT	"Innate proteolytic antibodies: Failed D-VIPase response to the D-				
RT	enantiomer of VIP and identification of L-VIPase VL domains.";				
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF516283; AAM64201.1; -				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00409; Ig; 1.				
DR	SMART; SM00406; IGv; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
FT	NON_TER	1			
FT	NON_TER	112			
SQ	SEQUENCE	112 AA;	11953 MW;	4716887FADB543BD CRC64;	
Query Match					
Best local Similarity 87.5%; Score 42; DB 11; Length 112;					
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	1 QORSSYPFT 9				
DB	88 QORSSYPFT 96				

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RESULT 2
Q8VDD0
ID Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Anti-MOG 212 variable light chain (Fragment).
GN ANTI-MOG KAPPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembli P.;
RT "Targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416331; CAC94866.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14525 MW; CDF8E2236E2D0CF CRC64;

Query Match 79.2%; Score 38; DB 11; Length 134;
Best Local Similarity 87.5%; Pred. No. 3.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRSSYPFT 9
Db 111 QRSSYPFT 118

RESULT 3
Q9U410
ID Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
DE variable region (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
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FT NON_TER 1 1
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 77.1%; Score 37; DB 5; Length 106;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db 88 QQRSSYPFT 96

RESULT 4
Q18582
ID Q18582 PRELIMINARY; PRT; 269 AA.
AC Q18582;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 30.8 kDa protein.
GN C42D8.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Hallsworth K.;
RT "The sequence of C. elegans cosmid C42D8.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U56966; AAA98721.2; -.
DR WormPep; C42D8.1; CE27844.
KW Hypothetical protein.
SQ SEQUENCE 269 AA; 30847 MW; 32D2B7A1C0102F93 CRC64;

Query Match 77.1%; Score 37; DB 5; Length 269;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9
Db 225 QQRSSYPFT 233

RESULT 5
Q8U25
ID Q8U25 PRELIMINARY; PRT; 289 AA.
AC Q8U25;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Orthodenticle-related homeobox 5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
```

RN [1];  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21624608; PubMed=11753388;  
RA Gamse J.T., Liang J.O., Shen Y.-C., Raymond P., Thisse B., Thisse C.,  
RA Halpern M.E.;  
RT "Otx5 regulates genes that show circadian expression in the zebrafish  
RT pineal complex.";  
RL Nat. Genet. 30:117-121(2002).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL; AY036005; AAK62029.1; -.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR003025; Otx\_TF.  
DR InterPro; IPR007104; Paired\_homeo.  
DR Pfam; PF00046; homeobox; 1.  
DR Pfam; PF03529; TF\_Otx; 1.  
DR PRINTS; PR01255; OTXHOMEBOX.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS50071; HOMEBOX\_2; 1.  
DR PROSITE; PS50552; PAX; 1.  
KW Homeobox; DNA-binding; Nuclear protein.  
SQ SEQUENCE 289 AA; 31422 MW; 542FA0F69AE90DAC CRC64;

Query Match 77.1%; Score 37; DB 13; Length 289;  
Best Local Similarity 87.5%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QRSSYPFT 9  
Db 177 QRSSYPMT 184

RESULT 6  
Q8EZ70 PRELIMINARY; PRT; 489 AA.  
AC Q8EZ70;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Putative Na(+)/H(+) exchanger.  
GN LA3988.  
OS Leptospira interrogans.  
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.  
OX NCBI\_TaxID=173;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;  
RA Ren S.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE011554; AAN51186.1; -.  
KW Complete proteome.  
SQ SEQUENCE 489 AA; 53349 MW; 40F609F6E5AC2DD5 CRC64;

Query Match 77.1%; Score 37; DB 16; Length 489;  
Best Local Similarity 75.0%; Pred. No. 23;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QQRSSYPF 8  
Db 395 QQRASYPF 402

RESULT 7  
O9VM23 PRELIMINARY; PRT; 1501 AA.  
ID O9VM23;  
AC O9VM23;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE CG5125 protein.  
GN NINAC OR CG5125.  
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclele J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
RA Ferriera S., Frise E., Galie R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
RA Ibegwan C., Jatali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
RA Paclele J., Paragas V., Park S., Patel S., Pfeiffer B.,  
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RT "Sequencing of Drosophila melanogaster genome.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,  
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
RT "Annotation of Drosophila melanogaster genome.";



RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003617; AAF52504.3; -.  
DR HSSP; P08799; 1MND.  
DR FlyBase; FBgn0002938; ninac.  
DR InterPro; IPR000048; IQ\_region.  
DR InterPro; IPR001609; myosin\_head.  
DR InterPro; IPR00719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00612; IQ; 2.  
DR Pfam; PF00663; myosin\_head; 1.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000355; myosin\_head; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00015; IQ; 2.  
DR SMART; SM00242; MYSC; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; TyRKc; 1.  
DR PROSITE; PS50096; IQ; 2.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Transferase.  
SQ SEQUENCE 1501 AA; 174299 MW; 164DF87DDA7EB3D1 CRC64;

Query Match 77.1%; Score 37; DB 5; Length 1501;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYP 7  
Db 1352 QORSSYP 1358

RESULT 8  
Q8EXK4 PRELIMINARY; PRT; 380 AA.  
AC Q8EXK4;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Mannosyltransferase A.  
GN MTPA OR LB204.  
OS Leptospira interrogans.  
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.  
OX NCBI\_TaxID=173;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;  
RA Ren S.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE011608; AAN51763.1; -.  
KW Transferase; Complete proteome.  
SQ SEQUENCE 380 AA; 43772 MW; FB289EA9C63D6D6F CRC64;

Query Match 75.0%; Score 36; DB 16; Length 380;  
Best Local Similarity 66.7%; Pred. No. 29;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
Db 224 EQNSSYPFS 232

RESULT 9  
Q9KC72

ID Q9KC72 PRELIMINARY; PRT; 886 AA.  
AC Q9KC72;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Penicillin-binding proteins 1A/1B.  
GN PONA OR BH1702.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis";  
RL Nucleic Acids Res. 28:4317-4331(2000).  
DR EMBL; AP001512; BAB05421.1; -.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR001264; Glyco\_trans\_51.  
DR InterPro; IPR001460; Transpeptidase.  
DR Pfam; PF00041; fn3; 1.  
DR Pfam; PF00912; Transglycosyl; 1.  
DR Pfam; PF00905; Transpeptidase; 1.  
DR ProDom; PD001895; Glyco\_trans\_51; 1.  
DR SMART; SM00060; FN3; 1.  
KW Hydrolyase; Complete proteome.  
SQ SEQUENCE 886 AA; 98280 MW; 0662807F75148534 CRC64;

Query Match 75.0%; Score 36; DB 16; Length 886;  
Best Local Similarity 75.0%; Pred. No. 69;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYP 8  
Db 282 QERESYPF 289

RESULT 10  
Q8VIJ0 PRELIMINARY; PRT; 108 AA.  
ID Q8VIJ0;  
AC Q8VIJ0;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Anti-DNA light chain (Fragment).  
GN VK19.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H/HeJ-lpr/lpr;  
RX MEDLINE=96409289; PubMed=8814271;  
RA Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;  
RT "Differences in V kappa gene utilization and VH CDR3 sequence among  
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis.";  
RL Eur. J. Immunol. 26:2225-2233(1996).  
DR EMBL; U59155; AAB02917.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW NON\_TER  
FT NON\_TER  
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 72.9%; Score 35; DB 11; Length 108;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
Db 89 QQYNSYPFT 97

## RESULT 11

Q12744

PRELIMINARY; PRT; 133 AA.

AC Q12744;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)  
DE Hypothetical ORF IDENTICAL to ORF NOTED in RAD10 5' region A22726.  
GN YML094C-A.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AB972;  
RA Gentles S., Bowman S.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AB972;  
RA Barrel B., Rajandream M.A.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 2-133 FROM N.A.  
RX MEDLINE=85284950; PubMed=3896774;  
RA Weiss W.A., Friedberg E.C.;  
RT "Molecular cloning and characterization of the yeast RAD10 gene and  
expression of RAD10 protein in E. coli."  
RL EMBL J. 4:1575-1582(1985).  
DR EMBL; Z46660; CAA86643.1; -.  
DR EMBL; X02591; CAA26432.1; -.  
DR SGD; S0004561; YML094C-A.  
DR InterPro; IPR002016; Peroxidase.  
DR PROSITE; PS00435; PEROXIDASE\_1; 1.  
SQ SEQUENCE 133 AA; 15007 MW; B93007588867456 CRC64;

Query Match 72.9%; Score 35; DB 3; Length 133;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
Db 101 QORSSYPFT 109

## RESULT 12

Q8X6Y8

PRELIMINARY; PRT; 341 AA.

AC Q8X6Y8;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)  
DE Putative capsid protein of prophage CP-933X (Putative major capsid  
protein).  
GN Z1888 OR ECS2174 OR ECS1635.  
OS Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=83334;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
RX MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
RL Nature 409:529-533(2001).

## [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / RIMD 0509952;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,  
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohemorrhagic Escherichia coli  
O157:H7 and genomic comparison with a laboratory strain K-12";  
RL DNA Res. 8:11-22(2001).  
DR EMBL; AE005330; AAG55985.1; -.  
DR EMBL; AP002557; BAB35597.1; -.  
DR EMBL; AP002555; BAB35058.1; -.  
DR InterPro; IPR005564; Phage\_cap\_E.  
DR Pfam; PF03864; Phage\_cap\_E; 1.  
KW Complete proteome.  
SQ SEQUENCE 341 AA; 38123 MW; C0310C4DE97C0037 CRC64;

Query Match 70.8%; Score 34; DB 16; Length 341;  
Best Local Similarity 85.7%; Pred. No. 67;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RSSYPFT 9  
Db 29 RESYPFT 35

## RESULT 13

Q8FEW0

PRELIMINARY; PRT; 341 AA.

AC Q8FEW0;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)  
DE Putative capsid protein of prophage.  
GN C3168.  
OS Escherichia coli O6.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=217992;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;  
RX MEDLINE=22388234; PubMed=12471157;  
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
RT "Extensive mosaic structure revealed by the complete genome sequence  
of uropathogenic Escherichia coli."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).  
DR EMBL; AE016765; AAN81620.1; -.  
KW Complete proteome.  
SQ SEQUENCE 341 AA; 38075 MW; D986172AB796B014 CRC64;

Query Match 70.8%; Score 34; DB 16; Length 341;  
Best Local Similarity 85.7%; Pred. No. 67;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RSSYPFT 9  
Db 29 RESYPFT 35

RESULT 14  
Q9SWC7 PRELIMINARY; PRT; 363 AA.  
AC Q9SWC7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Putative cysteine proteinase GMPM33.  
GN GMPM33.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Shi-Shi;  
RA Chow T.Y., Lin S.M., Lin T.Y., Hsing Y.I.C.;  
RT "Characterization of soybean seed maturation protein, PM33."  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF167986; AAD46920.1; -.  
DR HSSP; P25779; LAIM.  
DR InterPro; IPR000668; Peptidase\_C1.  
DR InterPro; IPR000169; SHprot\_acsite.  
DR Pfam; PF00112; Peptidase\_C1; 1.  
DR PRINTS; PR00705; PAPA1N.  
DR ProDom; PD000158; Peptidase\_C1; 1.  
DR SMART; SM00645; Pept\_C1; 1.  
DR PROSITE; PS00640; THIOI\_PROTEASE\_ASN; 1.  
DR PROSITE; PS00139; THIOI\_PROTEASE\_CYS; 1.  
DR PROSITE; PS00639; THIOI\_PROTEASE\_HIS; 1.  
KW Hydrolase; Protease; Thiol protease.  
SQ SEQUENCE 363 AA; 39685 MW; 55C46B8F2CAC8EFB CRC64;  
  
Query Match 70.8%; Score 34; DB 10; Length 363;  
Best Local Similarity 55.6%; Pred. No. 72;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 QQRSSYPFT 9  
::|||:|  
Db 213 EEESSTPYT 221  
  
RESULT 15  
O24324  
ID O24324 PRELIMINARY; PRT; 377 AA.  
AC O24324;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Cysteine proteinase precursor.  
OS Phaseolus vulgaris (Kidney bean) (French bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
OX NCBI\_TaxID=3885;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Moldavian; TISSUE=Cotyledon;  
RA Senyuk V., Becker C., Muentz K.;  
RT "Isolation of cDNA clone encoding cysteine proteinase (CP4) from a  
cotyledon-specific cDNA library of germinating kidney bean seeds."  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z99955; CAB17077.1; -.  
DR HSSP; P25779; LAIM.  
DR InterPro; IPR000668; Peptidase\_C1.  
DR InterPro; IPR000169; SHprot\_acsite.  
DR Pfam; PF00112; Peptidase\_C1; 1.  
DR ProDom; PD000158; Peptidase\_C1; 1.  
DR SMART; SM00645; Pept\_C1; 1.  
DR PROSITE; PS00640; THIOI\_PROTEASE\_ASN; 1.  
DR PROSITE; PS00139; THIOI\_PROTEASE\_CYS; 1.  
KW Hydrolase; Protease; Signal; Thiol protease.

FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 138 377 CYSTEINE PROTEINASE.  
SQ SEQUENCE 377 AA; 41827 MW; 6576DEF3F1B26DA9 CRC64;  
  
Query Match 70.8%; Score 34; DB 10; Length 377;  
Best Local Similarity 55.6%; Pred. No. 75;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 QQRSSYPFT 9  
::|||:|  
Db 228 EEESSTPYT 236  
  
Search completed: July 30, 2003, 09:42:44  
Job time : 9.07789 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 9 Seconds  
(without alignments)  
158.727 Million cell updates/sec

Title: US-09-865-198-6  
Perfect score: 48  
Sequence: 1 QQRSSYPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: \*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	21	AAV97234
2	48	100.0	9	22	AAE13142
3	48	100.0	9	22	AAE25961
4	48	100.0	9	22	AAE25963
5	48	100.0	9	23	AAE25954
6	48	100.0	9	23	AAU74411
7	48	100.0	9	24	AAU74411
8	48	100.0	106	22	AAE13144
9	48	100.0	106	23	AAU74418

10	48	100.0	106	24	ABJ26730	VEGF binding relat
11	48	100.0	107	22	AAE25961	Amino acid sequenc
12	48	100.0	108	21	AAV97236	Variable light cha
13	48	100.0	108	22	AAE25961	VEGF antagonist an
14	48	100.0	108	23	AAE25956	Mouse anti-KDR p1c
15	48	100.0	108	23	AAU74413	Antigen-binding pr
16	48	100.0	108	24	ABJ26725	VEGF binding relat
17	48	100.0	125	22	AAE13146	Chimeric p1c11 lig
18	48	100.0	125	22	AAE25961	VEGF antagonist an
19	48	100.0	125	23	AAE28917	c-p1c11 vector lig
20	48	100.0	125	23	AAE25966	Mouse anti-KDR p1c
21	48	100.0	131	23	ABE79727	Anti-Streptococcus
22	48	100.0	238	23	AAE25963	KDR binding immuno
23	48	100.0	238	23	AAU74420	KDR binding immuno
24	48	100.0	238	23	AAU74420	Antigen-binding pr
25	48	100.0	238	24	ABJ26732	VEGF binding relat
26	48	100.0	240	23	AAE25960	KDR binding immuno
27	48	100.0	240	23	AAU74419	Antigen-binding relat
28	48	100.0	240	24	ABJ26731	VEGF binding relat
29	48	100.0	330	22	AAE70842	SNV-env leader/hum
30	45	93.8	9	19	AAW73171	CDR3 of light chai
31	45	93.8	9	20	AAE28392	Peptide fragment f
32	45	93.8	9	22	AAE83165	Mouse ganglioside
33	45	93.8	52	24	ABU56913	BONT/A Hc binding
34	45	93.8	52	24	ABU56914	BONT/A Hc binding
35	45	93.8	107	22	AAE83159	Mouse ganglioside
36	45	93.8	107	22	AAE83167	Ganglioside GM2 an
37	45	93.8	129	15	AAE53329	KM-796 and KM-750
38	45	93.8	129	20	AAE28385	Anti-GM2 light cha
39	45	93.8	129	20	AAE28357	Antibody chain use
40	45	93.8	130	19	AAW73179	Fragment of gangli
41	45	93.8	130	19	AAW73180	Fragment of gangli
42	45	93.8	130	19	AAW73181	Fragment of gangli
43	45	93.8	130	19	AAW73182	Fragment of gangli
44	45	93.8	130	19	AAW73183	Fragment of gangli
45	45	93.8	130	19	AAW73184	Fragment of gangli

ALIGNMENTS

RESULT 1	
AAV97234	
ID	AAV97234 standard; Protein; 9 AA.
AC	AAV97234;
XX	
DT	19-DEC-2000 (first entry)
XX	
DE	Complementary determining region (CDRL3) of anti-SI (KDR) antibody.
XX	
KW	Immunoglobulin; antibody; complementary determining region; CDR;
KW	VEGF; vascular endothelial growth factor; KDR;
KW	kinase insert domain containing receptor; multivalent; monovalent;
KW	humanised antibody; chimeric antibody; tumour; diabody; triabody;
KW	glioblastoma multiforme; hemangioblastoma; AIDS;
KW	central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
KW	acquired immune deficiency syndrome; AIDS; human.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200044777-A1.
XX	
PD	03-AUG-2000.
XX	
PF	28-JAN-2000; 2000WO-US02180.
XX	
PR	29-JAN-1999; 99US-0117726.
PR	29-JAN-1999; 99US-0240736.
XX	
PA	(IMCL-) IMCLONE SYSTEMS INC.
XX	

PI Zhu Z, Witte L;  
XX  
DR WPI; 2000-505966/45.  
DR N-PSDB; AAA53766.  
XX  
PT Novel immunoglobulin molecules binding kinase insert domain-containing  
PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growth  
XX  
PS Claim 3; Page 50; 55pp; English.  
XX  
CC New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Kaposi's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulin of the invention.  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
|||  
1 QORSSYPFT 9  
Db

RESULT 2  
AAE13142  
ID AAE13142 standard; peptide; 9 AA.  
XX  
AC AAE13142;  
XX

DT 28-JAN-2002 (first entry)  
XX

DE Humanised antibody murine light chain hypervariable region (VL) CDR3.  
XX

KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytosstatic; light chain hypervariable region; VL; myelocytic leukaemia;  
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;  
KW Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.  
XX

OS Mus sp.  
XX

PN WO200174296-A2.  
XX

PD 11-OCT-2001.  
XX

PF 30-MAR-2001; 2001WO-US10504.  
XX

PR 31-MAR-2000; 2000US-0540770.  
XX

PA (IMCL-) IMCLONE SYSTEMS INC.  
PA (CORR ) CORNELL RES FOUND INC.  
XX

PI Witte L, Rafil S;  
XX

DR WPI; 2001-662942/76.  
DR

DR N-PSDB; AAD21668.  
XX

PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with

PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
PS Claim 8; Page 15; 68pp; English.  
XX

CC The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains mouse complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised  
CC antibody murine light chain hypervariable region (VL) CDR-3 used in the  
CC exemplification of the invention.  
XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
|||  
1 QORSSYPFT 9  
Db

RESULT 3  
AAB82708  
ID AAB82708 standard; peptide; 9 AA.  
XX

AC AAB82708;  
XX

DT 15-OCT-2001 (first entry)  
XX

DE VEGF antagonist antibody IMC-1C11 VL CDR-3.  
XX

KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; light chain; CDR;  
KW complementarity determining region.  
XX

OS Chimeric - Mus sp.  
XX

OS Chimeric - Homo sapiens.  
XX

PN WO200154723-A1.  
XX

PD 02-AUG-2001.  
XX

PF 29-JAN-2001; 2001WO-US02839.  
XX

PR 28-JAN-2000; 2000US-0178791.  
XX

PR 31-MAR-2000; 2000US-0539692.  
XX

PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX

PI Kerbel R;  
XX

DR WPI; 2001-514531/56.  
XX

PT Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX

PS Disclosure; Page 37; 42pp; English.



XX The present sequence is that of complementarity determining region  
CC 3 of the light chain variable region (see also AAB82702) of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
| | | | | | | | |  
Db 1 QORSSYPFT 9

RESULT 4

AAG63993 ID AAG63993 standard; peptide; 9 AA.

XX AC AAG63993;

XX DT 26-NOV-2001 (first entry)

XX DE Complementarity determining region of light chain of antibody 2C4.

XX KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;

KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;  
KW leukemia; eosinophil.

XX OS Mus sp.

XX PN WO200166126-A1.

XX PD 13-SEP-2001.

XX PF 05-MAR-2001; 2001WO-US07193.

XX PR 07-MAR-2000; 2000US-0187595.

XX PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;

XX PI Schleimer R;

XX DR WPI; 2001-570749/64.

XX PT Novel monoclonal antibody specific for human sialoadhesin factor-2 for  
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases  
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal -  
XX PS Claim 10; Page 34; 35pp; English.

CC AAG63991-93 represent the complementarity determining regions (CDRs)

CC of the light chain variable region of murine monoclonal antibody 2C4.  
CC This antibody binds to human sialoadhesin factor-2 (SAF-2). The  
CC antibody is useful for treating or preventing allergic rhinitis,  
CC allergies, asthma, anemia, eczema or diseases such as lymphoma,  
CC leukemia or systemic mastocytosis in a mammal. It is also useful for  
CC detecting the presence of a cell, especially eosinophil in a sample,  
CC by detecting binding of the antibody to SAF-2. The antibody can be  
CC coupled to toxins, antiproliferative drugs or radionuclides to  
CC kill cells in areas of excessive SAF-2 expression.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
| | | | | | | | |  
Db 1 QORSSYPFT 9

RESULT 5

AAE25954 ID AAE25954 standard; peptide; 9 AA.

XX AC AAE25954;

XX DT 15-NOV-2002 (first entry)

XX DE Mouse anti-KDR p1C11 scFv antibody CDR13 peptide.

XX KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;

KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;

KW VEGF; tumour growth; light chain complementarity determining region 3;

XX KW CDR13; angiogenesis; p1C11; scFv antibody.

XX OS Mus musculus.

XX PN US2002064528-A1.

XX PD 30-MAY-2002.

XX PF 12-OCT-2001; 2001US-0976787.

XX PR 28-JAN-2000; 2000US-0493539.

XX PA (ZHUZ/) ZHU Z.

PA (WITT/) WITTE L.

XX PI Zhu Z, Witte L;

XX DR WPI; 2002-589175/63.

XX DR N-PSDB; AAD42819.

XX PS Claim 3; Page 11; 34pp; English.

CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody  
CC light chain complementarity determining region 3 (CDRL3) protein.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
| | | | |  
Db 1 QORSSYPFT 9

## RESULT 6

AAU74411  
ID AAU74411 standard; peptide; 9 AA.

XX AC AAU74411;

DT 26-MAR-2002 (first entry)

DE light chain complementarity determining region L3 (CDRL3).

XX KW Complementarity determining region; CDR; CDRL3; antigen; cytostatic;  
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;  
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;  
KW antibody light chain variable domain.

XX OS Mus sp.

XX PN WO200190192-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US16924.

XX PR 24-MAY-2000; 2000US-206749P.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;

XX DR WPI; 2002-106189/14.

XX DR N-PSDB; AAS20282.

PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides

XX PS Claim 55; Page 57; 64pp; English.

XX CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (CL domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This peptide sequence represents the light chain variable domain  
CC complementarity determining region L3 (CDRL3) incorporated into an  
CC antigen-binding protein described in the method of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
| | | | |  
Db 1 QORSSYPFT 9

## RESULT 7

ABJ26723  
ID ABJ26723 standard; Peptide; 9 AA.

XX AC ABJ26723;

DT 01-MAY-2003 (first entry)

DE VEGF binding related peptide SEQ ID No 6.

XX KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.

XX OS Mus sp.

XX PN WO2003002144-A1.

XX PD 09-JAN-2003.

XX PF 26-JUN-2002; 2002WO-US20332.

XX PR 26-JUN-2001; 2001US-301299P.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;

XX DR WPI; 2003-201468/19.

XX DR N-PSDB; ABT23301.

PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors

XX PS Claim 6; Page 49; 98pp; English.

XX CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse peptide relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
| | | | |  
Db 1 QORSSYPFT 9

## RESULT 8

AAE13144  
ID AAE13144 standard; Protein; 106 AA.

XX AC AAE13144;

XX XX

DT 28-JAN-2002 (first entry)  
XX  
DE Humanised antibody light chain fragment.  
XX  
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;  
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;  
KW human; chimeric.  
XX  
OS Chimeric - Homo sapiens.  
OS Chimeric - Mus sp.  
XX  
PN WO200174296-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US10504.  
XX  
PR 31-MAR-2000; 2000US-0540770.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Witte L, Rafil S;  
XX  
DR WPI; 2001-662942/76.  
DR N-PSDB; AAD21670.  
XX  
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with  
PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
PS Claim 8; Page 16; 68pp; English.  
XX  
CC The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised  
CC antibody light chain fragment used in the exemplification of the  
CC invention.  
XX  
SQ Sequence 106 AA;  
XX  
Query Match 100.0%; Score 48; DB 22; Length 106;  
Best Local Similarity 100.0%; Pred. No. 0.086;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QORSSYPFT 9  
Db 88 QORSSYPFT 96

RESULT 9  
AAU74418  
ID AAU74418 standard; peptide; 106 AA.  
XX  
AC AAU74418;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Antigen-binding protein light chain variable domain (VH) #2.  
XX  
KW Antigen-binding protein; antibody light chain variable domain;  
KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;

KW cell proliferation inhibitor.  
XX  
OS Mus sp.  
XX  
PN WO200190192-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US16924.  
XX  
PR 24-MAY-2000; 2000US-206749P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2002-106189/14.  
DR N-PSDB; AAU20289.  
XX  
XX New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides -  
XX  
PS Claim 61; Page 61; 64pp; English.  
XX  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (CL domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This sequence represents a light chain variable domain (VH) incorporated  
CC into Fv, an engineered protein containing a heavy chain variable domain  
CC and a light chain variable domain in one polypeptide chain, described in  
CC the method of the invention.  
XX  
SQ Sequence 106 AA;  
XX  
Query Match 100.0%; Score 48; DB 23; Length 106;  
Best Local Similarity 100.0%; Pred. No. 0.086;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QORSSYPFT 9  
Db 88 QORSSYPFT 96

RESULT 10  
ABJ26730  
ID ABJ26730 standard; Protein; 106 AA.  
XX  
AC ABJ26730;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE VEGF binding related protein SEQ ID No 23.  
XX  
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.

XX OS Mus sp.  
XX PN WO2003002144-A1.  
XX PD 09-JAN-2003.  
XX PF 26-JUN-2002; 2002WO-US20332.  
XX PR 26-JUN-2001; 2001US-301299P.  
XX PA (IMCL-) IMCLONE SYSTEMS INC.  
XX PI Zhu Z;  
XX DR WPI; 2003-201468/19.  
XX DR N-PSDB; ABT23308.  
XX PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -  
XX PS Disclosure; Page 54; 98pp; English.  
XX CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse protein relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX SQ Sequence 106 AA;  
XX Query Match 100.0%; Score 48; DB 24; Length 106;  
XX Best Local Similarity 100.0%; Pred. No. 0.086;  
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QQRSSYPFT 9  
Db 88 QQRSSYPFT 96  
RESULT 11  
AAG63987  
ID AAG63987 standard; Protein; 107 AA.  
XX AC AAG63987;  
XX DT 26-NOV-2001. (first entry)  
XX DE Amino acid sequence of light chain variable region of antibody 2C4.  
XX KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;  
KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;  
KW leukemia; eosinophil.  
XX OS Mus sp.  
XX PN WO200166126-A1.  
XX PD 13-SEP-2001.  
XX PF 05-MAR-2001; 2001WO-US07193.  
XX PR 07-MAR-2000; 2000US-0187595.  
XX PA (SMIK ) SMETHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.

PA (UYJO ) UNIV JOHNS HOPKINS.  
XX ABrahamsen JA, Bochner B, Erickson-Miller CL, Kikly KK;  
PI Schleimer R;  
XX WPI; 2001-570749/64.  
XX DR N-PSDB; AAH78184.  
XX PT Novel monoclonal antibody specific for human sialoadhesin factor-2 for  
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases  
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal -  
XX PS Claim 11; Fig 2; 35pp; English.  
XX CC The present sequence represents the light chain variable region of murine  
CC monoclonal antibody 2C4. This antibody binds to human sialoadhesin  
CC factor-2 (SAF-2). The antibody is useful for treating or preventing  
CC allergic rhinitis, allergies, asthma, anemia, eczema or diseases such  
CC as lymphoma, leukemia or systemic mastocytosis in a mammal. It is also  
CC useful for detecting the presence of a cell, especially eosinophil in  
CC a sample, by detecting binding of the antibody to SAF-2. The antibody  
CC can be coupled to toxins, antiproliferative drugs or radionuclides to  
CC kill cells in areas of excessive SAF-2 expression.  
XX SQ Sequence 107 AA;  
XX Query Match 100.0%; Score 48; DB 22; Length 107;  
XX Best Local Similarity 100.0%; Pred. No. 0.087;  
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QQRSSYPFT 9  
Db 88 QQRSSYPFT 96  
RESULT 12  
AAY97236  
ID AAY97236 standard; Protein; 108 AA.  
XX AC AAY97236;  
XX DT 19-DEC-2000 (first entry)  
XX DE Variable light chain fragment of anti-SI(KDR) antibody.  
XX KW Immunoglobulin; antibody; complementary determining region; CDR;  
KW VEGF; vascular endothelial growth factor; KDR;  
KW kinase insert domain containing receptor; multivalent; monovalent;  
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;  
KW glioblastoma multiforme; hemangioblastoma; AIDS;  
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;  
KW acquired immune deficiency syndrome; AIDS; human.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO200044777-A1.  
XX PD 03-AUG-2000.  
XX PF 28-JAN-2000; 2000WO-US02180.  
XX PR 29-JAN-1999; 99US-0117726.  
XX PR 29-JAN-1999; 99US-0240736.  
XX PA (IMCL-) IMCLONE SYSTEMS INC.  
XX PI Zhu Z, Witte L;  
XX WPI; 2000-505966/45.  
XX DR N-PSDB; AAA53768.  
XX PT Novel immunoglobulin molecules binding kinase insert domain-containing



PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growth  
XX  
PS Claim 4; Page 51; 55pp; English.  
XX  
CC New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Kaposi's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulins of the invention.  
XX  
SQ Sequence 108 AA;  
  
Query Match 100.0%; Score 48; DB 21; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.088;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QQRSSYPFT 9  
    |||||  
DB 88 QQRSSYPFT 96  
  
RESULT 13  
AAB82710  
ID AAB82710 standard; Protein; 108 AA.  
XX  
AC AAB82710;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE VEGF antagonist antibody IMC-1C11 light chain variable region.  
XX  
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; light chain.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 24..33  
    /label= CDR-L1  
FT Region /note= "complementarity determining region 1"  
    49..55  
    /label= CDR-L2  
FT Region /note= "complementarity determining region 2"  
    88..96  
    /label= CDR-L3  
    /note= "complementarity determining region 3"  
XX  
PN WO200154723-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 29-JAN-2001; 2001WO-US02839.  
XX  
PR 28-JAN-2000; 2000US-0178791.  
XX 31-MAR-2000; 2000US-0539692.  
XX  
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.

PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Kerbel R;  
XX  
DR WPI; 2001-514531/56.  
DR N-PSDB; AAH26406.  
XX  
PT Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX  
PS Disclosure; Page 38-39; 42pp; English.  
XX  
CC The present sequence is that of the light chain variable region of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
SQ Sequence 108 AA;  
  
Query Match 100.0%; Score 48; DB 22; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.088;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QQRSSYPFT 9  
    |||||  
DB 88 QQRSSYPFT 96  
  
RESULT 14  
AAE25956  
ID AAE25956 standard; Protein; 108 AA.  
XX  
AC AAE25956;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Mouse anti-KDR p1C11 scFv antibody VL region #1.  
XX  
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; light chain variable region; VL; angiogenesis;  
KW p1C11; scFv antibody.  
XX  
OS Mus musculus.  
XX  
PN US2002064528-A1.  
XX  
PD 30-MAY-2002.  
XX  
PF 12-OCT-2001; 2001US-0976787.  
XX  
PR 28-JAN-2000; 2000US-0493539.  
XX  
PA (ZHUZ/) ZHU Z.  
PA (WITT/) WITTE L.  
XX



PI Zhu Z, Witte L;  
XX  
DR WPI; 2002-589175/63.  
DR N-PSDB; AAD42821.  
XX  
PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR  
XX  
PS Claim 4; Page 11; 34pp; English.  
XX  
CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (Flk)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody  
CC light chain variable region (VL).  
XX  
SQ Sequence 108 AA;

Query Match 100.0%; Score 48; DB 23; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.088;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QQRSSYPFT 9  
|||  
Db 88 QQRSSYPFT 96

RESULT 15  
AAU74413

ID AAU74413 standard; peptide; 108 AA.

XX AAU74413;

DT 26-MAR-2002 (first entry)

DE Antigen-binding protein light chain variable domain (VH) #1.

KW Antigen-binding protein; antibody light chain variable domain;  
KW cytoskeletal; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;  
KW cell proliferation inhibitor.

OS Mus sp.

PN WO200190192-A2.

PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US16924.

PR 24-MAY-2000; 2000US-206749P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

DR WPI; 2002-106189/14.

DR N-PSDB; AAS20284.

PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides  
XX  
PS Claim 57; Page 57; 64pp; English.

CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an

CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (CL domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This sequence represents a light chain variable domain (VH) incorporated  
CC into Fv, an engineered protein containing a heavy chain variable domain  
CC and a light chain variable domain in one polypeptide chain, described in  
CC the method of the invention.

SQ Sequence 108 AA;

Query Match 100.0%; Score 48; DB 23; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.088;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QQRSSYPFT 9  
|||  
Db 88 QQRSSYPFT 96

Search completed: July 30, 2003, 09:36:47  
Job time : 9 secs

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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:42:53 ; Search time 11.0631 Seconds  
(without alignments)  
96.613 Million cell updates/sec

Title: US-09-865-198-6  
Perfect score: 48  
Sequence: 1 QQRSSYPFT 9

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

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8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	9	US-09-976-787-6 Sequence 6, Appli
2	48	100.0	9	10	US-09-865-198-6 Sequence 6, Appli
3	48	100.0	9	11	US-09-798-689-6 Sequence 6, Appli
4	48	100.0	9	15	US-10-232-187-10 Sequence 10, Appli
5	48	100.0	106	9	US-09-976-787-24 Sequence 24, Appli
6	48	100.0	106	10	US-09-865-198-23 Sequence 23, Appli
7	48	100.0	106	11	US-09-798-689-8 Sequence 8, Appli
8	48	100.0	107	15	US-10-232-187-4 Sequence 4, Appli
9	48	100.0	108	9	US-09-976-787-8 Sequence 8, Appli
10	48	100.0	108	10	US-09-865-198-8 Sequence 8, Appli
11	48	100.0	131	9	US-09-881-823-6 Sequence 6, Appli
12	48	100.0	238	9	US-09-976-787-29 Sequence 29, Appli
13	48	100.0	238	10	US-09-865-198-28 Sequence 28, Appli
14	48	100.0	238	11	US-09-798-689-21 Sequence 21, Appli
15	48	100.0	240	9	US-09-976-787-28 Sequence 28, Appli

16	48	100.0	240	10	US-09-865-198-27	Sequence 27, Appli
17	45	93.8	9	15	US-10-195-752-110	Sequence 110, App
18	45	93.8	107	10	US-09-144-886-88	Sequence 88, Appli
19	45	93.8	112	10	US-09-144-886-89	Sequence 89, Appli
20	45	93.8	130	15	US-10-195-752-111	Sequence 111, App
21	45	93.8	130	15	US-10-195-752-113	Sequence 113, App
22	45	93.8	256	15	US-10-247-488-2	Sequence 2, Appli
23	45	93.8	258	15	US-10-247-488-4	Sequence 4, Appli
24	44	91.7	9	14	US-10-032-482-14	Sequence 14, Appli
25	44	91.7	92	14	US-10-032-482-4	Sequence 4, Appli
26	43	89.6	9	9	US-09-808-037-17	Sequence 17, Appli
27	43	89.6	9	9	US-09-808-037-19	Sequence 19, Appli
28	43	89.6	9	15	US-10-162-889-17	Sequence 17, Appli
29	43	89.6	9	15	US-10-162-889-19	Sequence 19, Appli
30	43	89.6	119	9	US-09-808-037-28	Sequence 28, Appli
31	43	89.6	119	15	US-10-162-889-28	Sequence 28, Appli
32	43	89.6	239	9	US-09-808-037-6	Sequence 6, Appli
33	43	89.6	239	15	US-10-162-889-6	Sequence 6, Appli
34	40	83.3	9	9	US-09-808-037-18	Sequence 18, Appli
35	40	83.3	9	15	US-10-162-889-18	Sequence 18, Appli
36	40	83.3	107	10	US-09-144-886-75	Sequence 75, Appli
37	40	83.3	242	16	US-10-259-087A-18	Sequence 18, Appli
38	39	81.2	9	10	US-09-910-059-28	Sequence 28, Appli
39	39	81.2	107	10	US-09-910-059-50	Sequence 50, Appli
40	39	81.2	107	10	US-09-910-059-61	Sequence 61, Appli
41	39	81.2	107	10	US-09-910-059-65	Sequence 65, Appli
42	39	81.2	107	10	US-09-910-059-71	Sequence 71, Appli
43	39	81.2	108	10	US-09-910-059-9	Sequence 9, Appli
44	39	81.2	235	10	US-09-910-059-17	Sequence 17, Appli
45	39	81.2	235	10	US-09-910-059-52	Sequence 52, Appli

ALIGNMENTS

RESULT 1  
US-09-976-787-6  
; Sequence 6, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-976-787-6

Query Match 100.0%; Score 48; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSSYPFT 9  
Db 1 QQRSSYPFT 9

RESULT 2  
US-09-865-198-6  
; Sequence 6, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping

; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methd  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-6

Query Match 100.0%; Score 48; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
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Db 1 QORSSYPFT 9

RESULT 3  
US-09-798-689-6  
; Sequence 6, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; TITLE OF INVENTION: Combined With Radiation and Chemotherapy  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/326,552  
; PRIOR FILING DATE: 1994-10-20  
; PRIOR APPLICATION NUMBER: 08/196,041  
; PRIOR FILING DATE: 1994-02-10  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-798-689-6

Query Match 100.0%; Score 48; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
|||  
Db 1 QORSSYPFT 9

RESULT 4  
US-10-232-187-10  
; Sequence 10, Application US/10232187  
; Publication No. US20030092091A1  
; GENERAL INFORMATION:  
; APPLICANT: Abrahamson, Julie A.  
; APPLICANT: Bochner, Bruce  
; APPLICANT: Erickson-Miller, Connie L.

; APPLICANT: Kikly, Kristine K.  
; APPLICANT: Schleimer, Robert  
; APPLICANT: Nulku, Turkan E.  
; TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies  
; FILE REFERENCE: GH50042-1  
; CURRENT APPLICATION NUMBER: US/10/232,187  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/187,595  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: PCT/US01/07193  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/315,943  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/349,830  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: 60/394,741  
; PRIOR FILING DATE: 2002-07-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-232-187-10

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Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
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Db 1 QORSSYPFT 9

RESULT 5  
US-09-976-787-24  
; Sequence 24, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 24  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-24

Query Match 100.0%; Score 48; DB 9; Length 106;  
Best Local Similarity 100.0%; Pred. No. 0.09;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
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Db 88 QORSSYPFT 96

RESULT 6  
US-09-865-198-23  
; Sequence 23, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho

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; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23
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Query Match      100.0%; Score 48; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 QORSSYPFT 9
        |||||
        88 QORSSYPFT 96
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## RESULT 7

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US-09-798-689-8
; Sequence 8, Application US/09798689
; Publication No. US20030103973A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; FILE REFERENCE: Sequence listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-8
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Query Match      100.0%; Score 48; DB 11; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 QORSSYPFT 9
        |||||
        88 QORSSYPFT 96
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## RESULT 8

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US-10-232-187-4
; Sequence 4, Application US/10232187
; Publication No. US20030092091A1
; GENERAL INFORMATION:
; APPLICANT: Abrahamson, Julie A.
; APPLICANT: Bochner, Bruce
; APPLICANT: Erickson-Miller, Connie L.
; APPLICANT: Kikily, Kristine K.
```

```
; APPLICANT: Schleimer, Robert
; APPLICANT: Nulku, Turkan E.
; TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
; FILE REFERENCE: GH50042-1
; CURRENT APPLICATION NUMBER: US/10/232,187
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/187,595
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: PCT/US01/07193
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/315,943
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/349,830
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/394,741
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-232-187-4
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Query Match      100.0%; Score 48; DB 15; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 QORSSYPFT 9
        |||||
        88 QORSSYPFT 96
```

## RESULT 9

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US-09-976-787-8
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-8
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Query Match      100.0%; Score 48; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 QORSSYPFT 9
        |||||
        88 QORSSYPFT 96
```

## RESULT 10

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US-09-865-198-8
; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
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; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-8

Query Match          100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QORSSYPFT 9
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        88 QORSSYPFT 96
Db

RESULT 11
US-09-881-823-6
; Sequence 6, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-6

Query Match          100.0%; Score 48; DB 9; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QORSSYPFT 9
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        110 QORSSYPFT 118
Db

RESULT 12
US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
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; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29

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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QORSSYPFT 9
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        220 QORSSYPFT 228
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RESULT 13
US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28

Query Match          100.0%; Score 48; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QORSSYPFT 9
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        220 QORSSYPFT 228
Db

RESULT 14
US-09-798-689-21
; Sequence 21, Application US/09798689
; Publication No. US20030103973A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 238
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; TYPE: PRT  
; ORGANISM: Mouse  
US-09-798-689-21

Query Match 100.0%; Score 48; DB 11; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
|||  
Db 220 QORSSYPFT 228

RESULT 15  
US-09-976-787-28  
; Sequence 28, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 28  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-28

Query Match 100.0%; Score 48; DB 9; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
|||  
Db 220 QORSSYPFT 228

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Job time : 11.0631 secs

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OM protein - protein search, using sw model

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(without alignments)  
131.295 Million cell updates/sec

Title: US-09-865-198-6  
Perfect score: 48  
Sequence: 1 QORSSYPFT 9

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Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	45	93.8	9	2 US-08-483-528B-99	Sequence 99, Appl
4	45	93.8	9	4 US-09-393-385B-110	Sequence 110, App
5	45	93.8	129	2 US-08-116-778E-2	Sequence 2, Appli
6	45	93.8	129	2 US-08-438-562-2	Sequence 2, Appli
7	45	93.8	129	2 US-08-483-528B-92	Sequence 92, Appl
8	45	93.8	130	4 US-09-393-385B-111	Sequence 111, App
9	45	93.8	133	2 US-08-116-778E-37	Sequence 37, Appl
10	45	93.8	133	2 US-08-438-562-37	Sequence 37, Appl
11	45	93.8	133	2 US-08-483-528B-101	Sequence 101, App
12	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
13	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
14	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
15	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
16	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
17	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
18	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
19	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
20	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
21	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
22	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
23	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
24	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
25	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
26	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli
27	45	93.8	270	2 US-08-652-507-2	Sequence 2, Appli

28	39	81.2	281	4	US-09-423-439-44	Sequence 44, Appl
29	39	81.2	666	4	US-09-423-439-51	Sequence 51, Appl
30	38	79.2	108	2	US-08-378-939-32	Sequence 32, Appl
31	38	79.2	108	2	US-08-378-939-34	Sequence 34, Appl
32	37	77.1	105	3	US-08-434-000A-12	Sequence 12, Appl
33	37	77.1	105	4	US-09-312-157-12	Sequence 12, Appl
34	37	77.1	233	4	US-09-485-737B-102	Sequence 102, App
35	37	77.1	233	4	US-09-485-737B-69	Sequence 69, Appl
36	37	77.1	235	4	US-09-485-737B-93	Sequence 93, Appl
37	37	77.1	240	4	US-09-485-737B-91	Sequence 91, Appl
38	37	77.1	267	4	US-09-485-737B-2	Sequence 2, Appli
39	37	77.1	541	4	US-09-485-737B-85	Sequence 85, Appl
40	36	75.0	108	3	US-09-157-370-4	Sequence 90, Appl
41	36	75.0	130	2	US-08-659-567-2	Sequence 4, Appli
42	36	75.0	239	4	US-10-092-246-33	Sequence 2, Appli
43	36	75.0	240	4	US-10-092-246-36	Sequence 33, Appl
44	36	75.0	240	4	US-10-092-246-36	Sequence 36, Appl
45	36	75.0	240	4	US-10-092-246-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1  
US-08-116-778E-11  
; Sequence 11, Application US/08116778E  
; Patent No. 5830470  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KUMANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/116,778E  
; FILING DATE: 07-SEP-93  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 249-59  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-116-778E-11  
Query Match 93.8%; Score 45; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. NO. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0;  
QY 1 QORSSYPFT 9  
|||||||:|

Db 1 QORSSYPYT 9

## RESULT 2

US-08-438-562-11  
; Sequence 11, Application US/08438562  
; Patent No. 5874255

## ; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO; APPLICANT: KIWANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 49

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON &amp; VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/438,562

; FILING DATE: 10-MAY-95

; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/116,778

; FILING DATE: 07-SEP-93

## ; ATTORNEY/AGENT INFORMATION:

; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 249-76

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4000

; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 11:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-438-562-11

Query Match 93.8%; Score 45; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;QY 1 QORSSYPYT 9  
|||||:|

Db 1 QORSSYPYT 9

## RESULT 3

US-08-483-528B-99

; Sequence 99, Application US/08483528B  
; Patent No. 5939532

## ; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO; APPLICANT: KIWANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 103

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON &amp; VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,528B

; FILING DATE: 07-JUN-95

## ; CLASSIFICATION: 536

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4000

; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 99:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-483-528B-99

Query Match 93.8%; Score 45; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;QY 1 QORSSYPYT 9  
|||||:|

Db 1 QORSSYPYT 9

## RESULT 4

US-09-393-385B-110

; Sequence 110, Application US/09393385B  
; Patent No. 6423511

## ; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO; APPLICANT: KIWANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 113

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON &amp; VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/393,385B

; FILING DATE: 27-JUN-96

## ; CLASSIFICATION:

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4000

; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 110:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; US-09-393-385B-110

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-393-385B-110

Query Match 93.8%; Score 45; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYPPT 9  
DB 1 QORSSYPPT 9

RESULT 5  
US-08-116-778E-2  
Sequence 2, Application US/08116778E  
Patent No. 5830470  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUMANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/116,778E  
FILING DATE: 07-SEP-93  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 249-59  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: -22..-1  
IDENTIFICATION METHOD: BY SIMILARITY  
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED  
IDENTIFICATION METHOD: CONSENSUS  
FEATURE:  
NAME/KEY: domain  
LOCATION: 24..33  
IDENTIFICATION METHOD: BY SIMILARITY  
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED  
IDENTIFICATION METHOD: CONSENSUS  
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"  
FEATURE:  
NAME/KEY: domain  
LOCATION: 49..55  
IDENTIFICATION METHOD: BY SIMILARITY  
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED

IDENTIFICATION METHOD: CONSENSUS  
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"  
FEATURE:  
NAME/KEY: domain  
LOCATION: 88..96  
IDENTIFICATION METHOD: BY SIMILARITY  
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED  
IDENTIFICATION METHOD: CONSENSUS  
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"  
US-08-116-778E-2

Query Match 93.8%; Score 45; DB 2; Length 129;  
Best Local Similarity 88.9%; Pred. No. 0.15;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYPPT 9  
DB 110 QORSSYPPT 118

RESULT 6  
US-08-438-562-2  
Sequence 2, Application US/08438562  
Patent No. 5874255  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUMANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,562  
FILING DATE: 10-MAY-95  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/116,778  
FILING DATE: 07-SEP-93  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 249-76  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: -22..-1  
IDENTIFICATION METHOD: BY SIMILARITY  
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED  
IDENTIFICATION METHOD: CONSENSUS  
FEATURE:



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NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-438-562-2
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Query Match 93.8%; Score 45; DB 2; Length 129;  
Best Local Similarity 88.9%; Pred. No. 0.15;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9  
Db 110 QORSSYPPT 118

## RESULT 7

US-08-483-528B-92

Sequence 92, Application US/08483528B

Patent No. 5939532

GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU

APPLICANT: KOIKE, MASAMICHI

APPLICANT: SHITARA, KENYA

APPLICANT: HANAI, NOBUO

APPLICANT: KUMANA, YOSHIHISA

APPLICANT: HASEGAWA, MAMORU

TITLE OF INVENTION: HUMANIZED ANTIBODIES

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON &amp; VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,528B

FILING DATE: 07-JUN-95

CLASSIFICATION: 536

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 129 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE-TYPE: protein

FEATURE:

NAME/KEY: sig\_peptide

LOCATION: -22...-1

IDENTIFICATION METHOD:

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IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE TO AN
IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
FEATURE:
NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-483-528B-92
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Query Match 93.8%; Score 45; DB 2; Length 129;  
Best Local Similarity 88.9%; Pred. No. 0.15;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPPT 9  
Db 110 QORSSYPPT 118

## RESULT 8

US-09-393-385B-111

Sequence 111, Application US/09393385B

Patent No. 6423511

GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU

APPLICANT: KOIKE, MASAMICHI

APPLICANT: SHITARA, KENYA

APPLICANT: HANAI, NOBUO

APPLICANT: KUMANA, YOSHIHISA

APPLICANT: HASEGAWA, MAMORU

TITLE OF INVENTION: HUMANIZED ANTIBODIES

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON &amp; VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/393,385B

FILING DATE: 27-JUN-96

CLASSIFICATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 111:

SEQUENCE CHARACTERISTICS:

LENGTH: 130 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE-TYPE: protein

US-09-393-385B-111

Query Match 93.8%; Score 45; DB 4; Length 130;  
Best Local Similarity 88.9%; Pred. No. 0.15;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
Db 110 QORSSYPFT 118

## RESULT 9

US-09-393-385B-113  
Sequence 113, Application US/09393385B  
Patent No. 6423511

## GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KIWANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/393,385B  
FILING DATE: 27-JUN-96  
CLASSIFICATION:

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-393-385B-113

Query Match 93.8%; Score 45; DB 4; Length 130;  
Best Local Similarity 88.9%; Pred. No. 0.15;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
Db 110 QORSSYPFT 118

## RESULT 10

US-08-116-778E-37  
Sequence 37, Application US/08116778E  
Patent No. 5830470

## GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KIWANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES

NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/116,778E  
FILING DATE: 07-SEP-93

## CLASSIFICATION: 424

## ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 249-59

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 133 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-116-778E-37

Query Match 93.8%; Score 45; DB 2; Length 133;  
Best Local Similarity 88.9%; Pred. No. 0.16;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
Db 110 QORSSYPFT 118

## RESULT 11

US-08-438-562-37  
Sequence 37, Application US/08438562  
Patent No. 5874255

## GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KIWANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49

## CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,562  
FILING DATE: 10-MAY-95  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/116,778  
FILING DATE: 07-SEP-93

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 249-76  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-438-562-37

Query Match 93.8%; Score 45; DB 2; Length 133;  
Best Local Similarity 88.9%; Pred. No. 0.16;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
|||:|  
Db 110 QORSSYPFT 118

## RESULT 12

US-08-483-528B-101  
Sequence 101, Application US/08483528B  
Patent No. 5939532

## GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUMANA, YOSHITAKA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,528B  
FILING DATE: 07-JUN-95

## CLASSIFICATION: 536

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 133 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-528B-101

Query Match 93.8%; Score 45; DB 2; Length 133;  
Best Local Similarity 88.9%; Pred. No. 0.16;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
|||:|  
Db 110 QORSSYPFT 118

## RESULT 13

US-08-652-507-2

Sequence 2, Application US/08652507

Patent No. 5876691

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon & Vanderhaye, P.C.

STREET: 1100 No. 5876691th Glebe Road, 8th Floor

CITY: Arlington

STATE: Virginia

COUNTRY: USA

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,507

FILING DATE: 02-Jul-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Arthur R. Crawford

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 117-211

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4000

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 270 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-507-2

Query Match 87.5%; Score 42; DB 2; Length 270;  
Best Local Similarity 88.9%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QORSSYPFT 9  
|||:|  
Db 249 QORSSYPFT 257

## RESULT 14

US-08-661-052-16

Sequence 16, Application US/08661052

Patent No. 5837243

GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo

APPLICANT: Joel Goldstein

APPLICANT: Robert Graziano

APPLICANT: Chezia Somasundaram

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED

TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,052  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-661-052-16

Query Match 87.5%; Score 42; DB 2; Length 553;  
Best Local Similarity 88.9%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
|||||||  
Db 499 QORSSYPFT 507

## RESULT 15

US-09-188-082-16  
Sequence 16, Application US/09188082

Patent No. 6270765

GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo

APPLICANT: Joel Goldstein

APPLICANT: Robert Graziano

APPLICANT: Chezian Somasundaram

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED

TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/188,082

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/661,052

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: MXI-043CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein  
US-09-188-082-16

Query Match 87.5%; Score 42; DB 3; Length 553;  
Best Local Similarity 88.9%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QORSSYPFT 9  
|||||||  
Db 499 QORSSYPFT 507

Search completed: July 30, 2003, 09:38:30  
Job time : 2.90033 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 5.02658 Seconds  
(without alignments)  
325.245 Million cell updates/sec

Title: US-09-865-198-21  
Perfect score: 101  
Sequence: 1 WIDPENGDSYAPKFOG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	93.1	82	2	A36025 Ig heavy chain V r
2	86	85.1	118	2	S25174 Ig heavy chain V r
3	84	83.2	136	2	S04576 Ig heavy chain pre
4	82	81.2	116	2	S15672 Ig heavy chain V r
5	78	77.2	137	2	S52445 Ig heavy chain V r
6	68	67.3	143	1	E1HUND Ig heavy chain pre
7	67	66.3	85	2	E37262 Ig heavy chain V r
8	64	63.4	86	2	S54912 Ig heavy chain V r
9	63	62.4	98	2	S26938 Ig heavy chain V r
10	63	62.4	98	2	S26912 Ig heavy chain V r
11	63	62.4	99	2	D37262 Ig heavy chain V r
12	63	62.4	107	2	PH1013 Ig heavy chain V r
13	63	62.4	108	2	PH1012 Ig heavy chain V r
14	63	62.4	117	2	S31680 Ig heavy chain V r
15	63	62.4	117	2	S18551 Ig heavy chain V r
16	63	62.4	118	2	S36265 Ig heavy chain V r
17	63	62.4	120	2	S03471 Ig heavy chain V-D
18	63	62.4	122	2	S06823 Ig heavy chain V r
19	63	62.4	123	2	D33548 Ig heavy chain V-1
20	63	62.4	123	2	PH1403 Ig heavy chain V r
21	63	62.4	129	2	S46393 Ig heavy chain V r
22	63	62.4	135	2	S49530 anti-Sm antibody V
23	62	61.4	178	2	S29594 Ig gamma chain (WM
24	61	60.4	120	2	S03484 Ig heavy chain V-D
25	61	60.4	221	2	S49220 Ig gamma-1 chain -
26	60	59.4	77	2	S46465 Ig heavy chain V r
27	60	59.4	98	2	S26918 Ig heavy chain V r
28	60	59.4	98	2	S26909 Ig heavy chain V r
29	60	59.4	132	2	S31596 Ig heavy chain V r

30	60	59.4	136	2	S31600 Ig heavy chain V r
31	59	58.4	86	2	S29544 Ig heavy chain V r
32	59	58.4	97	2	S16028 Ig heavy chain V r
33	59	58.4	98	2	S26921 Ig heavy chain V r
34	59	58.4	116	2	S24289 Ig gamma chain V r
35	58	57.4	114	2	PH1667 Ig heavy chain V r
36	58	57.4	118	2	PH1666 Ig heavy chain V r
37	57.5	56.9	98	2	S26911 Ig heavy chain V r
38	57	56.4	110	2	PH1670 Ig heavy chain V r
39	57	56.4	115	2	S03482 Ig heavy chain V-D
40	57	56.4	120	2	S31999 Ig heavy chain V r
41	57	56.4	171	2	S23623 Ig heavy chain V r
42	56	55.4	107	2	A27646 Ig heavy chain V r
43	56	55.4	126	2	I44151 Ig heavy chain V r
44	56	55.4	127	2	S34014 Ig heavy chain V r
45	55	54.5	99	2	C37262 Ig heavy chain V r

## ALIGNMENTS

RESULT 1  
A36025  
Ig heavy chain V region (PR8-1) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 11-Jan-1991 #sequence\_revision 11-Jan-1991 #text\_change 23-Jul-1999  
C/Accession: A36025; E36025  
R/Caton, A.J.; Kopyrowski, H.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6450-6454, 1990  
A/Title: Influenza virus hemagglutinin-specific antibodies isolated from a combinatorial  
A/Reference number: A36025; MUID:90349634; PMID:1696733  
A/Accession: A36025  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-82 <CAT>  
A/Cross-references: GB:M55999; NID:g194955; PIDN:AAA38112.1; PID:g194956  
A/Note: PR8-1  
A/Accession: E36025  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 19-82 <CA2>  
A/Cross-references: GB:M57273; NID:g194963; PIDN:AAA38116.1; PID:g194964  
A/Note: clone PR8-21  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 93.1%; Score 94; DB 2; Length 82;  
Best Local Similarity 88.2%; Pred. No. 6e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGDSYAPKFOG 17  
Db 12 WIDPENGDTETAPKFOG 28

RESULT 2  
S25174  
Ig heavy chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C/Accession: S25174; S33133  
R/Monestier, M.; Fasy, T.M.; Loeman, M.J.; Novick, K.E.; Muller, S.  
Submitted to the EMBL Data Library, July 1992  
A/Description: Structure and binding properties of monoclonal antibodies to core histone  
A/Reference number: S25174  
A/Accession: S25174  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-118 <MON>  
A/Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259  
A/Accession: S33133  
A/Status: preliminary  
A/Molecule type: mRNA

A;Residues: 1-118 <MO2>  
A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 86; DB 2; Length 118;  
Best Local Similarity 82.4%; Pred. No. 1.7e-06;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFOG 17  
DB 50 WIDPENGDTYASKFOG 66

## RESULT 3

S04576  
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000  
C;Accession: S04576  
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th  
Eur. J. Immunol. 17, 91-95, 1987  
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involve  
A;Reference number: S04573; MUID:87133856; PMID:3102255  
A;Accession: S04576  
A;Molecule type: mRNA  
A;Residues: 1-136 <KOF>  
A;Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 84; DB 2; Length 136;  
Best Local Similarity 82.4%; Pred. No. 4.2e-06;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFOG 17  
DB 69 WIDPENGDTYASKFOG 85

## RESULT 4

S15672  
Ig heavy chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C;Accession: S15672  
R;Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris,  
Bio/Technology 9, 266-271, 1991  
A;Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi  
A;Reference number: S15672; MUID:91337412; PMID:1367535  
A;Accession: S15672  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-116 <TEM>  
A;Cross-references: EMBL:X58635; NID:g51978; PIDN:CAA41644.1; PID:g51979  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 82; DB 2; Length 116;  
Best Local Similarity 82.4%; Pred. No. 7.3e-06;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFOG 17  
DB 50 WIDPENGDTYASKFOG 66

## RESULT 5

S52445  
Ig heavy chain V region precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C;Accession: S52445  
R;Berdoz, J.; Kraehenbuhl, J.P.  
submitted to the EMBL Data Library, November 1994  
A;Description: Specific amplification by the polymerase chain reaction of rearranged ge  
A;Reference number: S52445  
A;Accession: S52445  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-137 <BER>  
A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440  
C;Genetics:  
A;Intons: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;34-115/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 78; DB 2; Length 137;  
Best Local Similarity 76.5%; Pred. No. 3.8e-05;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFOG 17  
DB 69 WIDPENGNTYDPAKFOG 85

## RESULT 6

E1HUND  
Ig heavy chain precursor V-I region (Nd) - human (fragments)  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1981 #sequence\_revision 05-Apr-1983 #text\_change 21-Jan-2000  
C;Accession: A93933; A02026  
R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.;  
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982  
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin eps  
A;Reference number: A93933; MUID:83065234; PMID:6815656  
A;Accession: A93933  
A;Molecule type: mRNA  
A;Residues: 1-143 <KEN>  
R;Benich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.  
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3  
A;Reference number: A94418  
A;Contents: annotation; partial sequence  
A;Note: this epsilon chain was isolated from a myeloma protein  
C;Genetics:  
A;Gene: GDB:IGHV@  
A;Cross-references: GDB:128528; OMIM:147070  
A;Map position: 14q32.33-14q32.33  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin; pyroglytamic acid  
F;1-15/Domain: signal sequence #status predicted <SIG>  
F;16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>  
F;30-113/Domain: immunoglobulin homology <IMM>  
F;16/Modified site: pyrolydione carboxylic acid (Gln) (in mature form) #status experime  
F;37-111/Disulfide bonds: #status experimental

Query Match 67.3%; Score 68; DB 1; Length 143;  
Best Local Similarity 58.8%; Pred. No. 0.0016;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFOG 17  
DB 65 WIPNPGGTNYAPRFOG 81

## RESULT 7

E37262  
Ig heavy chain V region (6H2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 09-May-1997

C;Accession: E37262  
R;Goshorn, S.C.; Retzel, E.; Jemerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A;Title: Common structural features among monoclonal antibodies binding the same antigen  
A;Reference number: A38601; MUID:91115823; PMID:1703527  
A;Accession: E37262  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-85 <GOS>  
A;Cross-references: GB:M57991  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.3%; Score 67; DB 2; Length 85;  
Best Local Similarity 75.0%; Pred. No. 0.0013;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFOG 17  
DB 29 IDPANGDTRYDPKFOG 44

RESULT 8  
S54912  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 17-Feb-1998 #sequence\_revision 26-Feb-1998 #text\_change 21-Jan-2000  
C;Accession: S54912  
R;Tomlinson, M.; Walter, G.; Cook, X.Y.Z.; Winter, G.  
submitted to the EMBL Data Library, November 1992  
A;Reference number: S54912  
A;Accession: S54912  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-86 <TOM>  
A;Cross-references: EMBL:Z18904; NID:g840779; PIDN:CAA79341.1; PID:g840780  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 64; DB 2; Length 86;  
Best Local Similarity 64.7%; Pred. No. 0.004;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17  
DB 38 WIDPENGSPSYAKKFOG 54

RESULT 9  
S26938  
Ig heavy chain V region (DP-75) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 17-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S26938  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A;Reference number: S26885; MUID:93021117; PMID:1404388  
A;Accession: S26938  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-98 <TOM>  
A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 98;  
Best Local Similarity 58.8%; Pred. No. 0.0066;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17

DB 50 WIDPNSGCTNYAQKFOG 66

RESULT 10  
S26912  
Ig heavy chain V region (DP-8) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S26912  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A;Reference number: S26885; MUID:93021117; PMID:1404388  
A;Accession: S26912  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-98 <TOM>  
A;Cross-references: EMBL:Z12310; NID:g32979; PIDN:CAA78180.1; PID:g32980  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 98;  
Best Local Similarity 58.8%; Pred. No. 0.0066;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17  
DB 50 WIDPNSGCTNYAQKFOG 66

RESULT 11  
D37262  
Ig heavy chain V region (2E5) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 21-Jan-2000  
C;Accession: D37262  
R;Goshorn, S.C.; Retzel, E.; Jemerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A;Title: Common structural features among monoclonal antibodies binding the same antigen  
A;Reference number: A38601; MUID:91115823; PMID:1703527  
A;Accession: D37262  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-99 <GOS>  
A;Cross-references: GB:M57990; NID:g195046; PIDN:AAA63328.1; PID:g195047  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 99;  
Best Local Similarity 68.8%; Pred. No. 0.0067;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFOG 17  
DB 43 IDPANGTKYDPKFOG 58

RESULT 12  
PH1013  
Ig heavy chain V region (clone 111.67) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH1013  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
A;Reference number: PH0971; MUID:92381444; PMID:1512540  
A;Accession: PH1013  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA

A;Residues: 1-107 <TIL>  
A;Experimental source: B cell, strain [NZB x NZW]F1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 107;  
Best Local Similarity 73.3%; Pred. No. 0.0073;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPENGSDSYAPKFG 16  
DB 51 IDPANGNTKYAPKFG 65

## RESULT 13

PH1012  
Ig heavy chain V region (clone 17p.73) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH1012

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells  
A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1012

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-108 <TIL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 108;  
Best Local Similarity 73.3%; Pred. No. 0.0074;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPENGSDSYAPKFG 16  
DB 51 IDPANGNTKYAPKFG 65

## RESULT 14

S31680

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S31680

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the

A;Reference number: S31585

A;Accession: S31680

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-117 <CUI>

A;Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796

C;Genetics: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 117;  
Best Local Similarity 58.8%; Pred. No. 0.0081;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFG 17  
DB 69 WINPNSGCTNYAQKFG 85

## RESULT 15

S18551

Ig heavy chain V region precursor (VI-2) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 06-Jun-1997 #text\_change 23-Jul-1999

C;Accession: S18551; S23625

R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.;

EMBO J. 10, 3641-3645, 1991

A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl

A;Reference number: S18551; MUID:92037524; PMID:1935893

A;Accession: S18551

A;Molecule type: DNA

A;Residues: 1-117 <SHI>

A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832

R;Olee, T.; Lu, B.W.; Huang, D.F.; Soto-Gil, R.W.; Defcos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from r

A;Reference number: S23623; MUID:92156804; PMID:1740665

A;Accession: S23625

A;Molecule type: DNA

A;Residues: 1-117 <OLB>

A;Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553

C;Genetics: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 63; DB 2; Length 117;  
Best Local Similarity 58.8%; Pred. No. 0.0081;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDSYAPKFG 17  
DB 69 WINPNSGCTNYAQKFG 85

Search completed: July 30, 2003, 09:44:10  
Job time : 6.02658 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:35 ; Search time 2.65449 Seconds  
(without alignments)  
301.171 Million cell updates/sec

Title: US-09-865-198-21  
Perfect score: 101  
Sequence: 1 WIDPENGDSYAPKFG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	67.3	147	1	HVIC_HUMAN P01744 homo sapien
2	52	51.5	117	1	HVIG_HUMAN P23083 homo sapien
3	51	50.5	117	1	HVIB_HUMAN P01743 homo sapien
4	51	50.5	350	1	NUD9_HUMAN Q9bw91 homo sapien
5	47	46.5	1709	1	SN_HUMAN Q9bz22 homo sapien
6	46	45.5	117	1	HVI2_MOUSE P01756 mus musculu
7	46	45.5	117	1	HVI3_MOUSE P01757 mus musculu
8	46	45.5	117	1	HVS2_MOUSE P06327 mus musculu
9	46	45.5	118	1	HVS1_MOUSE P06330 mus musculu
10	45	44.6	1387	1	PUR4_ARATH G9m8d3 arabidopsis
11	44	43.6	402	1	MCE1_SCHPO P40997 schizosacch
12	44	43.6	944	1	CHS2_NEUCR P30589 neurospora
13	43	42.6	120	1	HV03_MOUSE P01747 mus musculu
14	43	42.6	238	1	YIGB_ECOLI P23306 escherichia
15	43	42.6	511	1	C772_SOLME P37124 solanum mel
16	43	42.6	776	1	HYPF_AZOVI P40596 azotobacter
17	43	42.6	977	1	DLP3_RAT P97838 rattus norv
18	43	42.6	3329	1	BRC2_MOUSE P97929 mus musculu
19	42	41.6	140	1	HV02_MOUSE P01746 mus musculu
20	41.5	41.1	117	1	HV03_CAICR P03982 caiman croc
21	41.5	41.1	551	1	YG1F_YEAST P53214 saccharomyc
22	41.5	41.1	597	1	ETFD_CAEEL Q11190 c probable
23	41	40.6	117	1	HV06_MOUSE P01750 mus musculu
24	41	40.6	120	1	HV50_MOUSE P06329 mus musculu
25	41	40.6	526	1	THRC_ARATH Q987b5 arabidopsis
26	41	40.6	783	1	HELS_HUMAN Q9hmv6 halobacteri
27	41	40.6	830	1	SREC_HUMAN Q14162 homo sapien
28	41	40.6	977	1	DLP1_HUMAN Q14490 homo sapien
29	41	40.6	992	1	DLP1_RAT P97836 rattus norv
30	41	40.6	1005	1	EP48_HUMAN P29322 homo sapien
31	41	40.6	1338	1	PUR4_HUMAN O15067 homo sapien
32	41	40.6	1343	1	PUR4_CAEEL Q19311 caenorhabdi
33	41	40.6	1354	1	PUR4_DROME P35421 drosophila

34	41	40.6	1857	1	FAS2_PENPA P15368 p fatty aci
35	40.5	40.1	205	1	DNBI_ADE12 P36704 human adeno
36	40	39.6	117	1	HV1A_HUMAN P01742 homo sapien
37	40	39.6	153	1	RNH_XYLEA Q9pb16 xylella fas
38	40	39.6	156	1	RNP_HUMAN P07998 homo sapien
39	40	39.6	227	1	YG24_HAEIN P44276 haemophilus
40	40	39.6	254	1	MOX1_YEAST P50221 homo sapien
41	40	39.6	297	1	YMY9_HUMAN Q03161 saccharomyc
42	40	39.6	416	1	PA12_RAT P29524 rattus norv
43	40	39.6	496	1	PACR_MOUSE P70205 mus musculu
44	40	39.6	523	1	PACR_RAT P32215 rattus norv
45	40	39.6	712	1	GPA1_CANAL P53704 candida alb

ALIGNMENTS

RESULT 1	
HVIC_HUMAN	STANDARD; PRT; 147 AA.
ID HVIC_HUMAN	
AC P01744;	
DT 21-JUL-1986 (Rel. 01, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 15-SEP-2003 (Rel. 42, Last annotation update)	
DE Ig heavy chain V-I region ND precursor (Fragments).	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX NCBI_Taxid=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=83065234; PubMed=6815656;	
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,	
RA Bell L.O., Gould H.J.;	
RT "Cloning and sequence determination of the gene for the human	
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";	
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).	
RN [2]	
RP SEQUENCE OF 20-147.	
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;	
RL (in) Bach M.K. (eds.);	
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,	
RL Marcel Dekker, New York (1978).	
CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA	
CC PROTEIN.	
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.	
DR HSSP; P01789; IMCP.	
DR GO; GO:0005576; C:extracellular; NAS.	
DR GO; GO:0003823; F:antigen binding activity; NAS.	
DR GO; GO:0006955; P:immune response; NAS.	
DR InterPro; IPR007110; Ig-like.	
DR InterPro; IPR003006; Ig_MHC.	
DR InterPro; IPR003596; Ig_V.	
DR Pfam; PF00047; Ig; 1.	
DR SMART; SM00406; IGV; 1.	
DR PROSITE; PS50835; IG_LIKE; 1.	
DR Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.	
KW SIGNAL.	
FT CHAIN 1	
FT CHAIN 20	
FT DOMAIN 20	
FT MOD RES 20	
FT DISULFID 41	
FT CONFLICT 21	
FT CONFLICT 53	
FT CONFLICT 67	
FT CONFLICT 125	
FT NON TER 147	
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;	

Query Match 67.3%; Score 68; DB 1; Length 147;  
Best Local Similarity 58.8%; Pred. No. 0.00087;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;



QY 1 WIDPENGSDYAPKFOG 17  
DB 69 WINPNSGCTNYAPKFOG 85

## RESULT 2

HV1G\_HUMAN STANDARD; PRT; 117 AA.  
AC P23083;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DE Ig heavy chain V-I region V35 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88296408; PubMed=2841108;  
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,  
RA Ohno H., Fukuhara S., Honjo T.;  
RT "Dispersed localization of D segments in the human immunoglobulin  
heavy-chain locus."  
RL EMBL J. 7:1047-1051(1988).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -----  
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CC -----  
DR EMBL: X07448; -; NOT\_ANNOTATED\_CDS.  
DR PIR: S00476; HVH035.  
DR HSSP: P01772; 2FB4.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.  
FT DOMAIN 20 >117 IG-LIKE.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;  
Query Match 51.5%; Score 52; DB 1; Length 117;  
Best Local Similarity 56.2%; Pred. No. 0.23;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFOG 17

DB 70 INPNSGCTNYAPKFOG 85

## RESULT 3

HV1B\_HUMAN STANDARD; PRT; 117 AA.  
AC P01743;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-I region HG3 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83144028; PubMed=6298778;  
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;  
RT "Evolutionary aspects of immunoglobulin heavy chain variable region  
(VH) gene subgroups."  
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -----  
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CC -----  
DR EMBL: J00240; AAA52988.1; -.  
DR PIR: A02024; HVH0HG.  
DR HSSP: P01772; 2FB4.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.  
FT DOMAIN 20 >117 IG-LIKE.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

QY 2 IDPENGSDYAPKFOG 17  
DB 70 INPNSGCTNYAPKFOG 85

QY 2 IDPENGSDYAPKFOG 17  
DB 70 INPNSGCTNYAPKFOG 85

## RESULT 4

NUD9\_HUMAN STANDARD; PRT; 350 AA.  
AC Q9BW91;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DE ADP-ribose pyrophosphatase (EC 3.6.1.13) (ADP-ribose diphosphatase)  
DE (Adenosine diphosphoribose pyrophosphatase) (ADPR-PPase) (ADP-ribose  
DE phosphohydrolase) (Nucleoside diphosphate-linked moiety X motif 9).  
GN NUDT9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=21279171; PubMed=11385575;  
RA Perraud A.-L., Fleig A., Dunn C.A., Bagley L.A., Launay P.,  
RA Schmitz C., Stokes A.J., Zhu Q., Bessman M.J., Penner R., Kinet J.-P.,  
RT "ADP-ribose gating of the calcium-permeable LTRPC2 channel revealed by  
RT Nudix motif homology."  
RL Nature 411:595-599(2001).  
RN [2]

RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loqueillano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- CATALYTIC ACTIVITY: ADP-ribose + H(2)O = AMP + D-ribose 5-  
CC phosphate.  
CC -1- TISSUE SPECIFICITY: Ubiquitous.  
CC -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. NUDF SUBFAMILY.  
CC -----  
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CC -----  
CC  
DR EMBL; AY026252; AAK07671.1; -.  
DR EMBL; BC000542; AAH00542.1; -.  
DR Genew; HGNC:8056; NUDT9.  
DR MIM; 606022; -.  
DR GO; GO:0005622; C:intracellular; NAS.  
DR GO; GO:0019144; F:ADP-sugar diphosphatase activity; NAS.  
DR GO; GO:0005227; F:calcium activated cation channel activity; NAS.  
DR GO; GO:0006812; P:cation transport; NAS.  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
DR PROSITE; PS00893; NUDIX; FALSE\_NEG.  
KW Hydrolase.  
FT DOMAIN 215 237 NUDIX BOX.  
SQ SEQUENCE 350 AA; 39125 MW; 2EA5B24B88FB3420 CRC64;  
  
Query Match 50.5%; Score 51; DB 1; Length 350;  
Best Local Similarity 46.7%; Pred. No. 1.1;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKF 15  
| | | : | : | | |  
Db 110 WADPQISESNFSPKF 124

RESULT 5  
SN\_HUMAN STANDARD; PRT: 1709 AA.  
ID SN\_HUMAN  
AC Q9BZZ2; Q96DL4; Q9GZS5; Q9H1H6; Q9H1H7; Q9H7L7;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Sialoadhesin precursor (Sialic acid binding Ig-like lectin-1) (Siglec-  
DE 1) (CD169 antigen).  
GN SN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.  
RC TISSUE=Monocytes;  
RX MEDLINE=20575418; PubMed=11133773;  
RA Hartnell A., Steel J., Turley H., Jones M., Jackson D.G.,  
RA Crocker P.R.;  
RT "Characterization of human sialoadhesin, a sialic acid binding  
RT receptor expressed by resident and inflammatory macrophage  
RT populations.";  
RL Blood 97:288-296(2001).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RX MEDLINE=21638749; PubMed=11780052;  
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lehaeslaaho M.H., Leverisa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConnachie L.J., McElay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
RN [3]  
RP SEQUENCE OF 733-1709 FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Spleen;  
RX MEDLINE=21082933; PubMed=11214971;  
RA Hattori A., Okumura K., Nagase T., Kikuno R., Hirose M., Ohara O.;  
RT "Characterization of long cDNA clones from human adult spleen.";  
RL DNA Res. 7:357-366(2000).  
RN [4]  
RP SEQUENCE OF 1539-1709 FROM N.A. (ISOFORM 3).  
RC TISSUE=Thymus;  
RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,  
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,  
RA Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,  
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,  
RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,  
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,  
RA Wakamatsu A., Ishii S., Yamashita H., Matsuo K., Nakamura Y.,  
RA Nishikawa T., Kimura K., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,  
RA Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K.,  
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,  
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;  
RT "NEDO human cDNA sequencing project.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Macrophage-restricted adhesion molecule that mediates  
CC sialic-acid dependent binding to lymphocytes, including  
CC granulocytes, monocytes, natural killer cells, B-cells and CD8 T-  
CC cells. Preferentially binds to alpha2,3-linked sialic acid (By  
CC similarity). Binds to SPN/CD43 on T-cells (By similarity). May  
CC play a role in hemopoiesis.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and  
CC soluble (isoform 2).  
CC -1- ALTERNATIVE PRODUCTS:

```

CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC Isoid=Q9BZ22-1; Sequence=Displayed;
CC Name=2;
CC Isoid=Q9BZ22-2; Sequence=VSP_002571;
CC Name=3;
CC Isoid=Q9BZ22-3; Sequence=VSP_002572;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Expressed by macrophages in various tissues.
CC High levels are found in spleen, lymph node, perivascular
CC macrophages in brain and lower levels in bone marrow, liver
CC Kupffer cells and lamina propria of colon and lung. Also expressed
CC by inflammatory macrophages in rheumatoid arthritis.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC
CC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 16 immunoglobulin-like C2-type domains.
CC -1- DATABASE: NAME=PROW; NOTE=PROW 2:18-22(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/985165905_g.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF230073; AAK0757.1; -.
DR EMBL; AL109804; CAC17543.1; -.
DR EMBL; AL109804; CAC17542.1; -.
DR EMBL; AK024462; BAB15752.1; -.
DR EMBL; AK024459; BAB15749.1; -.
DR EMBL; AK024479; BAB15769.1; -.
DR EMBL; AK057560; BAB71527.1; -.
DR HSSP; Q62230; IQFO.
DR Genew; HGNC:11127; SN.
DR MIM; 600751; -.
DR GO; GO:0016021; C:Integral to membrane; NAS.
DR GO; GO:0005530; F:Lectin; NAS.
DR GO; GO:0016337; P:cell-cell adhesion; NAS.
DR GO; GO:0007160; P:cell-matrix adhesion; NAS.
DR GO; GO:0006954; P:inflammatory response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 14.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PS50835; IG_LIKE; 14.
KW Cell adhesion; Lectin; Antigen; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat; Alternative splicing; Polymorphism.
FT SIGNAL 1 19
FT CHAIN 20 1709
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FT DOMAIN 1663 1709
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FT DOMAIN 411 507
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FT DOMAIN 601 705
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FT DOMAIN 799 89
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	FT	DISULFID	36	166	BY SIMILARITY.
	FT	DISULFID	41	98	BY SIMILARITY..
	FT	DISULFID	160	217	BY SIMILARITY.
	FT	DISULFID	262	305	BY SIMILARITY.
	FT	DISULFID	346	390	BY SIMILARITY.
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	FT	DISULFID	531	575	BY SIMILARITY.
	FT	DISULFID	624	689	BY SIMILARITY.
	FT	DISULFID	729	774	BY SIMILARITY.
	FT	DISULFID	817	876	BY SIMILARITY.
	FT	DISULFID	916	960	BY SIMILARITY.
	FT	DISULFID	1005	1067	BY SIMILARITY.
	FT	DISULFID	1107	1149	BY SIMILARITY.
	FT	DISULFID	1193	1241	BY SIMILARITY.
	FT	DISULFID	1281	1324	BY SIMILARITY.
	FT	DISULFID	1367	1425	BY SIMILARITY.
	FT	DISULFID	1465	1511	BY SIMILARITY.
	FT	DISULFID	1554	1613	BY SIMILARITY.
	FT	CABOHYD	159	159	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	265	265	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	339	339	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	499	499	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	697	697	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	726	726	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	730	730	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	741	741	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	886	886	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	1104	1104	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	1138	1138	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	1251	1251	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	1462	1462	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	CABOHYD	1476	1476	N-LINKED (GLCNAC. . ) (POTENTIAL).
	FT	VARSPLIC	1632	1709	ALHRIHOFOQLTWLGLVGLVLILLGAGCYTTRRRVCCK QSMGENSVEMAFQKETTLDPDAATCETSTCAPLLG -> GGEGRLHPGHSAOKPS (in isoform 2'). /FTid=VSP_002571. RARRRVCKQSMGENSVEMAFQKETTLDPDAATCETSTCAP PLG -> SSLIMQPHVRFPPVPFWADQCCLPSGGSGQ NL (in isoform 3). /FTid=VSP_002572. K -> R (in dbSNP:625372). /FTid=VAR_014136.
	FT	VARIANT	239	239	
	Query Match		46.5%;	Score 47; DB 1; Length 1709; #	
	Best Local Similarity		58.3%;	Pred. No. 27;	
	Matches	7; Conservative	4; Mismatches	1; Indels	0; Gaps
OY	6 NGDSDDYPAPFKQG 17	:	:   :::  :		
Db	456 SGSDSHSFRFG 467				
RESULT 6	HV12_MOUSE	STANDARD;	PRT;	117 AA.	\$
ID	HV12_MOUSE				
AC	P01756;				
DT	21-JUN-1986 (Rel. 01, Created)				
DT	21-JUN-1986 (Rel. 01, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Ig heavy chain V region MOFC 104E.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxId=10090;				
RN	[1]				
RP	SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.				
RX	MEDLINE=83075344; PubMed=6816276;				
RA	Kenny M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley G.H., Hood L.E.;				
RA	"Complete amino acid sequence of a mouse mu chain: homology among heavy chain constant region domains.";				
RL	Biochemistry 21:5415-5424(1982).				

```
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02039; MEMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFGQ 17
   |||||:|:|:|
Db 51 INPNNGTSTYNQKFKG 66

RESULT 7
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MEMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFGQ 17
   |||||:|:|:|
Db 51 INPNNGTSTYNQKFKG 66
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RESULT 8
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M13787; AAA38499.1; -.
DR PIR; A02029; HVMSA1.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 45.5%; Score 46; DB 1; Length 117;
Best Local Similarity 47.1%; Pred. No. 2;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFGQ 17
   |||||:|:|:|
Db 69 WIVPGDGSTYNEKFKG 85

RESULT 9
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```



RP SEQUENCE.  
RX MEDLINE=84182519; PubMed=62201362;  
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;  
RT "A V region determinant (idiotope) expressed at high frequency in B  
lymphocytes is encoded by a large set of antibody structural genes.";  
RL EMO J. 3:517-523(1984).  
DR PIR; A02040; MHMS38.  
DR HSRP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 98 V SEGMENT.  
FT DOMAIN 99 104 D SEGMENT.  
FT DOMAIN 105 118 J SEGMENT.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON\_TER 118 118  
SQ SEQUENCE 118 AA; 12934 MW; 94F7BBE4C762A018 CRC64;  
Query Match 45.5%; Score 46; DB 1; Length 118;  
Best Local Similarity 50.0%; Pred. No. 2.1;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 2 IDPENGSDSYAPKFG 17  
Db 51 INPNNGTSTYNQKFKG 66  
RESULT 10  
PUR4\_ARATH STANDARD; PRT; 1387 AA.  
AC Q9M8D3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Probable phosphoribosylformylglycinamide synthase, chloroplast  
precursor (EC 6.3.5.3) (FGAM synthase) (FGAMS) (Formylglycinamide  
ribotide amidotransferase) (FGARAT) (Formylglycinamide ribotide  
synthetase).  
GN AT1G74260 OR F1017.7.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=21016719; PubMed=11130712;  
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,  
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
Gill J.B., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,  
Miltischer J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,  
Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
Utecherback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
thaliana.";  
RL Nature 408:816-820(2000).  
CC -i- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-  
ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-

CC (formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine + L-glutamate.  
CC -i- PATHWAY: De novo purine biosynthesis; fourth step.  
CC -i- SUBCELLULAR LOCATION: Chloroplast (Probable).  
CC -i- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FGAMS  
FAMILY.  
CC -i- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.  
CC -----  
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CC -----  
DR EMBL; AC020579; AAG52403.1; -.  
DR PIR; A96771; A96771.  
DR InterPro; IPR000728; AIRS\_related.  
DR Pfam; PF00586; AIRS; 1.  
DR Pfam; PF02769; AIRS\_C; 2.  
KW Purine biosynthesis; ligase; ATP-binding; Glutamine amidotransferase;  
KW Chloroplast; Transit peptide.  
FT TRANSIT 1 ?  
FT CHAIN ? 1387 CHLOROPLAST (POTENTIAL).  
FT PROBABLE  
FT PHOSPHORIBOSYLFORMYLGLYCINAMIDINE  
FT SYNTHASE.  
FT NP\_BIND 387 398 ATP (POTENTIAL).  
FT ACT\_SITE 1215 1215 GATASE (BY SIMILARITY).  
SQ SEQUENCE 1387 AA; 151778 MW; 65E9920DF83F0E95 CRC64;  
Query Match 44.6%; Score 45; DB 1; Length 1387;  
Best Local Similarity 64.3%; Pred. No. 44;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2 IDPENGSDSYAPKF 15  
Db 448 IDASNGASDYGKPF 461  
RESULT 11  
MCE1 SCHPO  
ID MCE1 SCHPO STANDARD; PRT; 402 AA.  
AC P40997;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE mRNA capping enzyme alpha subunit (mRNA guanylyltransferase)  
(EC 2.7.7.50) (GTP-RNA guanylyltransferase) (GTase).  
GN CEG1 OR PCE1 OR SPBC2F12.08C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95083638; PubMed=7991582;  
RA Shuman S., Liu Y., Scher B.;  
RT "Covalent catalysis in nucleotidyl transfer reactions: essential  
RT motifs in Saccharomyces cerevisiae RNA capping enzyme are conserved  
RT in Schizosaccharomyces pombe and viral capping enzymes and among  
RT polynucleotide ligases.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:12046-12050(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Fresco L.D., Woo S., Buratowski S.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,



RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,  
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakowski G.V., Usery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of *Schizosaccharomyces pombe*.";  
 RL Nature 415:871-880(2002).  
 CC -I- FUNCTION: SECOND STEP OF M-RNA CAPPING. TRANSFER OF THE GMP MOIETY  
 CC OF GTP TO THE 5' END OF RNA YIELDING A 52 KDA ENZYME-GMP COVALENT  
 CC REACTION INTERMEDIATE (BY SIMILARITY).  
 CC -I- CATALYTIC ACTIVITY: GTP + (5') PP-pur-mRNA = diphosphate +  
 CC G(5')PPP-pur-mRNA.  
 CC -I- SUBUNIT: THE M-RNA CAPPING ENZYME IS COMPOSED OF TWO SEPARATE  
 CC CHAINS ALPHA AND BETA, RESPECTIVELY A MRNA GUANYLYLTRANSFERASE AND  
 CC AN RNA 5'-TRIPHOSPHATASE (BY SIMILARITY).  
 CC -I- SUBCELLULAR LOCATION: Nuclear.  
 CC -I- SIMILARITY: BELONGS TO THE EUKARYOTIC GTASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; U16143; AAA64996.1; -.  
 DR EMBL; U18811; AAA58715.1; -.  
 DR EMBL; Z97211; CAB10156.1; -.  
 DR PIR; T40133; T40133.  
 DR GenDB\_SPombe; SPBC2F12.08c; -.  
 DR InterPro; IPR001339; mRNA\_cap\_enzyme.  
 DR Pfam; PF03919; mRNA\_cap\_C; 1.  
 DR Pfam; PF01331; mRNA\_cap\_enzyme; 1.  
 KW Transferase; Nucleotidyltransferase; mRNA processing; mRNA capping;  
 KW Nuclear protein.  
 FT ACT\_SITE 67 GUANYLYLATION SITE.  
 FT MUTAGEN 67 K->A: LOSS OF FUNCTION.  
 SQ SEQUENCE 402 AA; 46875 MW; 76B1E2052DABB974 CRC64;

Query Match 43.6%; Score 44; DB 1; Length 402;  
 Best Local Similarity 60.0%; Pred. No. 16;  
 Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

OY 4 PENGDSBYA--PKFQ 16  
 DB 260 PEEGDIDYSAMPEFQ 274

RESULT 12  
 CHS2\_NEUCR STANDARD; PRT; 944 AA.  
 AC P30589;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Chitin synthase 2 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl  
 DE transferase 2).  
 GN CHS-2.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95039879; PubMed=7952169;  
 RA Din A.B., Yarden O.;  
 RT "The Neurospora crassa chs-2 gene encodes a non-essential chitin  
 RT synthase.";  
 RL Microbiology 140:2189-2197(1994).  
 RN [2]  
 RP SEQUENCE OF 250-438 FROM N.A.  
 RX MEDLINE=92115692; PubMed=1731323;  
 RA Bowen A.R., Chen-Wu J.L., Momany M., Young R., Szaniszlo P.J.,  
 RA Robbins P.W.;  
 RT "Classification of fungal chitin synthases.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:519-523(1992).  
 CC -I- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.  
 CC -I- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + {(1,4)-(N-acetyl-  
 CC beta-D-glucosaminyl)}(N) = UDP + {(1,4)-(N-acetyl-beta-D-  
 CC glucosaminyl)}(N+1).  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.  
 CC -I- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X77782; CAA54816.1; -.  
 DR EMBL; M82951; AAA33582.1; -.  
 DR PIR; B45189; B45189.  
 DR PIR; T47246; T47246.  
 DR InterPro; IPR004834; Chitin synth.  
 DR Pfam; PF01644; Chitin\_synth; 1.  
 DR ProDom; PD002998; Chitin\_synth; 1.  
 KW Transferase; Glycosyltransferase; Transmembrane; Cell wall;  
 KW Multigene family.  
 FT TRANSMEM 597 617 POTENTIAL.  
 FT TRANSMEM 634 654 POTENTIAL.  
 FT TRANSMEM 669 689 POTENTIAL.  
 FT TRANSMEM 713 733 POTENTIAL.  
 FT TRANSMEM 873 893 POTENTIAL.  
 SQ SEQUENCE 944 AA; 106816 MW; F70052AEE083060D CRC64;

Query Match 43.6%; Score 44; DB 1; Length 944;  
 Best Local Similarity 47.1%; Pred. No. 42;  
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 WIDPENGDSDYAPKFG 17  
 DB 917 WIKKKMGDADVKGFEG 933

RESULT 13  
 HV03\_MOUSE  
 ID HV03\_MOUSE STANDARD; PRT; 120 AA.  
 AC P01747;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 36-65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 42.6%; Score 43; DB 1; Length 120;
Best Local Similarity 47.1%; Pred. No. 6.2;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFCQ 17
Db 49 YINPGNGYTKYNEKFKG 65

RESULT 14
YIGB_ECOLI STANDARD; PRT; 238 AA.
AC P23306; P76757;
AT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein YIGB.
GN YIGB OR B3812 OR SF3890.
OS Escherichia coli, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=92358234; PubMed=1379743;
RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
RT "Analysis of the Escherichia coli genome: DNA sequence of the region
RT from 84.5 to 86.5 minutes.";
RL Science 257:771-778(1992).
RN [2]
RP REVISION TO 13.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=91072248; PubMed=2254268;
RA Colloms S.D., Sykora P., Szatmari G., Sherratt D.J.;
RT "Recombination at ColEI cer requires the Escherichia coli xerC gene
RT product, a member of the lambda integrase family of site-specific
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RT recombinases.";
RL J. Bacteriol. 172:6973-6980(1990).
RN [4]
RP SEQUENCE OF 183-238 FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=84272253; PubMed=6379604;
RA Finch P.W., Emerson P.T.;
RT "The nucleotide sequence of the uvrD gene of E. coli.";
RL Nucleic Acids Res. 12:5789-5799(1984).
RN [5]
RP SEQUENCE OF 183-238 FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=84169504; PubMed=6324092;
RA Easton A.M., Kushner S.R.;
RT "Transcription of the uvrd gene of Escherichia coli is controlled by
RT the lexa repressor and by attenuation.";
RL Nucleic Acids Res. 11:8625-8640(1983).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -I- SIMILARITY: TO E.COLI YIGB.
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CC -----
DR EMBL; M87049; AAA67608.1; -.
DR EMBL; AE000457; AAC76815.1; -.
DR EMBL; M38257; AAA24764.1; -.
DR EMBL; X00738; -, NOT_ANNOTATED_CDS.
DR EMBL; AE015395; AAN45326.1; -.
DR PIR; D37841; D37841.
DR Ecogene; EG11202; yigB.
DR InterPro; IPR006439; HAD_SF_A_V1.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
DR TIGRfams; TIGR01549; HAD-SF-IA-V1; 1.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 13 13 L -> V (IN REF. 1).
FT CONFLICT 200 200 S -> T (IN REF. 3).
SQ SEQUENCE 238 AA; 27122 MW; 9C1BDE710641E0D6 CRC64;

Query Match 42.6%; Score 43; DB 1; Length 238;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSD 8
Db 206 WIRPENGSD 213

RESULT 15
C772_SOLME STANDARD; PRT; 511 AA.
ID C772 SOLME
AC P37124;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 77A2 (EC 1.14.-.-) (CYPLXXVIIA2) (P-450EG5).
GN CYP77A2 OR CYP6G5.
```

OS Solanum melongena (Eggplant) (Aubergine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4111;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Sinsadoharanasu; TISSUE=Hypocotyl;  
RX MEDLINE=94139942; PubMed=8307197;

RA Toguri T., Tokugawa K.;  
RT "Cloning of eggplant hypocotyl cDNAs encoding cytochromes P450  
belonging to a novel family (CYP77).";  
RL FEBS Lett. 338:290-294(1994).

CC -1- SIMILARITY: Belongs to the cytochrome P450 family.

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DR EMBL; X71655; CAA50646.1; -.  
DR PIR; S41598; S41598.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR Pfam; PF00067; P450; 1.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Oxidoreductase; Monooxygenase; Heme; Multigene family.  
FT METAL 456 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
SQ SEQUENCE 511 AA; 58114 MW; 4B2A185D4DAFE023 CRC64;

Query Match 42.6%; Score 43; DB 1; Length 511;  
Best Local Similarity 43.8%; Pred.No. 31;  
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 WIDPENGSDSDYAPKQ 16  
| | | | | : | :  
Db 479 WADPENTRVDFTEKLE 494

Search completed: July 30, 2003, 09:45:09  
Job time : 3.65449 secs

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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 13.1595 Seconds  
(without alignments)  
333.364 Million cell updates/sec

Title: US-09-865-198-21  
Perfect score: 101  
Sequence: 1 WIDPENGSDYAPKFG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	75.2	468	11 Q99L31	Q99L31 mus musculu
2	60	59.4	497	4 Q8WY24	Q8WY24 homo sapien
3	59	58.4	614	4 Q96GA6	Q96GA6 homo sapien
4	58	57.4	109	11 Q9JL85	Q9JL85 mus musculu
5	57.5	56.9	150	4 Q9Y298	Q9Y298 homo sapien
6	56	55.4	125	4 Q9UL95	Q9UL95 homo sapien
7	55	54.5	119	4 Q9UL94	Q9UL94 homo sapien
8	55	54.5	480	11 Q8K0Z4	Q8K0Z4 mus musculu
9	54	53.5	481	11 Q8VCV5	Q8VCV5 mus musculu
10	51	50.5	124	4 Q9UL92	Q9UL92 homo sapien
11	51	50.5	300	4 Q8NCB9	Q8NCB9 homo sapien
12	51	50.5	350	4 Q96KB3	Q96KB3 homo sapien
13	51	50.5	350	4 Q8NBN1	Q8NBN1 homo sapien
14	51	50.5	350	11 Q8K1U4	Q8K1U4 mus musculu
15	51	50.5	350	11 Q8BVU5	Q8BVU5 mus musculu
16	50	49.5	500	4 Q9BRV0	Q9BRV0 homo sapien

17	48.5	48.0	474	11 Q8R3H6	Q8R3H6 mus musculu
18	48	47.5	102	11 Q9JL79	Q9JL79 mus musculu
19	48	47.5	147	11 Q925S3	Q925S3 mus musculu
20	48	47.5	323	10 Q9STS2	Q9STS2 arbidopsis
21	48	47.5	379	10 Q8RYD8	Q8RYD8 arbidopsis
22	48	47.5	403	10 Q8LSZ4	Q8LSZ4 arbidopsis
23	48	47.5	403	16 Q8Y1U7	Q8Y1U7 ralstonia s
24	48	47.5	484	11 Q9YLA6	Q9YLA6 mus musculu
25	48	47.5	526	17 Q8TJE3	Q8TJE3 methanosarc
26	48	47.5	643	16 Q8CXI6	Q8CXI6 oceanobacil
27	47	46.5	300	4 Q8NG26	Q8NG26 homo sapien
28	47	46.5	350	4 Q8NG25	Q8NG25 homo sapien
29	47	46.5	481	11 Q91WT1	Q91WT1 mus musculu
30	47	46.5	520	11 Q921T2	Q921T2 mus musculu
31	46	45.5	117	11 Q9QXE9	Q9QXE9 mus musculu
32	46	45.5	117	11 Q9QXF0	Q9QXF0 mus musculu
33	46	45.5	159	4 Q96QSO	Q96QSO homo sapien
34	46	45.5	666	2 Q8GAL9	Q8GAL9 athrobacte
35	46	45.5	1452	16 Q8PUJ7	Q8PUJ7 xanthomonas
36	46	45.5	1737	11 Q9JL04	Q9JL04 rattus norv
37	45.5	45.0	118	11 Q9ZIC4	Q9ZIC4 mus musculu
38	45	44.6	138	2 Q9FBN0	Q9FBN0 carboxydoth
39	45	44.6	168	17 Q27394	Q27394 methanobact
40	45	44.6	179	10 Q9XI82	Q9XI82 arbidopsis
41	45	44.6	318	10 Q9LME3	Q9LME3 arbidopsis
42	45	44.6	348	5 Q16334	Q16334 caenorhabdi
43	45	44.6	1289	10 Q8VYU2	Q8VYU2 vulgna ungui
44	44.5	44.1	462	16 Q8Y074	Q8Y074 ralstonia s
45	44	43.6	219	16 Q34915	Q34915 bacillus su

#### ALIGNMENTS

##### RESULT 1

Q99L31 PRELIMINARY; PRT; 468 AA.  
ID Q99L31  
AC Q99L31;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Similar to RIKEN CDNA 181066009 gene.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC003878; AA03878.1; -.  
DR HSSP; P01842; 7FAB.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; ig; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match Best Local Similarity 75.2%; Score 76; DB 11; Length 468;  
Matches 12; Conservativity 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 16  
Db 69 WIDPEDEGTYAPKFG 84

RESULT 2  
Q8WY24 PRELIMINARY; PRT; 497 AA.  
ID Q8WY24



AC Q8WY24;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE SNC66 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;  
RT "Identification and characterization of SNC66, a Ig-like gene which is  
RT down-regulated in colorectal cancer."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF283666; AAL36987.1; -  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 59.4%; Score 60; DB 4; Length 497;  
Best Local Similarity 47.1%; Pred. No. 0.48;  
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17  
|:::|:::|:::|  
Db 69 WMNPQTGNTTEFAKFOG 85

RESULT 3  
Q96GA6 PRELIMINARY; PRT; 614 AA.  
AC Q96GA6;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC009851; AAH09851.1; -  
DR InterPro; IPR000005; HTHARAC.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 58.4%; Score 59; DB 4; Length 614;  
Best Local Similarity 62.5%; Pred. No. 0.87;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 16  
|:::|:::|:::|  
Db 69 WITPENGNTNYAQKFOG 84

RESULT 4  
Q9JL85 PRELIMINARY; PRT; 109 AA.  
AC Q9JL85;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Anti-myosin immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Walkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of  
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
RT with cardiac myosin."  
RL Infect. Immun. 68:5803-5808(2000).  
DR EMBL; AF206021; AAF69319.1; -  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 1  
FT NON\_TER 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 57.4%; Score 58; DB 11; Length 109;  
Best Local Similarity 68.8%; Pred. No. 0.18;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPENGSDYAPKFOG 17  
|:::|:::|:::|  
Db 43 IDPATGHSKYDPKFOG 58

RESULT 5  
Q9Y298 PRELIMINARY; PRT; 150 AA.  
AC Q9Y298;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE IGG VH protein precursor (Fragment).  
GN IGG VH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98322155; PubMed=9657749;  
RA Jacquemin M.G., Vander Elst L.P.L.;  
RT "Mechanism and kinetics of factor VIII inactivation: study with an  
RT IgG4 monoclonal antibody derived from a hemophilia A patient with  
RT inhibitor."  
RL Blood 92:496-506(1998).  
DR EMBL; AJ224083; CAA11829.1; -  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Signal.

```
FT SIGNAL 1 19 POTENTIAL.
RT NON TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match
Best Local Similarity 56.9%; Score 57.5; DB 4; Length 150;
Matches 11; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

Qy 1 WI--DPENGSDDYAPKFOG 17
   ||:||||:|:|:|:|
Db 66 WVGSPDESGESITYAREFOG 85

RESULT 6
Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match
Best Local Similarity 55.4%; Score 56; DB 4; Length 125;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WIDPENGSDDYAPKFOG 17
   ||:|:|:|:|:|:|
Db 50 WINPNSGCTNYAQKVOG 66

RESULT 7
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
```

```
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match
Best Local Similarity 54.5%; Score 55; DB 4; Length 119;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WIDPENGSDDYAPKFOG 17
   ||:|:|:|:|:|:|
Db 50 WINPNSWTTNYAQKFOG 66

RESULT 8
Q8K024 PRELIMINARY; PRT; 480 AA.
AC Q8K024;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to expressed sequence A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029188; AAH29188.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
SQ SEQUENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;

Query Match
Best Local Similarity 54.5%; Score 55; DB 11; Length 480;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WIDPENGSDDYAPKFOG 17
   ||:|:|:|:|:|:|
Db 69 WISPGDGSSEYNEKFKG 85

RESULT 9
Q8VCV5 PRELIMINARY; PRT; 481 AA.
AC Q8VCV5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 52.3 kDa protein.
OS Mus musculus (Mouse).;
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast tumor;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC018455; AAH18455.1; -  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 53.5%; Score 54; DB 11; Length 481;  
Best Local Similarity 58.8%; Pred. No. 4;  
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFG 17  
Db 69 YIDPYNGSSYNQKFKG 85

## RESULT 10

O9UL92 PRELIMINARY; PRT; 124 AA.

AC Q9UL92;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035022; AAD56258.1; -  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
FT NON\_TER 1  
FT NON\_TER 124  
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 50.5%; Score 51; DB 4; Length 124;  
Best Local Similarity 56.2%; Pred. No. 2.6;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 IDPENGSDYAPKFG 17  
Db 51 INPSGGSTYAPKFG 66

## RESULT 11

O8NCB9 PRELIMINARY; PRT; 300 AA.

AC O8NCB9;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical protein FLJ90364.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,  
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,  
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,  
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;  
RT "NEDO human cDNA sequencing project.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK074845; BAC11239.1; -  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 300 AA; 33776 MW; 531993C757A82E49 CRC64;

Query Match 50.5%; Score 51; DB 4; Length 300;  
Best Local Similarity 46.7%; Pred. No. 7;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKF 15  
Db 60 WADPQISESNFSPKF 74

## RESULT 12

O96KB3 PRELIMINARY; PRT; 350 AA.

AC O96KB3;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Hypothetical protein FLJ14389.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
RA Ninomiya K., Iwayanagi T.;  
RT "NEDO human cDNA sequencing project.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK027295; BAB55021.1; -  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 350 AA; 39042 MW; 8BE1A31ECFB343D CRC64;

Query Match 50.5%; Score 51; DB 4; Length 350;  
Best Local Similarity 46.7%; Pred. No. 8.3;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKF 15  
Db 110 WADPQISESNFSPKF 124

## RESULT 13

Q8NBN1 PRELIMINARY; PRT; 350 AA.  
AC Q8NBN1;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Hypothetical protein NT2RP2002907.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBT\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,  
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,  
RA Nagahari K., Sugano S., Isogai T.;  
RT "HRI human cDNA sequencing project.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK075408; BAC11601.1;  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 350 AA; 39095 MW; 2EB6A14B9BE83420 CRC64;

Query Match 50.5%; Score 51; DB 4; Length 350;  
Best Local Similarity 46.7%; Pred. No. 8.3;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKF 15  
| | | : : : : | | |  
Db 110 WADPQISESNFSPKF 124

## RESULT 14

Q8K1J4 PRELIMINARY; PRT; 350 AA.  
ID Q8K1J4;  
AC Q8K1J4;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Similar to nudix (Nucleoside diphosphate linked motley X)-type motif  
DE 9.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBT\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC033921; AAH33921.1;  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
SQ SEQUENCE 350 AA; 38623 MW; 6FD9371307AB3366 CRC64;

Query Match 50.5%; Score 51; DB 11; Length 350;  
Best Local Similarity 46.7%; Pred. No. 8.3;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKF 15  
| | | : : : : | | |  
Db 110 WADPQISESNFSPKF 124

## RESULT 15

Q8BVU5 PRELIMINARY; PRT; 350 AA.  
ID Q8BVU5;  
AC Q8BVU5;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Nudix.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBT\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
DR EMBL; AK076500; BAC36366.1;  
SQ SEQUENCE 350 AA; 38604 MW; EDD9371307AB3373 CRC64;

Query Match 50.5%; Score 51; DB 11; Length 350;  
Best Local Similarity 46.7%; Pred. No. 8.3;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKF 15  
| | | : : : : | | |  
Db 110 WADPQISESNFSPKF 124

Search completed: July 30, 2003, 09:42:46  
Job time : 15.2706 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 17 Seconds  
(without alignments)  
158.727 Million cell updates/sec

Title: US-09-865-198-21  
Perfect score: 101  
Sequence: 1 WIDPENGSDYAPKFG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*  
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6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\*  
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20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	17	22	AAE13138 Humanised antibody
2	101	100.0	17	22	AAB82704 VEGF antagonist an
3	101	100.0	17	23	AAU74416 Heavy chain comple
4	101	100.0	17	24	ABJ26728 VEGF binding relat
5	101	100.0	117	22	AAE13143 Humanised antibody
6	101	100.0	117	22	AAB82709 VEGF antagonist an
7	101	100.0	117	23	AAU74417 Antigen-binding pr
8	101	100.0	117	24	ABJ26729 VEGF binding relat
9	101	100.0	135	23	AAE25965 Mouse anti-KDR p1C

10	101	100.0	136	22	AAE13145	Chimeric p1C11 hea
11	101	100.0	136	22	AAB82701	VEGF antagonist an
12	101	100.0	136	23	AAE28916	c-p1C11 vector hea
13	101	100.0	238	23	AAE25961	KDR binding immuno
14	101	100.0	238	23	AAE25963	KDR binding immuno
15	101	100.0	238	23	AAU74420	Antigen-binding pr
16	101	100.0	238	23	AAU74420	VEGF binding relat
17	94	93.1	17	20	AAW89162	Anti-p53 monoclonal
18	94	93.1	17	21	AAV97230	Complementary dete
19	94	93.1	17	23	AAE25950	Mouse anti-KDR p1C
20	94	93.1	17	23	AAU74407	Heavy chain comple
21	94	93.1	17	24	ABJ26719	VEGF binding relat
22	94	93.1	20	21	AAV70794	Anti-anti-p53 PA
23	94	93.1	112	20	AAW89173	Murine anti-p53 mo
24	94	93.1	116	21	AAV70787	Murine anti-p53 mo
25	94	93.1	117	21	AAV97235	Variable heavy cha
26	94	93.1	117	23	AAE25955	Mouse anti-KDR p1C
27	94	93.1	117	23	AAU74412	Antigen-binding pr
28	94	93.1	117	24	ABJ26724	VEGF binding relat
29	94	93.1	122	20	AAV39531	Humanised Murine C
30	94	93.1	124	15	AAR60565	Anti-carcinoembryo
31	94	93.1	124	15	AAR60566	Anti-carcinoembryo
32	94	93.1	124	20	AAV39528	Murine COL1 VH cha
33	94	93.1	124	20	AAV39530	Humanised Murine C
34	94	93.1	124	20	AAV39536	Humanised Murine C
35	94	93.1	124	20	AAV39537	Humanised Murine C
36	94	93.1	124	20	AAV39538	Humanised Murine C
37	94	93.1	124	20	AAV39539	Humanised Murine C
38	94	93.1	124	20	AAV39540	Humanised Murine C
39	94	93.1	124	20	AAV39541	Humanised Murine C
40	94	93.1	124	20	AAV39542	Humanised Murine C
41	94	93.1	124	20	AAV39543	Humanised Murine C
42	94	93.1	124	23	ABB83941	Mouse monoclonal a
43	94	93.1	124	23	ABB83943	Humanised mouse mo
44	94	93.1	124	23	ABB83947	Expressed humanise
45	94	93.1	124	23	AAU76632	Murine Col-1(CEA a

ALIGNMENTS

RESULT 1  
ID AAE13138 standard; peptide; 17 AA.  
AAE13138;  
AC AAE13138;  
XX  
DT 28-JAN-2002 (first entry)  
XX  
DE Humanised antibody murine heavy chain hypervariable region (VH) CDR2.  
XX  
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytosolic; heavy chain hypervariable region; VH; myelocytic leukaemia;  
KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;  
KW Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.  
XX  
OS Mus sp.  
XX  
PN WO200174296-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US10504.  
XX  
PR 31-MAR-2000; 2000US-0540770.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Witte L, Rafil S;  
XX  
DR WPI: 2001-662942/76.  
DR N-PSDB; AAD21664.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with  
PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
XX Claim 8; Page 14; 68pp; English.  
XX  
CC The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains mouse complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised  
CC antibody murine heavy chain hypervariable region (VH) CDR-2 used in the  
CC exemplification of the invention.  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 101; DB 22; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.3e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 WIDPENGSDSYAPKFG 17  
Db 1 WIDPENGSDSYAPKFG 17  
RESULT 2  
AAB82704 ID AAB82704 standard; Peptide; 17 AA.  
XX  
AC AAB82704;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE VEGF antagonist antibody IMC-1C11 VH CDR-2.  
XX  
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; heavy chain; CDR;  
KW complementarity determining region.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
PN WO200154723-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 29-JAN-2001; 2001WO-US02839.  
XX  
PR 28-JAN-2000; 2000US-0178791.  
PR 31-MAR-2000; 2000US-0539692.  
XX  
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Kerbel R;  
XX  
DR WPI; 2001-514531/56.  
XX  
PT Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a

PT Chemotherapeutic agent -  
XX  
PS Disclosure; Page 37; 42pp; English.  
XX  
CC The present sequence is that of complementarity determining region  
CC 2 of the heavy chain variable region (see also AAB82701) of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 101; DB 22; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.3e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 WIDPENGSDSYAPKFG 17  
Db 1 WIDPENGSDSYAPKFG 17  
RESULT 3  
AAU74416 ID AAU74416 standard; peptide; 17 AA.  
XX  
AC AAU74416;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Heavy chain complementarity determining region H2 (CDRH2) version #2.  
XX  
XX Complementarity determining region; CDR; CDRH2; antigen; cytostatic;  
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;  
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;  
KW antibody heavy chain variable domain.  
XX  
OS SMus sp.  
XX  
PN WO200190192-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US16924.  
XX  
PR 24-MAY-2000; 2000US-206749P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2002-106189/14.  
DR N-PSDB; AAS20287.  
XX  
PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides -  
XX  
PS Claim 59; Page 60; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (C<sub>L</sub> domain), and P2 has an antigen-binding  
CC site located to the N terminus of the C<sub>H</sub>1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This peptide sequence represents the heavy chain variable domain  
CC complementarity determining region H2 (CDRH2) version #2 incorporated  
CC into an antigen-binding protein described in the method of the invention.  
XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 101; DB 23; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.3e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFG 17  
|||  
Db 1 WIDPENGSDYAPKFG 17

## RESULT 4

ABJ26728  
ID ABJ26728 standard; Peptide; 17 AA.

XX AC ABJ26728;

XX DT 01-MAY-2003 (first entry)

XX DE VEGF binding related peptide SEQ ID No 21.

XX KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.

XX OS Mus sp.

XX PN WO2003002144-A1.

XX PD 09-JAN-2003.

XX PF 26-JUN-2002; 2002WO-US20332.

XX PR 26-JUN-2001; 2001US-301299P.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;

XX DR WPI; 2003-201468/19.

XX PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -

XX PS Claim 10; Page 53; 98pp; English.

XX CC The invention relates to a novel antibody having a first antigen binding

CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse peptide relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 101; DB 24; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.3e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFG 17  
|||  
Db 1 WIDPENGSDYAPKFG 17

## RESULT 5

AAE13143  
ID AAE13143 standard; Protein; 117 AA.

XX AC AAE13143;

XX DT 28-JAN-2002 (first entry)

XX DE Humanised antibody heavy chain fragment.

XX KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytosstatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;  
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;  
KW human; chimeric.

XX OS Chimeric - Homo sapiens.

XX OS Chimeric - Mus sp.

XX PN WO200174296-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US10504.

XX PR 31-MAR-2000; 2000US-0540770.

XX PA (IMCL-) IMCLONE SYSTEMS INC.  
PA (CORR ) CORNELL RES FOUND INC.

XX PI Witte L, Rafii S;

XX DR WPI; 2001-662942/76.

XX DR N-PSDB; AAD21669.

XX PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with  
PT an antagonist of a vascular endothelial growth factor receptor -

XX PS Claim 8; Page 15; 68pp; English.

XX CC The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains mouse complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised

CC antibody heavy chain frgment used in the exemplification of the  
CC invention.  
XX  
SQ Sequence 117 AA;  
Query Match 100.0%; Score 101; DB 22; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WIDPENGSDYAPKFOG 17  
|||||  
Db 50 WIDPENGSDYAPKFOG 66  
RESULT 6  
AAB82709  
ID AAB82709 standard; Protein; 117 AA.  
XX  
AC AAB82709;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE VEGF antagonist antibody IMC-1C11 heavy chain variable region.  
XX  
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; heavy chain.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 26.35  
FT /label= CDR-H1  
FT /note= "complementarity determining region 1"  
FT 50.66  
FT /label= CDR-H2  
FT /note= "complementarity determining region 2"  
FT 99.106  
FT Region /label= CDR-H3  
FT /note= "complementarity determining region 3"  
XX  
PN WO200154723-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 29-JAN-2001; 2001WO-US02839.  
XX  
PR 28-JAN-2000; 2000US-0178791.  
PR 31-MAR-2000; 2000US-0539692.  
XX  
PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Kerbel R;  
XX  
DR WPI; 2001-514531/56.  
DR N-PSDB; AAH26405.  
XX  
PT Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX  
PS Disclosure; Page 38; 42pp; English.  
XX  
CC The present sequence is that of the heavy chain variable region of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,

CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
SQ Sequence 117 AA;  
Query Match 100.0%; Score 101; DB 22; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WIDPENGSDYAPKFOG 17  
|||||  
Db 50 WIDPENGSDYAPKFOG 66  
RESULT 7  
AAU74417  
ID AAU74417 standard; peptide; 117 AA.  
XX  
AC AAU74417;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Antigen-binding protein heavy chain variable domain (VH) #2.  
XX  
KW Antigen-binding protein; antibody heavy chain variable domain;  
KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;  
KW cell proliferation inhibitor.  
XX  
OS Mus sp.  
XX  
PN WO200190192-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US16924.  
XX  
PR 24-MAY-2000; 2000US-206749P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2002-106189/14.  
DR N-PSDB; AAS20288.  
XX  
PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides -  
XX  
PS Claim 61; Page 60; 64pp; English.  
XX  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (CL domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;



CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This sequence represents a heavy chain variable domain (VH) incorporated  
CC into Fv, an engineered protein containing a heavy chain variable domain  
CC and a light chain variable domain in one polypeptide chain, described in  
CC the method of the invention.

CC XX Sequence 117 AA;

Query Match 100.0%; Score 101; DB 23; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17  
|||  
Db 50 WIDPENGSDYAPKFG 66

RESULT 8

ABJ26729  
ID ABJ26729 standard; Protein; 117 AA.

AC ABJ26729;

DT 01-MAY-2003 (first entry)

DE VEGF binding related protein SEQ ID No 22.

XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;

KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.

XX Mus sp.

PN WO2003002144-A1.

PD 09-JAN-2003.

PF 26-JUN-2002; 2002WO-US20332.

PR 26-JUN-2001; 2001US-301299P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

DR WPI; 2003-201468/19.

DR N-PSDB; ABT23307.

PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -

PS Disclosure; Page 53; 98pp; English.

XX The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic

CC methods. This sequence represents a mouse protein relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.

CC XX Sequence 117 AA;

Query Match 100.0%; Score 101; DB 24; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17  
|||  
Db 50 WIDPENGSDYAPKFG 66

RESULT 9

AAE25965  
ID AAE25965 standard; Protein; 135 AA.

AC AAE25965;

DT 15-NOV-2002 (first entry)

DE Mouse anti-KDR p1C11 scFv antibody VH region #2.

XX Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
KW p1C11; scFv antibody.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1.19  
FT /label= Signal-peptide

FT Protein 20.135  
FT /note= "Mouse p1C11 scFv antibody mature VH region"

FT Region 45.54  
FT /note= "Heavy chain complementarity

FT Region 69.85  
FT /note= "Heavy chain complementarity

FT Region 118.125  
FT /note= "Heavy chain complementarity

FT Region determining region 3 (CDR-H3)"

PN US2002064528-A1.

PD 30-MAY-2002.

PF 12-OCT-2001; 2001US-0976787.

PR 28-JAN-2000; 2000US-0493539.

PA (ZHUZ/) ZHU Z.  
PA (WITT/) WITTE L.

PI Zhu Z, Witte L;

DR WPI; 2002-589175/63.

DR N-PSDB; AAD42832.

PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR -

PS Disclosure; Fig 4; 34pp; English.

XX The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises



CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR pIC11 scFv antibody  
CC heavy chain variable region (VH).  
XX  
SQ Sequence 135 AA;  
Query Match 100.0%; Score 101; DB 23; Length 135;  
Best Local Similarity 100.0%; Pred. No. 4.9e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WIDPENGSDYAPKFOG 17  
|||||  
Db 69 WIDPENGSDYAPKFOG 85  
RESULT 10  
AAE13145  
ID AAE13145 standard; Protein; 136 AA.  
XX  
AC AAE13145;  
XX  
DT 28-JAN-2002 (first entry)  
XX  
DE Chimeric pIC11 heavy chain fragment.  
XX  
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytoskeletal; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;  
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;  
KW human; pIC11 vector.  
XX  
OS Chimeric - Homo sapiens.  
OS Chimeric - Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
/label= Leader\_peptide  
FT Protein 20..136  
/note= "Mature chimeric pIC11 heavy chain fragment"  
FT Region 45..54  
/label= CDR\_H1  
FT Region 69..85  
/label= CDR\_H2  
FT Misc-difference 84  
/note= "Residue 'O' is present at this location in the  
FT sequence shown in fig-11 of the specification"  
FT Misc-difference 101  
/note= "Residue 'O' is present at this location in the  
FT sequence shown in fig-11 of the specification"  
FT Region 119..125  
/label= CDR\_H3  
XX  
PN WO200174296-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US10504.  
XX  
PR 31-MAR-2000; 2000US-0540770.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Witte L, Rafii S;  
XX  
DR WPI; 2001-662942/76.  
DR N-PSDB; AAD21682.  
XX  
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with  
PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
PS Example 3; Fig 11; 68pp; English.

XX  
CC The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised region  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains mouse complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric  
CC pIC11 heavy chain fragment which is used for the construction of chimeric  
CC pIC11 IgG expression vector. Chimeric pIC11 heavy chain contains cloned  
CC domain (CH).  
XX  
SQ Sequence 136 AA;  
Query Match 100.0%; Score 101; DB 22; Length 136;  
Best Local Similarity 100.0%; Pred. No. 5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WIDPENGSDYAPKFOG 17  
|||||  
Db 69 WIDPENGSDYAPKFOG 85  
RESULT 11  
AAB82701  
ID AAB82701 standard; Protein; 136 AA.  
XX  
AC AAB82701;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE VEGF antagonist antibody IMC-1C11 heavy chain variable region  
XX  
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; heavy chain.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
/label= Signal\_peptide  
FT Protein 20..136  
/label= Mature\_protein  
FT Region 45..54  
/label= CDR-H1  
FT Region 59..85  
/note= "complementarity determining region 1"  
FT Region 118..125  
/label= CDR-H2  
FT Region 118..125  
/label= CDR-H3  
FT /note= "complementarity determining region 3"  
XX  
PN WO200154723-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 29-JAN-2001; 2001WO-US02839.  
XX  
PR 28-JAN-2000; 2000US-0178791.  
PR 31-MAR-2000; 2000US-0539692.  
XX

PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Kerbel R;  
XX  
DR WPI; 2001-514531/56.  
DR N-PSDB; AAH26413.  
XX  
PT Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent  
XX  
PS Disclosure; Fig 1; 42pp; English.  
XX  
CC The present sequence is that of the heavy chain variable region of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimizing or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
SQ Sequence 136 AA;  
OY  
Query Match 100.0%; Score 101; DB 22; Length 136;  
Best Local Similarity 100.0%; Pred. No. 5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WIDPENGSDYAPKFOG 17  
|||  
Db 69 WIDPENGSDYAPKFOG 85

RESULT 12  
AAE28916  
ID AAE28916 standard; Protein; 136 AA.  
XX  
AC AAE28916;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE c-p1C11 vector heavy chain (VH) protein.  
XX  
KW Human; tumour; vascular endothelial growth factor receptor; metastasis;  
KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;  
KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; VH.  
XX  
OS Chimeric - Unidentified.  
OS Chimeric - Homo sapiens.  
XX  
FH Key  
FT Region 1..19 Location/Qualifiers  
FT /note= "Leader peptide"  
FT Region 20..136  
FT /note= "Human heavy chain constant region"  
FT 45..54  
FT /note= "CDR1"  
FT 69..85  
FT /note= "CDR2"  
FT 118..125  
FT Region

FT /note= "CDR3"  
XX  
PN WO200270008-A1.  
XX  
PD 12-SEP-2002.  
XX  
PF 04-MAR-2002; 2002WO-US06762.  
XX  
PR 02-MAR-2001; 2001US-0798689.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
PA (ROCK/) ROCKWELL P.  
PA (GOLD/) GOLDSTEIN N I.  
XX  
DR WPI; 2002-691738/74.  
DR N-PSDB; AAD46315.  
XX  
PT Inhibiting tumor growth in humans involves administering vascular  
PT endothelial growth factor receptor antagonists in combination with  
PT radiation, chemotherapeutic agents, or epidermal growth factor receptor  
PT antagonists -  
XX  
PS Example 9; Fig 19; 151pp; English.  
XX  
CC The invention relates to a method of inhibiting tumour growth which  
CC involves administering, vascular endothelial growth factor receptor  
CC (VEGFR) antagonists in combination with radiation, chemotherapeutic  
CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method  
CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.  
CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,  
CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,  
CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over  
CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour  
CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.  
CC It is preferably useful for treating subjects with both solid tumours,  
CC preferably high vascular tumours and non-solid tumours. The inhibition  
CC or reduction of tumour growth includes prevention or inhibition of the  
CC progression of tumour, including cancerous and non-cancerous tumours,  
CC where the progression of tumours includes the invasiveness, metastasis,  
CC recurrence and increase in size of the tumour. The present sequence is  
CC c-p1C11 vector containing human heavy chain (VH) protein. This sequence  
CC is used to illustrate the method of the invention.  
XX  
SQ Sequence 136 AA;  
OY  
Query Match 100.0%; Score 101; DB 23; Length 136;  
Best Local Similarity 100.0%; Pred. No. 5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WIDPENGSDYAPKFOG 17  
|||  
Db 69 WIDPENGSDYAPKFOG 85

RESULT 13  
AAE25961  
ID AAE25961 standard; Protein; 238 AA.  
XX  
AC AAE25961;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE KDR binding immunoglobulin related mouse protein #2.  
XX  
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
KW p1C11; scFv antibody.  
XX  
OS Mus sp.  
OS  
XX  
PN US2002064528-A1.  
XX

PD 30-MAY-2002.  
XX  
PF 12-OCT-2001; 2001US-0976787.  
XX  
PR 28-JAN-2000; 2000US-0493539.  
XX  
PA (ZHUZ/) ZHU Z.  
XX (WITT/) WITTE L.  
XX  
PI Zhu Z, Witte L;  
XX  
DR WPI; 2002-589175/63.  
XX N-PSDB; AAD42825.  
XX  
PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR  
XX  
PS Disclosure; Page 17-18; 34pp; English.  
XX  
CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (Flk)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is KDR binding immunoglobulin related  
CC mouse protein.  
XX  
SQ Sequence 238 AA;  
XX  
Query Match 100.0%; Score 101; DB 23; Length 238;  
Best Local Similarity 100.0%; Pred. No. 9e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WIDPENGSDSDYAPKFOG 17  
Db 50 WIDPENGSDSDYAPKFOG 66  
RESULT 14  
AAE25963  
ID AAE25963 standard; Protein; 238 AA.  
XX  
AC AAE25963;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE KDR binding immunoglobulin related mouse protein #3.  
XX  
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; Flk-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
KW pIC11; scFv antibody.  
XX  
OS Mus sp.  
XX  
PN US2002064528-A1.  
XX  
PD 30-MAY-2002.  
XX  
PF 12-OCT-2001; 2001US-0976787.  
XX  
PR 28-JAN-2000; 2000US-0493539.  
XX  
PA (ZHUZ/) ZHU Z.  
XX (WITT/) WITTE L.  
XX  
PI Zhu Z, Witte L;  
XX  
DR WPI; 2002-589175/63.  
XX

PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR  
XX  
PS Disclosure; Page 17-18; 34pp; English.  
XX  
CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (Flk)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is KDR binding immunoglobulin related  
CC mouse protein.  
XX  
SQ Sequence 238 AA;  
XX  
Query Match 100.0%; Score 101; DB 23; Length 238;  
Best Local Similarity 100.0%; Pred. No. 9e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WIDPENGSDSDYAPKFOG 17  
Db 50 WIDPENGSDSDYAPKFOG 66  
RESULT 15  
AAU74420  
ID AAU74420 standard; Protein; 238 AA.  
XX  
AC AAU74420;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Antigen-binding protein, single chain variable fragment version #2.  
XX  
KW Antigen-binding protein; single chain variable fragment; scFv; antigen;  
KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;  
KW cell proliferation inhibitor.  
XX  
OS Mus sp.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT 1..117  
FT Region /label= VH  
FT /note= "Heavy chain variable domain. Specifically  
FT claimed in claim 61"  
FT  
FT Region 118..132  
FT /label= Linker  
FT /note= "15 amino acid linker joins the VH and VL  
FT regions of the single chain variable fragment  
FT protein. Encoded by AAS20285"  
FT  
FT Region 133..238  
FT /label= VL  
FT /note= "Light chain variable domain. Specifically  
FT claimed in claim 61"  
FT  
PN WO200190192-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US16924.  
XX  
PR 24-MAY-2000; 2000US-206749P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2002-106189/14.  
XX

XX New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides

PS Claim 63; Page 62-63; 64pp; English.

XX  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (C<sub>L</sub> domain), and P2 has an antigen-binding  
CC site located to the N terminus of the C<sub>H</sub>1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This is the amino acid sequence of a single chain variable fragment  
CC (scFv), an engineered protein containing a variable light and variable  
CC heavy domain on one polypeptide, described in the method of the  
CC invention.

XX  
SQ Sequence 238 AA;

Query Match 100.0%; Score 101; DB 23; Length 238;  
Best Local Similarity 100.0%; Pred. No. 9e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFOG 17  
|||  
Db 50 WIDPENGSDYAPKFOG 66

Search completed: July 30, 2003, 09:36:48  
Job time : 18 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: July 30, 2003, 09:42:53 ; Search time 20.897 Seconds  
(without alignments)  
96.613 Million cell updates/sec

Title: US-09-865-198-21  
Perfect score: 101  
Sequence: 1 WIDPENGSDSDYAPKFGQ 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
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- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	17	9 US-09-976-787-22	Sequence 22, Appli
2	101	100.0	17	10 US-09-865-198-21	Sequence 21, Appli
3	101	100.0	117	9 US-09-976-787-23	Sequence 23, Appli
4	101	100.0	117	10 US-09-865-198-22	Sequence 22, Appli
5	101	100.0	117	11 US-09-798-689-7	Sequence 7, Appli
6	101	100.0	238	9 US-09-976-787-29	Sequence 29, Appli
7	101	100.0	238	10 US-09-865-198-28	Sequence 28, Appli
8	101	100.0	238	11 US-09-798-689-21	Sequence 21, Appli
9	95	94.1	16	11 US-09-798-689-2	Sequence 2, Appli
10	94	93.1	17	9 US-09-976-787-2	Sequence 2, Appli
11	94	93.1	17	10 US-09-865-198-2	Sequence 2, Appli
12	94	93.1	17	14 US-10-032-482-18	Sequence 18, Appli
13	94	93.1	112	14 US-10-032-482-7	Sequence 7, Appli
14	94	93.1	117	9 US-09-976-787-7	Sequence 7, Appli
15	94	93.1	117	10 US-09-865-198-7	Sequence 7, Appli

	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

RESULT 1  
US-09-976-787-22  
Sequence 22, Application US/09976787  
Patent No. US20020064528A1  
GENERAL INFORMATION:  
APPLICANT: Zhu, Zhenping  
APPLICANT: Witte, Larry  
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
FILE REFERENCE: 11245/46505  
CURRENT APPLICATION NUMBER: US/09/976, 787  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 09/493, 539  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/117, 726  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 22  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Mouse  
US-09-976-787-22

Query Match 100.0%; Score 101; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.4e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDSDYAPKFGQ 17  
|||||  
DB 1 WIDPENGSDSDYAPKFGQ 17

RESULT 2  
US-09-865-198-21  
Sequence 21, Application US/09865198  
Patent No. US20020103345A1  
GENERAL INFORMATION:  
APPLICANT: Zhu, Zhenping

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; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-21

Query Match      100.0%; Score 101; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDSYAPKFOG 17
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Db      50 WIDPENGSDSYAPKFOG 66

RESULT 3
US-09-976-787-23
; Sequence 23, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23

Query Match      100.0%; Score 101; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDSYAPKFOG 17
      |||||||
Db      50 WIDPENGSDSYAPKFOG 66

RESULT 4
US-09-865-198-22
; Sequence 22, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
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; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22

Query Match      100.0%; Score 101; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDSYAPKFOG 17
      |||||||
Db      50 WIDPENGSDSYAPKFOG 66

RESULT 5
US-09-798-689-7
; Sequence 7, Application US/09798689
; Publication No. US20030103973A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-7

Query Match      100.0%; Score 101; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDSYAPKFOG 17
      |||||||
Db      50 WIDPENGSDSYAPKFOG 66

RESULT 6
US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
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TYPE: PRT  
ORGANISM: Mouse  
US-09-976-787-29

Query Match 100.0%; Score 101; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17  
|||||  
Db 50 WIDPENGSDYAPKFG 66

RESULT 7  
US-09-865-198-28

Sequence 28, Application US/09865198  
Patent No. US20020103345A1  
GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping  
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods  
FILE REFERENCE: 11245/47102

CURRENT APPLICATION NUMBER: US/09/865,198  
CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 60/206,749

PRIOR FILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 34

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 28

LENGTH: 238

TYPE: PRT

ORGANISM: Mouse

US-09-865-198-28

Query Match 100.0%; Score 101; DB 10; Length 238;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17  
|||||  
Db 50 WIDPENGSDYAPKFG 66

RESULT 8

US-09-798-689-21

Sequence 21, Application US/09798689

Patent No. US20030103973A1

GENERAL INFORMATION:

APPLICANT: Rockwell, Patricia

APPLICANT: Goldstein, Neil I.

TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists

FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP

CURRENT APPLICATION NUMBER: US/09/798,689

CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 09/401,163

PRIOR FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: 08/967,113

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 08/706,804

PRIOR FILING DATE: 1996-09-03

PRIOR APPLICATION NUMBER: 08/476,533

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 08/326,552

PRIOR FILING DATE: 1994-10-20

PRIOR APPLICATION NUMBER: 08/196,041

PRIOR FILING DATE: 1994-02-10

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 21

LENGTH: 238

TYPE: PRT

ORGANISM: Mouse

US-09-798-689-21

Query Match 100.0%; Score 101; DB 11; Length 238;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 17  
|||||  
Db 50 WIDPENGSDYAPKFG 66

RESULT 9

US-09-798-689-2

Sequence 2, Application US/09798689

Patent No. US20030103973A1

GENERAL INFORMATION:

APPLICANT: Rockwell, Patricia

APPLICANT: Goldstein, Neil I.

TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists

FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP

CURRENT APPLICATION NUMBER: US/09/798,689

CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 09/401,163

PRIOR FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: 08/967,113

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 08/706,804

PRIOR FILING DATE: 1996-09-03

PRIOR APPLICATION NUMBER: 08/476,533

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 08/326,552

PRIOR FILING DATE: 1994-10-20

PRIOR APPLICATION NUMBER: 08/196,041

PRIOR FILING DATE: 1994-02-10

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 16

TYPE: PRT

ORGANISM: Mouse

US-09-798-689-2

Query Match 94.1%; Score 95; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.7e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFG 16  
|||||  
Db 1 WIDPENGSDYAPKFG 16

RESULT 10

US-09-976-787-2

Sequence 2, Application US/09976787

Patent No. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping

APPLICANT: Witte, Larry

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245/46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 09/493,539

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 2

LENGTH: 17

TYPE: PRT

ORGANISM: Mus musculus

US-09-976-787-2

Query Match 93.1%; Score 94; DB 9; Length 17;  
Best Local Similarity 94.1%; Pred. No. 4.2e-08;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17  
DB 1 WIDPENGDSGYAPKFOG 17

RESULT 11

US-09-865-198-2  
; Sequence 2, Application US/09865198  
; Patent No. US2002010345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho  
; TITLE OF INVENTION: Production  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; PRIOR FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-2

Query Match 93.1%; Score 94; DB 10; Length 17;  
Best Local Similarity 94.1%; Pred. No. 4.2e-08;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17  
DB 1 WIDPENGDSGYAPKFOG 17

RESULT 12

US-10-032-482-18  
; Sequence 18, Application US/10032482  
; Publication No. US20020197270A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Irwin  
; APPLICANT: ROTTER, Varda  
; APPLICANT: Wolkowicz, Roland  
; APPLICANT: RUIZ, Pedro  
; APPLICANT: EREZ-ALON, Neta  
; APPLICANT: HERKEL, Johannes  
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR  
; TITLE OF INVENTION: IMMUNITY  
; FILE REFERENCE: COHEN42  
; CURRENT APPLICATION NUMBER: US/10/032,482  
; PRIOR FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: US/09/445,602  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: PCT/IL98/00266  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: IL 121041  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-032-482-18

Query Match 93.1%; Score 94; DB 14; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.2e-08;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17  
DB 1 WIDPENGDTYAPKFOG 17

RESULT 13

US-10-032-482-7  
; Sequence 7, Application US/10032482  
; Publication No. US20020197270A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Irwin  
; APPLICANT: ROTTER, Varda  
; APPLICANT: Wolkowicz, Roland  
; APPLICANT: RUIZ, Pedro  
; APPLICANT: EREZ-ALON, Neta  
; APPLICANT: HERKEL, Johannes  
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR  
; TITLE OF INVENTION: IMMUNITY  
; FILE REFERENCE: COHEN42  
; CURRENT APPLICATION NUMBER: US/10/032,482  
; PRIOR FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: US/09/445,602  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: PCT/IL98/00266  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: IL 121041  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-032-482-7

Query Match 93.1%; Score 94; DB 14; Length 112;  
Best Local Similarity 88.2%; Pred. No. 2.9e-07;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIDPENGSDYAPKFOG 17  
DB 47 WIDPENGDTYAPKFOG 63

RESULT 14

US-09-976-787-7  
; Sequence 7, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: WILTE, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 7  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-976-787-7

Query Match 93.1%; Score 94; DB 9; Length 117;  
Best Local Similarity 94.1%; Pred. No. 3e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 WIDPENGSDYAPKFOG 17
Db      50 WIDPENGDSGYAPKFOG 66
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## RESULT 15

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US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Wordperfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-7

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Query Match          93.1%;  Score 94;  DB 10;  Length 117;
Best Local Similarity 94.1%;  Pred. No. 3e-07;
Matches 16;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      1 WIDPENGSDSYAPKFGG 17
        |||||
Db       50 WIDPENGDSGYAPKFGG.66

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Search completed: July 30, 2003, 10:20:29  
Job time : 20.897 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:36:53 ; Search time 95.7309 Seconds  
(without alignments)  
154.559 Million cell updates/sec

Title: US-09-865-198-21  
Perfect score: 101  
Sequence: 1 WIDPENGSDSYAPKFOG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA Main:  
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4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep:\*  
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28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	17	1	PCT-US02-20332-21
2	101	100.0	17	1	PCT-US02-41372-21

3	101	100.0	17	19	US-09-539-692-2	Sequence 2, Appli
4	101	100.0	17	19	US-09-540-770-2	Sequence 2, Appli
5	101	100.0	17	19	US-09-559-019-21	Sequence 21, Appli
6	101	100.0	17	23	US-09-865-198-21	Sequence 21, Appli
7	101	100.0	17	25	US-09-976-787-22	Sequence 22, Appli
8	101	100.0	117	1	PCT-US02-20332-22	Sequence 22, Appli
9	101	100.0	117	1	PCT-US02-41372-22	Sequence 22, Appli
10	101	100.0	117	19	US-09-539-692-7	Sequence 7, Appli
11	101	100.0	117	19	US-09-540-770-7	Sequence 7, Appli
12	101	100.0	117	19	US-09-559-019-22	Sequence 22, Appli
13	101	100.0	117	23	US-09-798-689-7	Sequence 7, Appli
14	101	100.0	117	23	US-09-865-198-22	Sequence 22, Appli
15	101	100.0	117	25	US-09-976-787-23	Sequence 23, Appli
16	101	100.0	238	1	PCT-US02-20332-28	Sequence 28, Appli
17	101	100.0	238	1	PCT-US02-41372-28	Sequence 28, Appli
18	101	100.0	238	19	US-09-559-019-28	Sequence 28, Appli
19	101	100.0	238	22	US-09-798-689-21	Sequence 21, Appli
20	101	100.0	238	23	US-09-865-198-28	Sequence 28, Appli
21	101	100.0	238	25	US-09-976-787-29	Sequence 29, Appli
22	95	94.1	16	22	US-09-798-689-2	Sequence 2, Appli
23	94	93.1	17	1	PCT-US00-02180-2	Sequence 2, Appli
24	94	93.1	17	1	PCT-US02-20332-2	Sequence 2, Appli
25	94	93.1	17	1	PCT-US02-38229-14	Sequence 14, Appli
26	94	93.1	17	1	PCT-US02-41372-2	Sequence 2, Appli
27	94	93.1	17	18	US-09-445-602A-18	Sequence 18, Appli
28	94	93.1	17	18	US-09-493-503-2	Sequence 2, Appli
29	94	93.1	17	19	US-09-559-019-2	Sequence 2, Appli
30	94	93.1	17	23	US-09-865-198-2	Sequence 2, Appli
31	94	93.1	17	25	US-09-976-787-2	Sequence 2, Appli
32	94	93.1	17	26	US-10-032-482-18	Sequence 26, Appli
33	94	93.1	82	3	US-07-769-021-26	Sequence 26, Appli
34	94	93.1	82	3	US-07-909-295A-26	Sequence 26, Appli
35	94	93.1	112	18	US-09-445-602A-7	Sequence 7, Appli
36	94	93.1	112	26	US-10-032-482-7	Sequence 7, Appli
37	94	93.1	114	22	US-09-791-537-48124	Sequence 48124, A
38	94	93.1	114	22	US-09-791-537-103366	Sequence 103366,
39	94	93.1	115	22	US-09-791-537-102822	Sequence 102822,
40	94	93.1	116	1	PCT-US99-24443-2	Sequence 2, Appli
41	94	93.1	116	23	US-09-807-827-2	Sequence 2, Appli
42	94	93.1	117	1	PCT-US00-02180-7	Sequence 7, Appli
43	94	93.1	117	1	PCT-US02-20332-7	Sequence 7, Appli
44	94	93.1	117	1	PCT-US02-41372-7	Sequence 7, Appli
45	94	93.1	117	1	PCT-US91-02730-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1  
PCT-US02-20332-21  
; Sequence 21, Application PC/TUS0220332  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Antibodies That Bind to VEGF Receptors  
; FILE REFERENCE: 11245/48576  
; CURRENT APPLICATION NUMBER: PCT/US02/20332  
; PRIOR FILING DATE: 2002-06-27  
; PRIOR APPLICATION NUMBER: US 60/301,299  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 21  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mouse  
PCT-US02-20332-21

QY	1	WIDPENGSDSYAPKFOG 17	100.0%; Score 101; DB 1; Length 17;
			Best Local Similarity 100.0%; Pred. No. 1.1e-08;
			Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 WIDPENGSDSYAPKFOG 17

RESULT 2  
PCT-US02-41372-21  
; Sequence 21, Application PC/TUS0241372  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Antibodies That Bind to VEGF Receptors  
; FILE REFERENCE: 11245/485762  
; CURRENT APPLICATION NUMBER: PCT/US02/41372  
; PRIOR FILING DATE: 2002-12-24  
; PRIOR APPLICATION NUMBER: PCT/US02/20332  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: US 60/301,299  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 21  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mouse  
PCT-US02-41372-21

Query Match 100.0%; Score 101; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDSYAPKFOG 17  
Db 1 WIDPENGSDSYAPKFOG 17

RESULT 3  
US-09-539-692-2  
; Sequence 2, Application US/09539692  
; GENERAL INFORMATION:  
; APPLICANT: Kerbel, Robert  
; TITLE OF INVENTION: Therapeutic Method for Reducing Angiogenesis  
; FILE REFERENCE: Sequence Listings 1-16 for 11245-19  
; CURRENT APPLICATION NUMBER: US/09/539,692  
; CURRENT FILING DATE: 2000-03-31  
; EARLIER APPLICATION NUMBER: US 60/178791  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-539-692-2

Query Match 100.0%; Score 101; DB 19; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDSYAPKFOG 17  
Db 1 WIDPENGSDSYAPKFOG 17

RESULT 4  
US-09-540-770-2  
; Sequence 2, Application US/09540770  
; GENERAL INFORMATION:  
; APPLICANT: Witte, Larry  
; APPLICANT: Rafii, Shahin  
; TITLE OF INVENTION: Treatment of Non-Solid Mammalian Tumors with Vascular Endothelial  
; TITLE OF INVENTION: Growth Factor Receptor Antagonists  
; FILE REFERENCE: 11245/46701  
; CURRENT APPLICATION NUMBER: US/09/540,770  
; CURRENT FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-540-770-2

Query Match 100.0%; Score 101; DB 19; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDSYAPKFOG 17  
Db 1 WIDPENGSDSYAPKFOG 17

RESULT 5  
US-09-559-019-21  
; Sequence 21, Application US/09559019  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: Sequence Listings 1-34 for 381-71  
; CURRENT APPLICATION NUMBER: US/09/559,019  
; CURRENT FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-559-019-21

Query Match 100.0%; Score 101; DB 19; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDSYAPKFOG 17  
Db 1 WIDPENGSDSYAPKFOG 17

RESULT 6  
US-09-865-198-21  
; Sequence 21, Application US/09865198  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methc  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 21  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-21

Query Match 100.0%; Score 101; DB 23; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WIDPENGSDSYAPKFOG 17  
Db 1 WIDPENGSDSYAPKFOG 17

RESULT 7  
US-09-976-787-22

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; Sequence 22, Application US/09976787
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
; US-09-976-787-22

Query Match          100.0%; Score 101; DB 25; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDYAPKFG 17
Db      1 WIDPENGSDYAPKFG 17

RESULT 8
PCT-US02-20332-22
; Sequence 22, Application PC/TUS0220332
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Antibodies That Bind to VEGF Receptors
; FILE REFERENCE: 11245/48576
; CURRENT APPLICATION NUMBER: PCT/US02/20332
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US 60/301,299
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
; PCT-US02-20332-22

Query Match          100.0%; Score 101; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDYAPKFG 17
Db      50 WIDPENGSDYAPKFG 66

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; Sequence 22, Application PC/TUS0241372
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Antibodies That Bind to VEGF Receptors
; FILE REFERENCE: 11245/485762
; CURRENT APPLICATION NUMBER: PCT/US02/41372
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: PCT/US02/20332
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/301,299
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22

; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
; PCT-US02-41372-22

Query Match          100.0%; Score 101; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDYAPKFG 17
Db      50 WIDPENGSDYAPKFG 66

; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
; PCT-US02-41372-22

Query Match          100.0%; Score 101; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDYAPKFG 17
Db      50 WIDPENGSDYAPKFG 66

RESULT 10
US-09-539-692-7
; Sequence 7, Application US/09539692
; GENERAL INFORMATION:
; APPLICANT: Kerbel, Robert
; TITLE OF INVENTION: Therapeutic Method for Reducing Angiogenesis
; FILE REFERENCE: Sequence Listings 1-16 for 11245-19
; CURRENT APPLICATION NUMBER: US/09/539,692
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/178791
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
; US-09-539-692-7

Query Match          100.0%; Score 101; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDYAPKFG 17
Db      50 WIDPENGSDYAPKFG 66

RESULT 11
US-09-540-770-7
; Sequence 7, Application US/09540770
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; TITLE OF INVENTION: Treatment of Non-Solid Mammalian Tumors with Vascular Endothelial
; FILE REFERENCE: 11245/46701
; CURRENT APPLICATION NUMBER: US/09/540,770
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
; US-09-540-770-7

Query Match          100.0%; Score 101; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDYAPKFG 17
Db      50 WIDPENGSDYAPKFG 66

RESULT 12
US-09-559-019-22
; Sequence 22, Application US/09559019
; GENERAL INFORMATION:
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; APPLICANT: Zhu, Zhenping
; APPLICANT: Wille, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: Sequence Listings 1-34 for 381-71
; CURRENT APPLICATION NUMBER: US/09/559,019
; CURRENT FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-559-019-22
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Query Match          100.0%; Score 101; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WIDPENGSDSYAPKFG 17
        |||||
Db       50 WIDPENGSDSYAPKFG 66
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## RESULT 13

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US-09-798-689-7
; Sequence 7, Application US/09798689
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-7
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Query Match          100.0%; Score 101; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 WIDPENGSDSYAPKFG 17
        |||||
Db       50 WIDPENGSDSYAPKFG 66
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## RESULT 14

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US-09-865-198-22
; Sequence 22, Application US/09865198
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
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; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22
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Query Match          100.0%; Score 101; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WIDPENGSDSYAPKFG 17
        |||||
Db       50 WIDPENGSDSYAPKFG 66
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## RESULT 15

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US-09-976-787-23
; Sequence 23, Application US/09976787
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Wille, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-23
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Query Match          100.0%; Score 101; DB 25; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WIDPENGSDSYAPKFG 17
        |||||
Db       50 WIDPENGSDSYAPKFG 66
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Search completed: July 30, 2003, 10:13:22  
Job time : 95.7309 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 5.4784 Seconds  
(without alignments)  
131.295 Million cell updates/sec

Title: US-09-865-198-21  
Perfect score: 101  
Sequence: 1 WIDPENGSDSYAPKFOG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	94	93.1	124	1 US-08-017-570-4	Sequence 4, Appli
2	94	93.1	124	1 US-08-017-570-6	Sequence 6, Appli
3	94	93.1	124	1 US-08-471-426-4	Sequence 4, Appli
4	94	93.1	124	1 US-08-471-426-6	Sequence 6, Appli
5	94	93.1	124	4 US-09-672-609-1	Sequence 1, Appli
6	94	93.1	124	4 US-09-672-609-3	Sequence 3, Appli
7	94	93.1	124	4 US-09-672-609-4	Sequence 4, Appli
8	94	93.1	124	4 US-09-672-609-5	Sequence 5, Appli
9	94	93.1	124	4 US-09-672-609-6	Sequence 6, Appli
10	94	93.1	124	4 US-09-672-609-7	Sequence 7, Appli
11	94	93.1	124	4 US-09-672-609-8	Sequence 8, Appli
12	94	93.1	124	4 US-09-672-609-9	Sequence 9, Appli
13	94	93.1	124	4 US-09-672-609-10	Sequence 10, Appli
14	94	93.1	124	4 US-09-672-609-11	Sequence 11, Appli
15	94	93.1	124	4 US-09-672-609-12	Sequence 12, Appli
16	94	93.1	124	4 US-09-025-403A-1	Sequence 1, Appli
17	94	93.1	124	4 US-09-025-403A-3	Sequence 3, Appli
18	94	93.1	124	4 US-09-025-403A-4	Sequence 4, Appli
19	94	93.1	124	4 US-09-025-403A-5	Sequence 5, Appli
20	94	93.1	124	4 US-09-025-403A-6	Sequence 6, Appli
21	94	93.1	124	4 US-09-025-403A-7	Sequence 7, Appli
22	94	93.1	124	4 US-09-025-403A-8	Sequence 8, Appli
23	94	93.1	124	4 US-09-025-403A-9	Sequence 9, Appli
24	94	93.1	124	4 US-09-025-403A-10	Sequence 10, Appli
25	94	93.1	124	4 US-09-025-403A-11	Sequence 11, Appli
26	94	93.1	124	4 US-09-025-403A-12	Sequence 12, Appli
27	94	93.1	124	5 PCT-US94-01709-4	Sequence 4, Appli

28	94	93.1	124	5 PCT-US94-01709-6	Sequence 6, Appli
29	94	93.1	270	2 US-08-652-507-2	Sequence 2, Appli
30	94	93.1	535	4 US-08-983-035A-38	Sequence 38, Appli
31	94	93.1	553	2 US-08-661-052-16	Sequence 16, Appli
32	94	93.1	553	3 US-09-188-082-16	Sequence 16, Appli
33	94	93.1	553	4 US-09-364-088-16	Sequence 16, Appli
34	94	93.1	553	4 US-09-102-716-16	Sequence 16, Appli
35	90	89.1	17	3 US-09-171-945-31	Sequence 31, Appli
36	90	89.1	120	3 US-09-171-945-11	Sequence 11, Appli
37	90	89.1	120	3 US-09-171-945-55	Sequence 55, Appli
38	90	89.1	120	3 US-09-171-945-75	Sequence 75, Appli
39	90	89.1	120	3 US-09-171-945-81	Sequence 81, Appli
40	90	89.1	120	3 US-09-171-945-85	Sequence 85, Appli
41	90	89.1	120	3 US-09-171-945-89	Sequence 89, Appli
42	90	89.1	120	3 US-09-171-945-91	Sequence 91, Appli
43	90	89.1	255	3 US-09-171-945-19	Sequence 19, Appli
44	90	89.1	255	3 US-09-171-945-57	Sequence 57, Appli
45	90	89.1	255	3 US-09-171-945-57	Sequence 57, Appli

ALIGNMENTS

RESULT 1  
US-08-017-570-4  
; Sequence 4, Application US/08017570  
; Patent No. 5472693  
; GENERAL INFORMATION:  
; APPLICANT: GOURLIE, BRIAN B  
; APPLICANT: RIXON, MARK W  
; APPLICANT: MEZES, PETER S  
; APPLICANT: KAPLAN, DONALD A  
; APPLICANT: SCHLOM, JEFFREY  
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Duane C. Ulmer  
; STREET: P.O. Box 1967  
; CITY: Midland  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48641-1967  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/017,570  
; FILING DATE: 19930216  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ULMER, DUANE C  
; REGISTRATION NUMBER: 34,941  
; REFERENCE/DOCKET NUMBER: C-38,777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 636-8104  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 124 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-017-570-4  
Query Match 93.1%; Score 94; DB 1; Length 124;  
Best Local Similarity 88.2%; Pred. No. 8e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WIDPENGSDSYAPKFOG 17  
Db 50 WIDPENGDTETAPKFOG 66

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RESULT 2
US-08-017-570-6
; Sequence 6, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-017-570-6

Query Match          93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 8e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDYAPKFG 17
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Db      50 WIDPENGDTYAPKFG 66

RESULT 3
US-08-471-426-4
; Sequence 4, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
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      ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-426-4

Query Match          93.1%; Score 94; DB 1; Length 124;
Best Local Similarity 88.2%; Pred. No. 8e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 WIDPENGSDYAPKFG 17
      |||||:|||||
Db      50 WIDPENGDTYAPKFG 66

RESULT 4
US-08-471-426-6
; Sequence 6, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: (517) 636-8104  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 124 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-471-426-6

Query Match 93.1%; Score 94; DB 1; Length 124;  
Best Local Similarity 88.2%; Pred. No. 8e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFG 17  
|||:|||:  
Db 50 WIDPENGDTYAPKFG 66

## RESULT 5

US-09-672-609-1  
; Sequence 1, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:

APPLICANT: Anderson, W.H. Kerr  
APPLICANT: Tempest, Philip R.  
APPLICANT: Carr, Frank J.  
APPLICANT: Harris, William J.  
APPLICANT: Armour, Kathryn  
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/672,609  
CURRENT FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: 09/025,403  
PRIOR FILING DATE: 1998-02-18  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Microsoft Word 97 SR-2  
SEQ ID NO 1  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: Murine Col-1 VH  
LOCATION: 1..124  
US-09-672-609-1

Query Match 93.1%; Score 94; DB 4; Length 124;  
Best Local Similarity 88.2%; Pred. No. 8e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFG 17  
|||:|||:  
Db 50 WIDPENGDTYAPKFG 66

RESULT 6  
US-09-672-609-3  
; Sequence 3, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:

APPLICANT: Anderson, W.H. Kerr  
APPLICANT: Tempest, Philip R.  
APPLICANT: Carr, Frank J.  
APPLICANT: Harris, William J.  
APPLICANT: Armour, Kathryn  
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/672,609  
CURRENT FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: 09/025,403  
PRIOR FILING DATE: 1998-02-18  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Microsoft Word 97 SR-2  
SEQ ID NO 3

LENGTH: 124

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

NAME/KEY: Humanized COL-1 VH, HuVH  
LOCATION: 1..124  
OTHER INFORMATION: Humanized heavy chain variable region containing human  
OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,  
OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98  
US-09-672-609-3

Query Match 93.1%; Score 94; DB 4; Length 124;  
Best Local Similarity 88.2%; Pred. No. 8e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFG 17  
|||:|||:  
Db 50 WIDPENGDTYAPKFG 66

## RESULT 7

US-09-672-609-4  
; Sequence 4, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:

APPLICANT: Anderson, W.H. Kerr  
APPLICANT: Tempest, Philip R.  
APPLICANT: Carr, Frank J.  
APPLICANT: Harris, William J.  
APPLICANT: Armour, Kathryn  
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/672,609  
CURRENT FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: 09/025,403  
PRIOR FILING DATE: 1998-02-18  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Microsoft Word 97 SR-2  
SEQ ID NO 4  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: Humanized COL-1 VH, HuVHA  
LOCATION: 1..124  
OTHER INFORMATION: Humanized heavy chain variable region containing human  
OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,  
OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98  
US-09-672-609-4

Query Match 93.1%; Score 94; DB 4; Length 124;  
Best Local Similarity 88.2%; Pred. No. 8e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFG 17  
|||:|||:  
Db 50 WIDPENGDTYAPKFG 66

## RESULT 8

US-09-672-609-5  
; Sequence 5, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:

APPLICANT: Anderson, W.H. Kerr  
APPLICANT: Tempest, Philip R.  
APPLICANT: Carr, Frank J.  
APPLICANT: Harris, William J.  
APPLICANT: Armour, Kathryn  
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/672,609  
CURRENT FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Word 97 SR-2  
; SEQ ID NO 5  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Humanized COL-1 VH, HUVHAT  
; LOCATION: 1..124  
; OTHER INFORMATION: Humanized heavy chain variable region containing human  
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,  
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98  
US-09-672-609-5

Query Match 93.1%; Score 94; DB 4; Length 124;  
Best Local Similarity 88.2%; Pred. No. 8e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFOG 17  
Db 50 WIDPENGDTTEYAPKFOG 66

RESULT 9  
US-09-672-609-6

; Sequence 6, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.  
; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Word 97 SR-2  
; SEQ ID NO 6  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Humanized COL-1 VH, HUVHAA  
; LOCATION: 1..124  
; OTHER INFORMATION: Humanized heavy chain variable region containing human  
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,  
; OTHER INFORMATION: Ile-29, Lys-30, Ala-79, Asn-97, and Thr-98  
US-09-672-609-6

Query Match 93.1%; Score 94; DB 4; Length 124;  
Best Local Similarity 88.2%; Pred. No. 8e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFOG 17  
Db 50 WIDPENGDTTEYAPKFOG 66

RESULT 10

US-09-672-609-7  
; Sequence 7, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.

; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Word 97 SR-2  
; SEQ ID NO 7  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Humanized COL-1 VH, HUVHAY  
; LOCATION: 1..124  
; OTHER INFORMATION: Humanized heavy chain variable region containing human  
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,  
; OTHER INFORMATION: Ile-29, Lys-30, Tyr-80, Asn-97, and Thr-98  
US-09-672-609-7

Query Match 93.1%; Score 94; DB 4; Length 124;  
Best Local Similarity 88.2%; Pred. No. 8e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFOG 17  
Db 50 WIDPENGDTTEYAPKFOG 66

RESULT 11  
US-09-672-609-8

; Sequence 8, Application US/09672609  
; Patent No. 6333405  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, W.H. Kerr  
; APPLICANT: Tempest, Philip R.  
; APPLICANT: Carr, Frank J.  
; APPLICANT: Harris, William J.  
; APPLICANT: Armour, Kathryn  
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/672,609  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 09/025,403  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Word 97 SR-2  
; SEQ ID NO 8  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Humanized COL-1 VH, HUVHATAY  
; LOCATION: 1..124  
; OTHER INFORMATION: Humanized heavy chain variable region containing human  
; OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,  
; OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98  
US-09-672-609-8

Query Match 93.1%; Score 94; DB 4; Length 124;  
Best Local Similarity 88.2%; Pred. No. 8e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WIDPENGSDYAPKFOG 17  
Db 50 WIDPENGDTTEYAPKFOG 66

RESULT 12

US-09-672-609-9  
; Sequence 9, Application US/09672609  
; Patent No. 6333405

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: GENERAL INFORMATION:
: APPLICANT: Anderson, W.H. Kerr
: APPLICANT: Tempest, Philip R.
: APPLICANT: Carr, Frank J.
: APPLICANT: Harris, William J.
: APPLICANT: Armour, Kathryn
: TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/672,609
: CURRENT FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: 09/025,403
: PRIOR FILING DATE: 1998-02-18
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: Microsoft Word 97 SR-2
: SEQ ID NO 9
: LENGTH: 124
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: Humanized COL-1 VH, HUVHASTAY
: LOCATION: 1..124
: OTHER INFORMATION: Humanized heavy chain variable region containing human
: OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
: OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, Tyr-80, Asn-97, and
: OTHER INFORMATION: Thr-98
US-09-672-609-9

```

```

Query Match          93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 8e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      1 WIDPENGSDYAPKFOG 17
Db      50 WIDPENGDTETAPKFOG 66

```

```

RESULT 13
US-09-672-609-10
: Sequence 10, Application US/09672609
: Patent No. 6333405
: GENERAL INFORMATION:
: APPLICANT: Anderson, W.H. Kerr
: APPLICANT: Tempest, Philip R.
: APPLICANT: Carr, Frank J.
: APPLICANT: Harris, William J.
: APPLICANT: Armour, Kathryn
: TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/672,609
: CURRENT FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: 09/025,403
: PRIOR FILING DATE: 1998-02-18
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: Microsoft Word 97 SR-2
: SEQ ID NO 10
: LENGTH: 124
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: Humanized COL-1 VH, HUVHT
: LOCATION: 1..124
: OTHER INFORMATION: Humanized heavy chain variable region containing human
: OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
: OTHER INFORMATION: Ile-29, Lys-30, Thr-72, Asn-97, and Thr-98
US-09-672-609-10

```

```

Query Match          93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 8e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      1 WIDPENGSDYAPKFOG 17
Db      50 WIDPENGDTETAPKFOG 66

```

```

RESULT 14
US-09-672-609-11
: Sequence 11, Application US/09672609
: Patent No. 6333405
: GENERAL INFORMATION:
: APPLICANT: Anderson, W.H. Kerr
: APPLICANT: Tempest, Philip R.
: APPLICANT: Carr, Frank J.
: APPLICANT: Harris, William J.
: APPLICANT: Armour, Kathryn
: TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/672,609
: CURRENT FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: 09/025,403
: PRIOR FILING DATE: 1998-02-18
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: Microsoft Word 97 SR-2
: SEQ ID NO 11
: LENGTH: 124
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: Humanized COL-1 VH, HUVHS
: LOCATION: 1..124
: OTHER INFORMATION: Humanized heavy chain variable region containing human
: OTHER INFORMATION: NEMM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
: OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Asn-97, and Thr-98
US-09-672-609-11

```

```

Query Match          93.1%; Score 94; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 8e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      1 WIDPENGSDYAPKFOG 17
Db      50 WIDPENGDTETAPKFOG 66

```

```

RESULT 15
US-09-672-609-12
: Sequence 12, Application US/09672609
: Patent No. 6333405
: GENERAL INFORMATION:
: APPLICANT: Anderson, W.H. Kerr
: APPLICANT: Tempest, Philip R.
: APPLICANT: Carr, Frank J.
: APPLICANT: Harris, William J.
: APPLICANT: Armour, Kathryn
: TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/672,609
: CURRENT FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: 09/025,403
: PRIOR FILING DATE: 1998-02-18
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: Microsoft Word 97 SR-2
: SEQ ID NO 12
: LENGTH: 124
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: Humanized COL-1 VH, HUVHSTAY
: LOCATION: 1..124
: OTHER INFORMATION: Humanized heavy chain variable region expressed from ATCC
: OTHER INFORMATION: CRL-12208, and containing human NEMM VH FRs, murine COL-1 VH CDRs
: OTHER INFORMATION: and Phe-27, Asn-28, Ile-29, Lys-30, Ser-76, Thr-78, Ala-79,
: OTHER INFORMATION: Tyr-80, Asn-97, and Thr-98
US-09-672-609-12

```

```

Query Match          93.1%; Score 94; DB 4; Length 124;

```



Best Local Similarity 88.2%; Pred. No. 8e-08;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 WIDPENGSDYAPKFOG 17  
|||:|||||  
Db 50 WIDPENGDTREYAPKFOG 66

Search completed: July 30, 2003, 09:38:30  
Job time : 5.4784 secs

---

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: July 30, 2003, 09:31:34 ; Search time 34.5947 Seconds  
(without alignments)  
325.245 Million cell updates/sec

Title: US-09-865-198-22

Sequence: 1 QVKLQQSGAELVSGGASVKL.....AYYGDEGYWGQGTIVSS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	511	81.0	136	2	S04576	Ig heavy chain pre
2	498.5	79.0	268	2	A56446	Ig heavy chain V r
3	496.5	78.7	116	2	S15672	Ig heavy chain V r
4	491	77.8	118	2	S25174	Ig heavy chain V r
5	481.5	76.3	137	2	S52445	Ig heavy chain V r
6	480	76.1	117	2	S17586	Ig heavy chain V r
7	479	75.9	221	2	S49220	Ig gamma-1 chain -
8	476	75.4	120	2	S03471	Ig heavy chain V-D
9	473.5	75.0	178	2	S29594	Ig gamma chain (WM
10	467	74.0	116	2	S24289	Ig gamma chain V r
11	465.5	73.8	114	4	A47271	nitrophenyl phosph
12	461.5	73.1	122	2	S06823	Ig heavy chain V r
13	459	72.7	233	2	JCS322	p53 specific singl
14	455	72.1	120	2	S03484	Ig heavy chain V-D
15	454	71.9	115	2	S03482	Ig heavy chain V-D
16	435	68.9	108	2	PH1012	Ig heavy chain V r
17	433	68.6	249	2	S41374	single chain Fv an
18	430.5	68.2	115	2	PL0246	Ig heavy chain V r
19	430	68.1	123	2	PH1403	Ig heavy chain V r
20	425.5	67.4	107	2	PH1013	Ig heavy chain V r
21	420.5	66.6	118	2	G37267	Ig heavy chain V r
22	416.5	66.0	139	2	PS0024	Ig heavy chain pre
23	410.5	65.1	115	2	A54378	Ig heavy chain V r
24	410	65.0	138	2	S21810	Ig heavy chain V r
25	406.5	64.4	120	2	B22769	Ig heavy chain V r
26	406	64.3	246	2	S38950	Ig gamma chain - m
27	404.5	64.1	107	2	S40295	Ig gamma-2a chain
28	404.5	64.1	107	2	A27646	Ig heavy chain V r
29	403.5	63.9	116	2	S53751	antibody Fab Jel 1

Iteration	Loss	Learning Rate	Model	Task
30	403.5	63.9	139	1 MHMS18
31	403.5	63.9	287	4 PC4402
32	400.5	63.5	120	2 S41394
33	399.5	63.3	133	2 PC1155
34	397.5	63.0	120	2 F28195
35	397	62.9	136	2 PL0208
36	396	62.8	119	2 D30562
37	394.5	62.5	136	2 JL0077
38	394.5	62.5	141	2 JL0076
39	394.5	62.5	469	2 S37483
40	394	62.4	116	2 S55542
41	394	62.4	131	2 A27472
42	393.5	62.4	119	2 A24672
43	393.5	62.4	120	2 G28195
44	393.5	62.4	288	2 S29690
45	392	62.1	99	2 D37262

## ALIGNMENTS

```

RESULT 1
S04576
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (Fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04576
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
Eur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involve
A;Reference number: S04573; MUID:87133856; PMID:3102255
A;Accession: S04576
A;Molecule type: mRNA
A;Residues: 1-136 <KOF>
A;Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (Fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

```

```

Query Match          81.0%; Score 511; DB 2; Length 136;
Best Local Similarity 82.9%; Pred. No. 3.5e-39;
Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY      1 QVKLQOQSGAELVSGSGAVKLSCTTSGFNICKDFYMHVWKQRPQGLEWIGWIDPENDSDY 60
      : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |
Db      20 EVQLQOQSGAELVPRGASVKLSCTASGFNIKDKDYNHWVKQRPEQGLEWIGWIDPENDTQY 79

QY      61 APKFQGKATMTADSSNSTAYLQLSLTSEDTAVYYCNAYYGDYEGYWGGTQTVYSS 117
      | ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db      80 ASKFQGKATMTADTSSNTTYLQLSLTSEDTAVYYCTTYGAYAMDYWGQGSTVYSS 136

```

## RESULT 2

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
 C/Accession: A56446  
 R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schneler, P.A.  
 J. Biol. Chem. 270, 7829-7835, 1995  
 A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical  
 A/Reference number: A56446; MUID:95229583; PMID:7713873  
 A/Accession: A56446  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-268 <TAN>  
 A/Cross-references: GB:U20617  
 C/Keywords: heterotetramer; immunoglobulin

Query Match	79.0%;	Score 498.5;	DB 2;	Length 268;
Best Local Similarity	83.1%;	Pred. NO. 9.5e-38;		

Matches	98; Conservative	5; Mismatches	14; Indels	1; Gaps	1;
QY	1 QVKLQOSGAELVGSASVKLSCTTSGFNKIDFYMHVWKORPEGLEWIGWIDPENDSDY	60			
Db	3 QVKLQESGAELVPGASVKLSCTTSGFNKIDTYMHVWKORPEGLEWIGRIAPANGITKY	62			
QY	61 APKFQGGKATMTADSSSNATYIQLSLTSEDYAVYYCNAYY-GDYEGYWGGTTVTSS	117			
Db	63 DPKFQGGKATIAADTSSSNATYIQLSLTSEDYAVYYCASYLYLTRENYWGGTTVTSS	120			

### RESULT 3

Ig heavy chain V region - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
 C/Accession: S15672  
 R/Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, Bio/Technology 9, 266-271, 1991  
 A/Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi  
 A/Reference number: S15672; WUID:91337412; PMID:1367535  
 A/Accession: S15672  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-116 <TEM>  
 A/Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA41644.1; PID:g51979  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match	78.7%;	Score 496.5;	DB 2;	Length 116;
Best Local Similarity	79.3%;	Pred. No. 6e-38;		
Matches 92;	Conservative 12;	Mismatches 11;	Indels 1;	Gaps 1;

```
Qy      2 VKLQQSGAELVSGASVKLSCTTSGFNKDFYMHMWKQRPBEGLEWIGWIDPENGBDYA    61
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2 VQLQXSTGLERSSGASVKLSCTASGFNKKDYYMMHMKQRPPDGLEWIGWIDPENDVDYA    61
```

```
Oy      62 PKFOGAKMTADSSSNTAYLQLSSLTSEDTAVYYCNAXYGDYEGYWGQTTIVSS 117
        |||||:::|||||:::|||||:::||:::|||||
Db      62 PKFOGAKMTADTSSNTAYLQLSLTFEDTAVYFCNWSGSDFD-HWGGQTIVVSS 116
```

## RESULT 4

Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S25174; S33133  
 R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.  
 submitted to the EMBL Data Library, July 1992  
 A:Description: Structure and binding properties of monoclonal antibodies to core histone  
 A:Reference number: S25174  
 A:Accession: S25174  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-118 <MON>  
 A:Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259  
 A:Accession: S33133  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-118 <MO2>  
 A:Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 P:15-98/Domain: immunoglobulin homology <IMM>

Query Match	77.8%;	Score 491;	DB 2;	Length 118;
Best Local Similarity	78.8%;	Pred. No. 1.9e-37;		
Matches 93;	Conservative 10;	Mismatches 13;	Indels 2;	Gaps 1;

```
QY      1 QVKLQOGSGAELVSGASVKLCSTTSGFNKIDFYHMHVKORPEOGLWIGWIDPENGSDY 60
       ::::| | | | | | | | | | : | | | | | | | | | | | | | | | | | | |
```

```

Db      1 EIQLQSGAELVYXXGASVKLSCTASGFNIKDDYLHWVKQRPEQGLEWIGMIDPENGDT EY 60
QY      61 APKFQGKATMTADSSSNLTAYLQLSLTSEDTAVYYCNAYYGYDYE--GYWGQGITVTS 116
        | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 ASKFOGKATITADTSSNTAYLQLSLTSEDTAVYYCSSPLVHLRTFAWGGQGITVTS 118

```

## RESULT 5

Ig heavy chain V region precursor - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
 C/Accession: S52445  
 R/Berdoz, J.; Kraehenbuhl, J.P.  
 submitted to the EMBL Data Library, November 1994  
 A/Description: Specific amplification by the polymerase chain reaction of rearranged genes  
 A/Reference number: S52445  
 A/Accession: S52445  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-137 <BER>  
 A/Cross-references: EMBL:X82690; NID:g673439; PIDN:CAAS8011.1; PTD:g673440  
 C/Genetics:  
 A/Introns: 16/1  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F;34-115/Domain: immunoglobulin homology <IMM>

Query Match	76.3%;	Score 481.5;	DB 2;	Length 137;
Best Local Similarity	78.2%;	Pred. No. 1.6e-36;		
Matches 93;	Conservative 11;	Mismatches 12;	Indels 3;	Gaps 2;

```
Qy      1 QVKLQSGAELVSGASVKLSCTTSGFNIDFYMHVWKQRPEQGLEWIGWDIPENDSDY 600
        :::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     20 EVQLQQSGAEIVRPGALVKLSCKASGFNIKDIYYMYWVKQRPEQGLEWIGWDIPENGNTIY 799
```

```

Qy      61 APKFOGKATMTADSSSNTAYLQLSSLTSEPTAVYYCNAYYGD--YEGYWGQGITVTIVSS 117
      |||||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      80 DPKFOGKASITADTSSNTAYLQLSSLASEPTAVYYC-AYYGTSYWFPYWGQGITVTIVSA 137

```

## RESULT 6

Ig heavy chain V region (E8) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C/Accession: S17586  
 R/Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowditch, K.; Getzoff, E.D.  
 J. Mol. Biol. 221, 455-462, 1991  
 A/Title: Biochemical implications from the variable gene sequences of an anti-cytochrome  
 forms.  
 A/Reference number: S17586; MUID:92015240; PMID:1656053  
 A/Accession: S17586  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-117 <MYL>  
 A/Cross-references: EMBL:X60683; NID:G51820; PIDN:CAA43095.1; PID:G51821  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match	76.1%;	Score 480;	DB 2;	Length 117;
Best Local Similarity	78.8%;	Pred. No. 1.9e-36;		
Matches	93;	Conservative	12;	Mismatches 11;
				Indels 2;
				Gaps 2;

```
QY      1 QVKTQQSGAEIVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGIDBPNCGSDSY   60  
       : ::::::::::::::::::::|:::|  
Db      1 EVQTQQSGAELVKPGASVKLSCTASGFNIDTYMHMWKQRPEKGLEWIGRIDPASGNTRY   60
```

```

Qy      61 APPKQGAATMTADSSSNAYLQLSLTSSEDTAVYYCNAY-YGDYEGYWGQGITVTSS 117
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 DPKFDKATITADTSSSNAYLQLSLTSSEDTAVYYCAGYDGNFD-YWGQGITVTSS 117

```











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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:35 ; Search time 18.2691 Seconds  
(without alignments)  
301.171 Million cell updates/sec

Title: US-09-865-198-22  
Perfect score: 631  
Sequence: 1 QVRLQSGAELVSGASVKL.....AYYGDYEGYMGQITVTSS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	403.5	63.9	139	1	HV07_MOUSE P01751 mus musculu
2	390	61.8	120	1	HV03_MOUSE P01747 mus musculu
3	385.5	61.1	137	1	HV11_MOUSE P01755 mus musculu
4	381	60.4	140	1	HV02_MOUSE P01746 mus musculu
5	377	59.7	117	1	HV12_MOUSE P01756 mus musculu
6	374	59.3	138	1	HV48_MOUSE P03980 mus musculu
7	368	58.3	117	1	HV13_MOUSE P01757 mus musculu
8	368	58.3	136	1	HV15_MOUSE P01759 mus musculu
9	366.5	58.1	120	1	HV50_MOUSE P06329 mus musculu
10	364.5	57.8	147	1	HV1C_HUMAN P01744 homo sapien
11	362.5	57.4	118	1	HV51_MOUSE P06330 mus musculu
12	348	55.2	121	1	HV01_MOUSE P01745 mus musculu
13	345	54.7	117	1	HV06_MOUSE P01750 mus musculu
14	343	54.4	117	1	HV09_MOUSE P01753 mus musculu
15	339	53.7	117	1	HV04_MOUSE P01748 mus musculu
16	336	53.2	117	1	HV49_MOUSE P06328 mus musculu
17	332	52.6	117	1	HV10_MOUSE P01754 mus musculu
18	332	52.6	117	1	HV52_MOUSE P06327 mus musculu
19	327	51.8	117	1	HV1B_HUMAN P01743 homo sapien
20	325	51.5	117	1	HV05_MOUSE P01749 mus musculu
21	323.5	51.3	119	1	HV40_MOUSE P01810 mus musculu
22	321.5	51.0	119	1	HV37_MOUSE P01807 mus musculu
23	320	50.7	117	1	HV14_MOUSE P01758 mus musculu
24	316.5	50.2	114	1	HV00_MOUSE P01741 mus musculu
25	314.5	49.8	119	1	HV38_MOUSE P01808 mus musculu
26	312	49.4	117	1	HV42_MOUSE P01812 mus musculu
27	309	49.0	117	1	HV1G_HUMAN P23083 homo sapien
28	308.5	48.9	136	1	HV16_MOUSE P01768 homo sapien
29	307.5	48.7	122	1	HV3G_HUMAN P01805 rattus norv
30	305	48.3	142	1	HV01_RAT P01742 homo sapien
31	303	48.0	117	1	HV1A_HUMAN P01809 mus musculu
32	296	46.9	118	1	HV39_MOUSE P01790 mus musculu
33	293.5	46.5	122	1	HV21_MOUSE

34	293	46.4	117	1	HV41_MOUSE P01811 mus musculu
35	291	46.1	123	1	HV24_MOUSE P01793 mus musculu
36	290	46.0	113	1	HV30_MOUSE P01799 mus musculu
37	290	46.0	115	1	HV32_MOUSE P01801 mus musculu
38	290	46.0	125	1	HV1F_HUMAN P06326 homo sapien
39	289	45.8	119	1	HV3L_HUMAN P01773 homo sapien
40	287	45.5	123	1	HV19_MOUSE P01788 mus musculu
41	286.5	45.4	116	1	HV3T_HUMAN P01781 homo sapien
42	286	45.3	113	1	HV3I_MOUSE P01800 mus musculu
43	285	45.2	113	1	HV27_MOUSE P01796 mus musculu
44	284	45.0	115	1	HV33_MOUSE P01802 mus musculu
45	283.5	44.9	122	1	HV3A_HUMAN P01762 homo sapien

ALIGNMENTS

RESULT 1  
HV07\_MOUSE STANDARD; PRT; 139 AA.  
ID HV07\_MOUSE  
AC P01751; P01752; (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region B1-8/186-2 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the Npb family of  
antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -I- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
(NPB ANTIBODIES).  
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CC  
CC EMBL; J00529; AAA38170.1; -.  
DR PIR; A90809; MEMS18.  
DR PDB; 1A6U; 27-MAY-98.  
DR PDB; 1A6W; 15-JUL-98.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal; 3D-structure.  
FT SIGNAL 1 19  
FT CHAIN 1 139  
FT DOMAIN 20 49 IG HEAVY CHAIN V REGION B1-8/186-2.  
FT DOMAIN 50 54 FRAMEWORK-1.  
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 69 85 FRAMEWORK-2.  
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 118 124 D SEGMENT.  
FT DOMAIN 125 139 JH2 SEGMENT.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 139 139  
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 63.9%; Score 403.5; DB 1; Length 139;  
Best Local Similarity 65.8%; Pred. No. 3.4e-33;  
Matches 79; Conservative 13; Mismatches 25; Indels 3; Gaps 2;

QY 1 QVQLQSGAELVSGASVYKLSCTTSGFNKDFYMHVWVKORPEQGLEWIGWIDPENGSDSY 60  
Db 20 QVQLQSGAELVSGASVYKLSCTTSGFNKDFYMHVWVKORPEQGLEWIGRIDPNSGCTKY 79  
QY 61 APKFGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA--YYG-DYEGYWGQGTITVSS 117  
Db 80 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARYDYGGSYFDYWGQGTITVSS 139

RESULT 2

HV03\_MOUSE  
ID HV03\_MOUSE STANDARD; PRT; 120 AA.  
AC P01747;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 36-65.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83131846; PubMed=6186498;  
RA Stekevitz M., Gelfer M.L., Brodeur P., Riblet R.,  
RA Marshak-Rothstein A.;  
RT "The genetic basis of antibody production: the dominant anti-arsonate  
RT idiotype response of the strain A mouse.";  
RL Eur. J. Immunol. 12:1023-1032(1982).  
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER  
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS  
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J  
CC SEGMENT, JH2.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Hybridoma.  
FT DOMAIN 1 111 IG-LIKE.  
FT NON TER 120  
SQ SEQUENCE 120 AA; 13307 MW; FF04EA167B654AF CRC64;  
Query Match 61.8%; Score 390; DB 1; Length 120;  
Best Local Similarity 62.5%; Pred. No. 6.2e-32;  
Matches 75; Conservative 19; Mismatches 22; Indels 4; Gaps 2;  
QY 2 VKLQSGAELVSGASVYKLSCTTSGFNKDFYMHVWVKORPEQGLEWIGWIDPENGSDSYA 61  
Db 1 VQLQSGAELVSGASVYKLSCTTSGFNKDFYMHVWVKORPEQGLEWIGYINPENGTYKN 60  
QY 62 PKFGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGD--YEGYWGQGTITVSS 117  
Db 61 EKFKGKTTLVDKSSSTAYMQLSSLTSEDSAVYYFCARSVYYGGSYFDYWGQGTITVSS 120

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NPB family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
CC (NPB ANTIBODIES).  
CC -----

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DR EMBL; J00539; AAA38172.1; -.  
DR PIR; A02038; G2MS43.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 FRAMEWORK-3.  
FT DOMAIN 86 117 FRAMEWORK-4.  
FT DOMAIN 118 122 D SEGMENT.  
FT DOMAIN 123 137 JH2 SEGMENT.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON TER 137 137  
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 61.1%; Score 385.5; DB 1; Length 137;  
Best Local Similarity 63.6%; Pred. No. 2e-31;  
Matches 75; Conservative 12; Mismatches 30; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVSGASVYKLSCTTSGFNKDFYMHVWVKORPEQGLEWIGWIDPENGSDSY 60  
Db 20 QVQLQSGAELVSGASVYKLSCTTSGFNKDFYMHVWVKORPEQGLEWIGRIDPNSGCTTY 79  
QY 61 APKFGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA--YGDYEGYWGQGTITVSS 117  
Db 80 NEHFRSKATLTIDKSSSTAYMQLSSLTSEDSAVYYCARYRLGRYFDYWGQGTITVSS 137

RESULT 4

HV02\_MOUSE  
ID HV02\_MOUSE STANDARD; PRT; 140 AA.  
AC P01746;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 93G7 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

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RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, J00493; AAA38128.1; -.
DR PIR; A94264; HVMSG7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON_TER 140 140
FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
SQ
Query Match 60.4%; Score 381; DB 1; Length 140;
Best Local Similarity 60.7%; Pred. No. 5.7e-31;
Matches 74; Conservative 22; Mismatches 20; Indels 6; Gaps 3;
QY 1 QVKLQSGAELVSGSASVKSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENDSDY 60
DB 20 EVQLQSGAELVRAGSSSVKMSCKASGYTFTSYGINVWKQRPQGLEWIGYINPGNGYIN 79
QY 61 APKFGKATMTADSSSNAYVLQSLTSEDTAVYYC--NAYYG--DYEGYWGQTTVTV 115
DB 80 NEKFKGKTTLTVDKSSSTAYWQLRSLTSEDSAVYFCARSHYGGSYDFD-YWGQGTPLTV 138
QY 116 SS 117
DB 139 SS 140
RESULT 5
HVI2_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RA [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83475344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.

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[illegible]



Matches 74; Conservative 17; Mismatches 25; Indels 4; Gaps 2;

OY 1 QVKLQSGAELVSGASVKSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
Db 20 QVQLQSGAELVPGASVQLSCKASGHTFTNYIHWKORPGQGLEWIGINPDGRSNY 79  
OY 61 APKFGKATMTADSSSNTAYLQLSLTSEDTAVYYC--NAYYGDYEGYWGQTTVTSS 117  
Db 80 NEKFKKATLTVDKSSSTAYMQLSLTPEEFAYVYCARSDGY-DWFVYWGQTLVTSSA 138

RESULT 7

HV13\_MOUSE STANDARD; PRT; 117 AA.  
AC P01757;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region J558.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=80078170; PubMed=6765983;  
RA Schilling J., Clevinger B., Davie J.M., Hood L.;  
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA  
rearrangements in heavy chain V-region gene segments.";  
RL Nature 283:35-40(1980).  
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO  
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF  
CC WHICH OCCUR IN THE D AND J SEGMENTS.  
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A26242; MHMSJ5.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 116 IG-LIKE.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 58.3%; Score 368; DB 1; Length 117;  
Best Local Similarity 61.3%; Pred. No. 9.1e-30;  
Matches 73; Conservative 16; Mismatches 26; Indels 4; Gaps 2;

OY 1 QVKLQSGAELVSGASVKSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
Db 1 EVQLQSGPELVPGASVKMSCKASGYTFTDYMKWKQSHGKSLIEWIGDINPNNGTSTY 60  
OY 61 APKFGKATMTADSSSNTAYLQLSLTSEDTAVYYC--NAYYGDYEGYWGQTTVTSS 117  
Db 61 NQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYVYCARDRYW--YFDVWAGATTVTSS 117

RESULT 8

HV15\_MOUSE STANDARD; PRT; 136 AA.  
AC P01759;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region BCL1 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82222262; PubMed=6806821;  
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,  
RA Blattner F.R.;  
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains  
by a cloned B-cell lymphoma: a single copy of the VH gene is shared  
by two adjacent CH genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC EMBL; J00494; AAA38130.1; -.  
DR PIR; A02042; HVMSB1.  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.  
FT DOMAIN 20 135 IG-LIKE.  
FT NON\_TER 136 136  
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 58.3%; Score 368; DB 1; Length 136;  
Best Local Similarity 59.0%; Pred. No. 1.1e-29;  
Matches 69; Conservative 17; Mismatches 31; Indels 0; Gaps 0;

OY 1 QVKLQSGAELVSGASVKSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
Db 20 QVQLQSGPELVPGASVKSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 79  
OY 61 APKFGKATMTADSSSNTAYLQLSLTSEDTAVYYC--NAYYGDYEGYWGQTTVTSS 117  
Db 80 NQKFKGKATMTVDKSSSTVHMEIARLTSEDSANLYCARYGNVFDYWGQTTVTSS 136

RESULT 9

HV50\_MOUSE STANDARD; PRT; 120 AA.  
AC P06329;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region AC38 15.3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

[1]  
RP SEQUENCE.  
RX MEDLINE=84182519; PubMed=6201362;  
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;  
RT "A V region determinant (idiotope) expressed at high frequency in B  
lymphocytes is encoded by a large set of antibody structural genes.";  
RL EMBO J. 3:517-523(1984).  
DR PIR; A02037; MHMS15.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 98 V SEGMENT.  
FT DOMAIN 99 105 D SEGMENT.  
FT DOMAIN 106 120 J SEGMENT.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 58.1%; Score 366.5; DB 1; Length 120;  
Best Local Similarity 58.2%; Pred. No. 1.3e-29;  
Matches 71; Conservative 16; Mismatches 28; Indels 7; Gaps 2;

QY 1 QVKLQSGAELVSGASYKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
DB 1 QVQLQPGTELVKPGASVNLSCKASGYFTSYMHVIRQRPQGLEWIGINPSNGTNY 60  
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDTAVYYCNAYGYDEG-----YWGQTTVTV 115  
DB 61 NEKFKSKATLTVDKSSSATYMWLTSTSEDSAVYYCARW--DYEGDRYFDVWGTTVTV 118

QY 116 SS 117  
DB 119 SS 120

RESULT 10  
HV1C\_HUMAN STANDARD; PRT; 147 AA.  
AC P01744;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-I region ND precursor (Fragments).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83065234; Pubmed=6815656;  
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
RA Bell L.O., Gould H.J.;  
RT "Cloning and sequence determination of the gene for the human  
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";  
RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).  
RN [2]  
RP SEQUENCE OF 20-147.  
RA Benrich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RL (In) Bach M.K. (eds.);  
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
RL Marcel Dekker, New York (1978).  
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA  
CC PROTEIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR HSSP; P01789; IMCP.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.  
FT SIGNAL 1 19  
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.  
FT DOMAIN 20 131 IG-LIKE.  
FT MOD\_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 41 115

FT CONFLICT 21 21 T -> V (IN REF. 2).  
FT CONFLICT 53 54 IH -> HI (IN REF. 2).  
FT CONFLICT 67 68 VG -> GV (IN REF. 2).  
FT CONFLICT 125 125 MISSING (IN REF. 2).  
FT NON\_TER 147 147  
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 57.8%; Score 364.5; DB 1; Length 147;  
Best Local Similarity 51.6%; Pred. No. 2.6e-29;  
Matches 66; Conservative 25; Mismatches 26; Indels 11; Gaps 2;

QY 1 QVKLQSGAELVSGASYKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
DB 20 QTVLVQSGAEVRKPGASVAVSVCKASGYTFIDSYTHVIRQAPGHLEWIGWIDPENGSDSY 79  
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDTAVYYC---NAYGYDEGY-----WGQ 109  
DB 80 APRFGKATMTADSSNTAYLQLSLTSEDTAVYYC---NAYGYDEGY-----WGQ 109  
QY 110 GTTVTVSS 117  
DB 140 GTTVTVSS 147

RESULT 11  
HV51\_MOUSE STANDARD; PRT; 118 AA.  
ID HV51\_MOUSE  
AC P06330;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region AC38 205.12.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=84182519; Pubmed=6201362;  
RA Dildrop R., Bovens J., Sikevitz M., Beyreuther K., Rajewsky K.;  
RT "A V region determinant (idiotope) expressed at high frequency in B  
RT lymphocytes is encoded by a large set of antibody structural genes";  
RL EMO J. 3:517-523(1984).  
RL PIR; A02040; MHMS38.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 98 V SEGMENT.  
FT DOMAIN 99 104 D SEGMENT.  
FT DOMAIN 105 118 J SEGMENT.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON\_TER 118 118  
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 57.4%; Score 362.5; DB 1; Length 118;  
Best Local Similarity 59.7%; Pred. No. 3.2e-29;  
Matches 71; Conservative 17; Mismatches 28; Indels 3; Gaps 2;

QY 1 QVKLQSGAELVSGASYKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
DB 1 EVQLQSGPELVKPGASVYKISCKASGYFTFDYVMWVKQSHGKSLIEWIGIDINPNNGTSY 60  
QY 61 APKFGKATMTADSSNTAYLQLSLTSEDTAVYYCNAYGYDEGY--WGQTTVTVSS 117  
DB 61 NQKFKKATLTVDKSSSATYMWLTSTSEDSAVYYCARGYG-YDPFDVWGTTVTVSS 118

RESULT 12

HV01\_MOUSE STANDARD; PRT; 121 AA.  
ID HV01\_MOUSE  
AC P01745;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region MPC11.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81053741; PubMed=6253904;  
RA Zakut R., Cohen J., Givol D.;  
RT "Cloning and sequence of the cDNA corresponding to the variable  
RL region of immunoglobulin heavy chain MPC11."  
RL Nucleic Acids Res. 8:3591-3601(1980).  
RN [2]  
RP REVISIONS.  
RA Zakut R., Cohen J., Givol D.;  
RL Nucleic Acids Res. 8:4839-4840(1980).  
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED  
CC FROM A MYELOMA THAT SECRETES IGG2B.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A93708; GWSM11.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 112 IG-LIKE.  
FT NON TER 121 121  
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;  
Query Match 55.2%; Score 348; DB 1; Length 121;  
Best Local Similarity 56.2%; Pred. No. 9e-28;  
Matches 68; Conservative 21; Mismatches 28; Indels 4; Gaps 2;  
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENDSDY 60  
DB 1 EAQLQSGAELVPGTGVKISKAGYFTNWKERPGHGLEWIGDIYPGGGFTNY 60  
QY 61 APKFGKATMTADSSNTAYLQSLTSEDTAVYYC--NAYYGD--YEGYWGQGTTVTVS 116  
DB 61 NDNLK GKATLTADTSSSTAYIQLSLTSEDSALYHCARGIYNSSPYFDSWGQGTTLTVS 120  
QY 117 S 117  
DB 121 S 121  
RESULT 13  
HV06\_MOUSE STANDARD; PRT; 117 AA.  
ID HV06\_MOUSE  
AC P01750;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 102 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6;  
MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;

RT "Heavy chain variable region contribution to the NPb family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region."  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY  
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
DR PIR; A02032; HVM502.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON TER 117 117  
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;  
Query Match 54.7%; Score 345; DB 1; Length 117;  
Best Local Similarity 67.4%; Pred. No. 1.7e-27;  
Matches 64; Conservative 13; Mismatches 18; Indels 0; Gaps 0;  
QY 2 VKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENDSDY 61  
DB 21 VQLQPGAELVKGASVKVSCASGYFTSYMHVWKORPEQGLEWIGRIHPSDSTNYN 80  
QY 62 PKFGKATMTADSSNTAYLQSLTSEDTAVYYC 96  
DB 81 QKFKGKATLTVDKSSSTAYMQSLTSEDSAVYYC 115  
RESULT 14  
HV09\_MOUSE STANDARD; PRT; 117 AA.  
ID HV09\_MOUSE  
AC P01753; P11271;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 186-1 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6;  
MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NPb family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region."  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY  
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
DR PIR; D90809; HVM561.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.  
FT DOMAIN 20 49 FRAMEWORK-1.



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 90.5681 Seconds  
(without alignments)  
333.364 Million cell updates/sec

Title: US-09-865-198-22  
Perfect score: 631  
Sequence: 1 QVKLQSGAELVSGASVKL.....AYYGDYEGYWGQTTVTSS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_23:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_virus:\*
  - 16: sp\_bacteriaph:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510	80.8	468	11 Q99L31	Q99L31 mus musculu
2	428	67.8	109	11 Q9JL85	Q9JL85 mus musculu
3	411.5	65.2	143	11 Q924P9	Q924P9 mus musculu
4	407	64.5	146	11 Q924R8	Q924R8 mus musculu
5	403.5	63.9	145	11 Q924Q7	Q924Q7 mus musculu
6	403	63.9	146	11 Q924Q3	Q924Q3 mus musculu
7	400.5	63.5	118	11 Q921C4	Q921C4 mus musculu
8	400.5	63.5	473	11 Q99L25	Q99L25 mus musculu
9	400.5	63.5	482	11 Q8K172	Q8K172 mus musculu
10	399	63.2	473	11 Q9D8L4	Q9D8L4 mus musculu
11	398.5	63.2	143	11 Q924Q5	Q924Q5 mus musculu
12	398.5	63.2	143	11 Q924R0	Q924R0 mus musculu
13	398	63.1	140	11 Q924R2	Q924R2 mus musculu
14	397	62.9	142	11 Q924Q1	Q924Q1 mus musculu
15	395.5	62.7	145	11 Q924R4	Q924R4 mus musculu
16	394.5	62.5	145	11 Q924R1	Q924R1 mus musculu

17	394	62.4	142	11 Q924Q2	Q924Q2 mus musculu
18	391.5	62.0	143	11 Q91V67	Q91V67 mus musculu
19	391.5	62.0	145	11 Q924Q9	Q924Q9 mus musculu
20	391	62.0	144	11 Q924P5	Q924P5 mus musculu
21	390.5	61.9	137	11 Q924R6	Q924R6 mus musculu
22	390.5	61.9	145	11 Q924Q6	Q924Q6 mus musculu
23	389.5	61.7	143	11 Q924P6	Q924P6 mus musculu
24	387.5	61.4	143	11 Q924R7	Q924R7 mus musculu
25	387	61.3	140	11 Q924P8	Q924P8 mus musculu
26	387	61.3	481	11 Q91WT1	Q91WT1 mus musculu
27	386.5	61.3	141	11 Q924Q4	Q924Q4 mus musculu
28	386.5	61.3	145	11 Q924P7	Q924P7 mus musculu
29	385.5	61.1	145	11 Q924R3	Q924R3 mus musculu
30	383.5	60.8	139	11 Q924R5	Q924R5 mus musculu
31	382.5	60.6	143	11 Q91VA2	Q91VA2 mus musculu
32	382.5	60.6	488	11 Q8K0F2	Q8K0F2 mus musculu
33	381	60.4	117	11 Q9QXF0	Q9QXF0 mus musculu
34	380	60.2	489	11 Q8VCX4	Q8VCX4 mus musculu
35	379.5	60.1	278	11 Q921K1	Q921K1 mus musculu
36	379.5	60.1	613	11 Q8VCX7	Q8VCX7 mus musculu
37	377	59.7	117	11 Q9QXE9	Q9QXE9 mus musculu
38	376	59.6	146	11 Q924Q8	Q924Q8 mus musculu
39	375	59.4	168	11 Q8VDC9	Q8VDC9 mus musculu
40	374	59.3	474	11 Q8R3H6	Q8R3H6 mus musculu
41	374	59.3	480	11 Q8K0Z4	Q8K0Z4 mus musculu
42	373.5	59.2	143	11 Q924Q0	Q924Q0 mus musculu
43	372	59.0	147	11 Q925S3	Q925S3 mus musculu
44	370.5	58.7	109	11 Q9JL75	Q9JL75 mus musculu
45	368	58.3	170	11 Q925S2	Q925S2 mus musculu

ALIGNMENTS

RESULT 1

Q99L31 PRELIMINARY; PRT; 468 AA.  
ID Q99L31  
AC Q99L31;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Similar to RIKEN CDNA 181060009 gene.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC003878; AA03878.1; -.  
DR HSSP; P01842; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 80.8%; Score 510; DB 11; Length 468;  
Best Local Similarity 80.7%; Pred. No. 2.2e-43;  
Matches 96; Conservative 9; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVKLQSGAELVSGASVKLSCTSGFNKDFYMHVYKORPEQGLEWIGWIDPENGSDY 60  
Db 20 EVQLQSGAELVRFPGASVKLSCTASGFNIKDSLHWYKORPEQGLEWIGWIDPEGETKY 79  
QY 61 APKFGKATMTADSSSNFAYQLSLTSEDTAVVYC--NAVYGDYEGYWGQTTVTSS 117  
Db 80 APKFGDKATITADTSSTNAYQLSLTSEDTAIVYCARNLLYGGYYDYWGQTTVTSS 138

RESULT 2  
Q9JL85  
ID Q9JL85 PRELIMINARY; PRT; 109 AA.  
AC Q9JL85;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Anti-myosin immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of  
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
RT with cardiac myosin."  
RL Infect. Immun. 68:5803-5808(2000).  
DR EMBL; AF206021; AAF69319.1; -.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig\_1-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_1 LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 109  
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;  
Query Match 67.8%; Score 428; DB 11; Length 109;  
Best Local Similarity 77.1%; Pred. No. 7.5e-36;  
Matches 84; Conservative 5; Mismatches 20; Indels 0; Gaps 0;  
Qy 9 AELVSGASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSDYAPKFGKA 68  
Db 1 AELVKPGASVKLSCTASGFNIEDTYMHVWKQRPQGLEWIGRIDPATGSKYDPKFGKA 60  
Qy 69 TMTADSSNTAYLQLSLTSEDYAVYYCNAYYGDYEGYWGQTTVTSS 117  
Db 61 TITSDTSSNTAYLQLSLTSEDYAVYYCVRRGAVVFDYWGQGTALTSS 109  
RESULT 3  
Q924P9  
ID Q924P9 PRELIMINARY; PRT; 143 AA.  
AC Q924P9;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE V303-D-J-C mu protein (Fragment).  
GN V303-D-J-C MU.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB069916; BAB63932.1; -.  
DR InterPro; IPR007110; Ig\_1-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_1 LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 143  
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;  
Query Match 65.2%; Score 411.5; DB 11; Length 143;  
Best Local Similarity 66.9%; Pred. No. 4.9e-34;  
Matches 79; Conservative 15; Mismatches 23; Indels 1; Gaps 1;  
Qy 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSDY 60  
Db 1 QVQLQDGAELVKGASVKLSCTASGYTFTSYMMHWKQRPQGLEWIGRIDPNSGCTKY 60  
Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYYC-NAYYGDYEGYWGQTTVTSS 117  
Db 61 NQKFKGATLTVDTSSTAYMQSLTSEDSAVYYCASHYGGSSSDYWGQGTTLTSS 118  
RESULT 4  
Q924R8  
ID Q924R8 PRELIMINARY; PRT; 146 AA.  
AC Q924R8;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE VH186.2-D-J-C mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB067781; BAB63266.1; -.  
DR InterPro; IPR007110; Ig\_1-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_1 LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 146  
SQ SEQUENCE 146 AA; 16216 MW; 92460F1FDP1B7538 CRC64;  
Query Match 64.5%; Score 407; DB 11; Length 146;  
Best Local Similarity 65.3%; Pred. No. 1.4e-33;  
Matches 79; Conservative 14; Mismatches 24; Indels 4; Gaps 2;  
Qy 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKQRPQGLEWIGWIDPENGDSDY 60  
Db 1 QVQLQDGAELVKGASVKLSCTASGYTFTSYMMHWKQRPQGLEWIGRIDPNSGCTKY 60  
Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYYC-NAYYGDYEGYWGQTTVTSS 116  
Db 61 NEKFKSKATLTVDKPSFAYMQSLTSEDSAVYYCARSYGSSLYYFDYWGQGTTLTSS 120  
Qy 117 S 117  
Db 121 S 121  
RESULT 5  
Q924Q7  
ID Q924Q7 PRELIMINARY; PRT; 145 AA.  
AC Q924Q7;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)



RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC003888; AAH03888.1; --  
DR HSSP; P01842; 7FAB.  
DR InterPro; IPR007110; Ig\_Like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 63.5%; Score 400.5; DB 11; Length 473;  
Best Local Similarity 63.7%; Pred. No. 2.8e-32;  
Matches 79; Conservative 16; Mismatches 22; Indels 7; Gaps 2;  
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
DB 20 QVQLQSGDAELVKGASVKISCKVSGYFTDHTIHVWKORPEQGLEWIGIYIPRDGSTKY 79  
QY 61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYC---NAVYG--DYEGWGQGTIV 113  
DB 80 NEKFKGKATLTADKSSSTAYMQLSLTSEDSAVCFCSRGGSIYGYGLYFDYWGQGTI 139  
QY 114 TVSS 117  
DB 140 TVSS 143

RESULT 9  
ID Q8K172 PRELIMINARY; PRT; 482 AA.  
AC Q8K172;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Similar to expressed sequence A1893585.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast tumor;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC028249; AAH28249.1; --  
DR InterPro; IPR007110; Ig\_Like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00407; IGV; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
SQ SEQUENCE 482 AA; 52121 MW; A06FF083E771D084 CRC64;

Query Match 63.5%; Score 400.5; DB 11; Length 482;  
Best Local Similarity 65.5%; Pred. No. 2.8e-32;  
Matches 78; Conservative 14; Mismatches 24; Indels 3; Gaps 2;  
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
DB 20 QVQLQSGAELVKGASVKISCKASGYFTSYMHVWKORPGGLEWIGRIDPNSGTTY 79  
QY 61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYCNAYYGYDEG--YWGQGTIVTSS 117  
DB 80 NEKFKGKATLTADKSSSTAYMQLSLTSEDSAVYYCTR-EGDYDAMYWGQGTIVTSS 137

RESULT 10  
ID Q9D8L4 PRELIMINARY; PRT; 473 AA.  
AC Q9D8L4;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE 181006009rik protein.  
GN IGH-1 OR 181006009RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L. M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,  
RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K. H., Weltz C., Whitaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK007918; BAB25349.1; --  
DR HSSP; P01842; 7FAB.  
DR MGD; MGI:96443; Igh-1.  
DR InterPro; IPR007110; Ig\_Like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 63.2%; Score 399; DB 11; Length 473;  
Best Local Similarity 64.7%; Pred. No. 3.9e-32;  
Matches 77; Conservative 18; Mismatches 22; Indels 2; Gaps 1;  
QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
DB 20 QVQLQSGAELVKGASVKISCKASGYFTDYINHWKORPGQGLEWIGKIGPGSGTTY 79  
QY 61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYC---NAVYGYDEGYWGQGTIVTSS 117  
DB 80 NEKFKGKATLTADKSSSTAYMQLSLTSEDSAVVFCARSGYDYDMFAYWGQGTIVTSSA 138

RESULT 11  
ID Q924Q5 PRELIMINARY; PRT; 143 AA.  
AC Q924Q5;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE VH186.2-D-J-C mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.



OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB067795; BAB63280.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 143  
SQ SEQUENCE 143 AA; 15908 MW; 55A2372870F0D568 CRC64;

Query Match 63.2%; Score 398.5; DB 11; Length 143;  
Best Local Similarity 65.5%; Pred. No. 1e-32;  
Matches 78; Conservative 14; Mismatches 24; Indels 3; Gaps 2;

OY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
DB 1 QVQLQPGALVKGASVKLSCKASGYTFTSYMHVWKORPGRGLEWIGRIDPNSGGTKY 60  
OY 61 APKFGKATMTADSSSNTAYLQLSLTSEPTAVYYCNAYGYDEGY--WGQGTTVTVSS 117  
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYYCARFY-DYEYFDVWGTTTVTVSS 118

RESULT 12  
O924R0 PRELIMINARY; PRT; 143 AA.  
AC Q924R0;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE VH186.2-D-J-C mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB067790; BAB63275.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 143  
SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

Query Match 63.2%; Score 398.5; DB 11; Length 143;  
Best Local Similarity 65.3%; Pred. No. 1e-32;  
Matches 77; Conservative 14; Mismatches 26; Indels 1; Gaps 1;

OY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
DB 1 QVQLQPGALVKGASVKLSCKASGYTFTSYMHVWKORPGRGLEWIGRIDPNSGGTKY 60  
OY 61 APKFGKATMTADSSSNTAYLQLSLTSEPTAVYYCNAYGYDEGY-DYEYFDVWGTTTVTVSS 117

DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYYCARWEDYAMDYWGQTSVTVSS 118

RESULT 13  
O924R2 PRELIMINARY; PRT; 140 AA.  
AC Q924R2;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE VH186.2-D-J-C mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB067788; BAB63273.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 140  
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match 63.1%; Score 398; DB 11; Length 140;  
Best Local Similarity 66.1%; Pred. No. 1.1e-32;  
Matches 78; Conservative 13; Mismatches 23; Indels 4; Gaps 2;

OY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
DB 1 QVQLQPGALVKGASVKLSCKASGYTFTSYMHVWKORPGRGLEWIGRIDPNSGGTKY 60  
OY 61 APKFGKATMTADSSSNTAYLQLSLTSEPTAVYYC-NAYGYDEGYWGQTTTVTVSS 117  
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYYCARIYAGD--YWGQTSVTVSS 115

RESULT 14  
O924Q1 PRELIMINARY; PRT; 142 AA.  
AC Q924Q1;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE V23-D-J-C mu protein (Fragment).  
GN V23-D-J-C MU.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB069913; BAB63929.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.





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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 117 Seconds  
(without alignments)  
158.727 Million cell updates/sec

Title: US-09-865-198-22

Perfect score: 631

Sequence: 1 QVKLQSGAEVLVSGASVKL.....AYYGDYEGYWGQGTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03:\*

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*

5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*

6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*

7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*

8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	631	100.0	117	22	AAE13143 Humanised antibody
2	631	100.0	117	23	AAB82709 VEGF antagonist an
3	631	100.0	117	23	AAU74417 Antigen-binding pr
4	631	100.0	117	24	ABJ26729 VEGF binding relat
5	631	100.0	136	22	AAB82701 VEGF antagonist an
6	631	100.0	136	23	AAE28916 c-p1C11 vector hea
7	631	100.0	238	23	AAE25963 KDR binding immuno
8	631	100.0	238	23	AAU74420 Antigen-binding pr
9	631	100.0	238	24	ABJ26732 VEGF binding relat

10	627	99.4	135	23	AAE25965
11	625	99.0	238	23	AAE25961
12	624	98.9	117	21	AAI97235
13	624	98.9	117	23	AAE25955
14	624	98.9	117	23	AAU74412
15	624	98.9	117	24	ABJ26724
16	624	98.9	240	23	AAE25960
17	624	98.9	240	23	AAU74419
18	624	98.9	240	24	ABJ26731
19	619	98.1	136	22	AAE13145
20	558.5	88.5	535	18	AAW28491
21	558.5	88.5	535	18	AAW28492
22	554.5	87.9	116	21	AAI70787
23	553.5	87.7	243	19	AAW60769
24	536.5	85.0	112	20	AAW89173
25	536.5	85.0	118	18	AAW01586
26	535	84.8	119	24	ABB99635
27	517.5	82.0	270	16	AAI75719
28	517.5	82.0	556	22	AAU97935
29	517.5	82.0	556	22	AAU80040
30	511.5	81.1	124	15	AAI60566
31	511.5	81.1	249	19	AAW60770
32	511.5	81.1	553	18	AAW11508
33	511.5	81.1	553	20	AAW73223
34	511.5	81.1	553	22	AAI85455
35	511.5	81.1	553	22	AAI61960
36	506.5	80.3	124	15	AAI60565
37	506.5	80.3	124	23	ABB83941
38	506.5	80.3	124	24	ABG75594
39	505.5	80.1	116	13	AAI24807
40	504.5	80.0	116	14	AAI42804
41	503.5	79.8	124	20	AAI39528
42	503.5	79.8	124	23	AAU76632
43	502.5	79.6	120	18	AAW41387
44	502.5	79.6	255	18	AAW41394
45	502.5	79.6	281	20	AAW82744

ALIGNMENTS

RESULT 1	
AAE13143	
ID	AAE13143 standard; Protein; 117 AA.
AC	AAE13143;
XX	
DT	28-JAN-2002 (first entry)
XX	
DE	Humanised antibody heavy chain fragment.
XX	
KW	Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW	cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW	monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW	human; chimeric.
XX	
OS	Chimeric - Homo sapiens.
OS	Chimeric - Mus sp.
XX	
PN	WO200174296-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US10504.
XX	
PR	31-MAR-2000; 2000US-0540770.
XX	
PA	(IMCL-) IMCLONE SYSTEMS INC.
PA	(CORR ) CORNELL RES FOUND INC.
XX	
PI	Witte L, Rafii S;
XX	
DR	WPI; 2001-662942/76.

Mouse anti-KDR p1C  
KDR binding immuno  
Variable heavy cha  
Mouse anti-KDR p1C  
Antigen-binding pr  
VEGF binding relat  
KDR binding immuno  
Antigen-binding pr  
VEGF binding relat  
Chimeric p1C11 hea  
Human p53 protein  
Human p53 protein  
Murine anti-p53 mo  
Single chain antib  
Anti-p53 monoclon  
Lead binding Mab 1  
2A2 monoclonal ant  
MFE-23 antibody.  
scFv-rearranged ca  
scFv-rearranged ca  
Anti-carcinoembryo  
Single chain antib  
Single chain anti-  
H22-anti-CEA antib  
Bispecific single  
Bispecific single  
Anti-carcinoembryo  
Mouse monoclonal a  
Mouse COL-1 Variab  
RSV19 VH. Mus mus  
RSV19 heavy chain  
Murine COL1 VH cha  
Murine Col-1(CEA a  
Anti-CEA antibody  
Chimeric anti-CEA  
Fusion protein p1C

DR N-PSDB; AAD21669.  
XX  
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
tumors such as leukemias or multiple myeloma comprises treatment with  
PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
PS Claim 8; Page 15; 68pp; English.  
XX  
CC The invention relates to a method for inhibiting the growth of non-solid  
tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains complementary determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised  
CC antibody heavy chain fragment used in the exemplification of the  
invention.  
XX  
SQ Sequence 117 AA;  
Query Match 100.0%; Score 631; DB 22; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
Db 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
QY 61 APKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYYGDYEGYWGQGTIVTVSS 117  
Db 61 APKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYYGDYEGYWGQGTIVTVSS 117  
RESULT 2  
AAB82709  
ID AAB82709 standard; Protein; 117 AA.  
XX  
AC AAB82709;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE VEGF antagonist antibody IMC-1C11 heavy chain variable region.  
XX  
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; heavy chain.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 26..35  
FT /label= CDR-H1  
FT /note= "complementarity determining region 1"  
FT 50..66  
FT /label= CDR-H2  
FT /note= "complementarity determining region 2"  
FT 99..106  
FT /label= CDR-H3  
FT /note= "complementarity determining region 3"  
XX  
PN WO200154723-A1.  
XX  
PD 02-AUG-2003.  
XX

PF 29-JAN-2001; 2001WO-US02839.  
XX  
XX 28-JAN-2000; 2000US-0178791.  
PR 31-MAR-2000; 2000US-0539692.  
XX  
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
XX Kerbel R;  
XX  
XX WPI; 2001-514531/56.  
DR N-PSDB; AAH26405.  
XX  
XX  
PT Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX  
PS Disclosure; Page 38; 42pp; English.  
XX  
XX The present sequence is that of the heavy chain variable region of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
SQ Sequence 117 AA;  
Query Match 100.0%; Score 631; DB 22; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
Db 1 QVKLOQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
QY 61 APKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYYGDYEGYWGQGTIVTVSS 117  
Db 61 APKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYYGDYEGYWGQGTIVTVSS 117  
RESULT 3  
AAU74417  
ID AAU74417 standard; peptide; 117 AA.  
XX  
XX AAU74417;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Antigen-binding protein heavy chain variable domain (VH) #2.  
XX  
KW Antigen-binding protein; antibody heavy chain variable domain;  
KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;  
KW cell proliferation inhibitor.  
XX  
OS Mus sp.  
OS  
XX  
PN WO200190192-A2.  
XX

XX		29-NOV-2001.	
PD			
XX			
PX	24-MAY-2001;	2001WO-US16924.	
XX			
PR	24-MAY-2000;	2000US-206749P.	
XX			
PA	(IMCL-) IMCLONE SYSTEMS INC.		
PI	Zhu Z;		
XX			
DR	WPI; 2002-106189/14.		
N-PSDB;	AAS20288.		
PT	New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides		
XX			
PS	Claim 61; Page 60; 64pp; English.		
CC	The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting VEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigations, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (VH) incorporated into Fv, an engineered protein containing a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in the method of the invention.		
CC			
XX	Sequence 117 AA;		
SQ			
	Query Match 100.0%; Score 631; DB 23; Length 117; Best Local Similarity 100.0%; Pred. No. 1.5e-47; Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Oy	1 QVKLQQSGAELVSGSVKLSCTTSGFNICKFYMHMWKORPEOGIEWIGIDPENDSDY 60 		
Db	1 QVKLQQSGAELVSGSAVKLSCTTSGFNICKFYMHMWKQRPEOGIEWIGIDPENDSDY 60 		
Oy	61 APKFQGATMTADSSSNNTAVYLQLSLTSEDYAVYYCNAYYGDEYWGQTTVTVSS 117 		
Db	61 APKFQGATMTADSSSNNTAVYLQLSLTSEDYAVYYCNAYYGDEYWGQTTVTVSS 117 		
RESULT 4			
ID	ABJ26729 standard; Protein; 117 AA.		
XX	ABJ26729;		
AC			
XX	01-MAY-2003 (first entry)		
DT			
DE	VEGF binding related protein SEQ ID No 22.		
XX			
KM	Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;		
KW	leukemia cell; vascular endothelial growth factor; tumour;		
KM	bispecific antigen-binding protein; mouse; murine.		
XX			

OS	Mus sp.
XX	PN WO2003002144-A1.
XX	PD 09-JAN-2003.
XX	PF 26-JUN-2002; 2002WO-US20332.
XX	PR 26-JUN-2001; 2001US-301299P.
PA	(IMCL-) IMCLONE SYSTEMS INC.
PI	Zhu Z;
XX	WPI; 2003-201468/19.
DR	N-PADB; ABT23307.
PT	New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
PS	Disclosure; Page 53; 98pp; English.
CC	The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF)
CC	receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
SQ	Sequence    117 AA;
OY	Query Match                  100.0%; Score 631; DB 24; Length 117; Best Local Similarity         100.0%; Pred.No.1.5e+47; Matches 117; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
Dd	1 QVKLQQSGAELVGSAGSVKLSCTTS GFNIKDFYMHWKQRPEQLGWIGIDPENGDSDY 60     1 QVKLQQSGAEIVGSGAVKLSC TTS GFNIKF YMHWKQRPEGLGWIGIDPENGDSDY 60
Oy	61 APKEQGATMTADSSNSTAYLLSLSTSEDTAAVVYCNAVYYDYEYGWGQTTVTVSS 117       61 APKFGKATMTADSSNSTAYLL SLSTSED TA VVCNA YYDY EGYWGQT TVTVSS 117
ID	AAB82701 standard; Protein; 136 AA.  AAB82701,  15-OCT-2001 (first entry)  DE VEGF antagonist antibody IMC-1C11 heavy chain variable region. Xx Km IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; Km vascular endothelial growth factor; angiogenesis; antiangiogenic; Km antitumour; neoplasm; collagen-vascular disease; autoimmune disease; Km tumour; breast carcinoma; lung carcinoma; prostate carcinoma; Km colon carcinoma; ovarian carcinoma; neuroblastoma; Km glioblastoma multiforme; melanoma; therapy; heavy chain. Xx Os Chimeric - Mus sp. Os Chimeric - Homo sapiens. FH Key Location/Qualifiers FT Peptide 1..19 /label= signal peptide



FT Protein 20..136  
FT /label= Mature\_protein  
FT Region 45..54  
FT /label= CDR-H1  
FT /note= "complementarity determining region 1"  
FT Region 59..85  
FT /label= CDR-H2  
FT /note= "complementarity determining region 2"  
FT Region 118..125  
FT /label= CDR-H3  
FT /note= "complementarity determining region 3"  
XX  
XX WO200154723-A1.  
XX  
XX 02-AUG-2001.  
XX  
XX 29-JAN-2001; 2001WO-US02839.  
XX  
XX 28-JAN-2000; 2000US-0178791.  
PR 31-MAR-2000; 2000US-0539692.  
XX  
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
XX Kerbel R;  
PI  
XX  
XX WPI; 2001-514531/56.  
DR N-PSDB; AAH26413.  
XX  
XX  
XX Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX  
XX  
XX Disclosure; Fig 1; 42pp; English.  
XX  
XX The present sequence is that of the heavy chain variable region of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
XX Sequence 136 AA;  
SQ  
Query Match 100.0%; Score 631; DB 22; Length 136;  
Best Local Similarity 100.0%; Pred. No. 1.7e-47;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKQRPDQGLWIGWIDPENGSDSY 60  
Db 20 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHVWKQRPDQGLWIGWIDPENGSDSY 79  
Qy 61 APKFGKATMTADSSNTAYLQLSLTSEDTAVYYCNAYGYDEGYWGQGTVTVSS 117  
Db 80 APKFGKATMTADSSNTAYLQLSLTSEDTAVYYCNAYGYDEGYWGQGTVTVSS 136  
RESULT 6  
AAE28916

ID AAE28916 standard; Protein; 136 AA.  
XX  
XX AAE28916;  
AC  
XX 27-DEC-2002 (first entry)  
DT  
XX  
XX c-p1C11 vector heavy chain (VH) protein.  
DE  
XX  
XX Human; tumour; vascular endothelial growth factor receptor; metastasis;  
KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;  
KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; VH.  
XX  
XX Chimeric - Unidentified.  
OS Chimeric - Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
FH Region 1..19  
FT /note= "Leader peptide"  
FT Region 20..136  
FT /note= "Human heavy chain constant region"  
FT Region 45..54  
FT /note= "CDR1"  
FT Region 69..85  
FT /note= "CDR2"  
FT Region 118..125  
FT /note= "CDR3"  
XX  
XX WO200270008-A1.  
XX  
XX 12-SEP-2002.  
XX  
XX 04-MAR-2002; 2002WO-US06762.  
XX  
XX 02-MAR-2001; 2001US-0798689.  
XX  
XX (IMCL-) IMCLONE SYSTEMS INC.  
PA (ROCK/) ROCKWELL P.  
PA (GOLD/) GOLDSTEIN N I.  
XX  
XX WPI; 2002-691738/74.  
DR N-PSDB; AAD46315.  
XX  
XX Inhibiting tumor growth in humans involves administering vascular  
PT endothelial growth factor receptor antagonists in combination with  
PT radiation, chemotherapeutic agents, or epidermal growth factor receptor  
PT antagonists -  
XX  
XX  
XX Example 9; Fig 19; 151pp; English.  
XX  
XX The invention relates to a method of inhibiting tumour growth which  
CC involves administering, vascular endothelial growth factor receptor  
CC (VEGFR) antagonists in combination with radiation, chemotherapeutic  
CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method  
CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.  
CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,  
CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,  
CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over  
CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour  
CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.  
CC It is preferably useful for treating subjects with both solid tumours,  
CC preferably high vascular tumours and non-solid tumours. The inhibition  
CC or reduction of tumour growth includes prevention or inhibition of the  
CC progression of tumour, including cancerous and non-cancerous tumours,  
CC where the progression of tumours includes the invasiveness, metastasis,  
CC recurrence and increase in size of the tumour. The present sequence is  
CC c-p1C11 vector containing human heavy chain (VH) protein. This sequence  
XX is used to illustrate the method of the invention.  
XX  
XX Sequence 136 AA;  
SQ  
Query Match 100.0%; Score 631; DB 23; Length 136;  
Best Local Similarity 100.0%; Pred. No. 1.7e-47;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





CC	(scFv), an engineered protein containing a variable light and variable heavy domain on one polypeptide, described in the method of the invention.
CC	
XX	
SQ	Sequence 238 AA;
OY	Query Match 100.0%; Score 631; DB 23; Length 238; Best Local Similarity 100.0%; Pred. No. 3.1e-47; Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 QVKLOOSGAEVLVSGASVKLSCTTSGFNKIDFYMHMWKORPEOGLWIGWIDPENGDSDY 60       1 QVKLQSGAELVSGASVKLSCTTSGFNKIDFYMHWKORPEOGLWIGWIDPENGDSDY 60
OY	61 APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCMAYYGDIYEGYWGQGTVTVSS 117       61 APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCMAYYGDIYEGYWGQGTVTVSS 117
Db	
RESULT 9	
ABJ26732	
ID	ABJ26732 standard; Protein; 238 AA.
XX	
AC	ABJ26732;
XX	
DT	01-MAY-2003 (first entry)
DE	
XX	VEGF binding related protein SEQ ID No 28.
KW	Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KM	leukaemia cell; vascular endothelial growth factor; tumour;
KM	bispecific antigen-binding protein; mouse; murine.
XX	
OS	Mus sp.
XX	
PX	WO2003002144-A1.
PN	
XX	
PD	09-JAN-2003.
XX	
PF	26-JUN-2002; 2002WO-US20332.
XX	
PR	26-JUN-2001; 2001US-301299P.
XX	
PA	(IMCL-) IMCLONE SYSTEMS INC.
XX	
PI	Zhu Z;
DR	WPI; 2003-201468/19.
XX	
PT	New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
PT	
PS	Disclosure; Page 56-57; 98pp; English.
XX	
CC	The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
CC	
CC	
XX	
SQ	Sequence 238 AA;
Query Match	100.0%; Score 631; DB 24; Length 238;
Best Local Similarity	100.0%; Pred. No. 3.1e-47;
Matches 117; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEOGLWIGWIDPENGSDSY	60
Db	1	QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEOGLWIGWIDPENGSDSY	60
QY	61	APKFGKATMTADSSSNTAVYLQISLTSSEDTAVYYCNAYYGDYEGYGQGTIVSS	117
Db	61	APKFGKATMTADSSSNTAVYLQISLTSSEDTAVYYCNAYYGDYEGYGQGTIVSS	117
RESULT 10			
ID	AAE25965	standard; Protein; 135 AA.	
XX	AAE25965;		
XX	15-NOV-2002	(first entry)	
DE	Mouse anti-KDR p1C11 scFv antibody VH region #2.		
XX			
KW	Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;		
KW	foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;		
KW	VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;		
KM	p1C11; scFv antibody.		
XX			
OS	Mus musculus.		
XX			
FT	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT	Protein	/label= Signal-peptide	
FT	Region	/note= "Mouse p1C11 scFv antibody mature VH region"	
FT	Region	/note= "Heavy chain complementarity determining region 1 (CDR-H1)"	
FT	Region	/note= "Heavy chain complementarity determining region 2 (CDR-H2)"	
FT	Region	/note= "Heavy chain complementarity determining region 3 (CDR-H3)"	
PN	US2002064528-A1.		
XX			
PD	30-MAY-2002.		
XX			
PF	12-OCT-2001; 2001US-0976787.		
XX			
PR	28-JAN-2000; 2000US-0493539.		
XX			
PA	(ZHUZ/) ZHU Z.		
XX	(WITT/) WITTE L.		
PI	Zhu Z, Witte L;		
XX			
DR	WPI; 2002-589175/63.		
DR	N-PSDB; AAD42832.		
XX			
PT	Novel immunoglobulin molecule for reducing tumor growth, binds to		
PT	kinase insert domain-containing receptor with an affinity comparable to		
PT	human vascular endothelial growth factor, and neutralizes activation of		
PT	KDR		
XX			
PS	Disclosure; Fig 4; 34pp; English.		
XX			
CC	The present invention relates to novel immunoglobulin molecules that bind		
CC	to kinase insert domain-containing receptor (KDR) (a human homologue of		
CC	mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable		
CC	to human vascular endothelial growth factor (VEGF) and that neutralises		
CC	activation of KDR. Sequences of the invention are useful for neutralising		
CC	the activation of KDR, for reducing tumour growth and for inhibiting		
CC	angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody		
CC	heavy chain variable region (VH).		
XX			

SQ Sequence 135 AA;  
Query Match 99.4%; Score 627; DB 23; Length 135;  
Best Local Similarity 100.0%; Pred. No. 3.8e-47;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHWKQRPQGLEWIGWIDPENGDSY 60  
Db 20 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHWKQRPQGLEWIGWIDPENGDSY 79

QY 61 APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDEGYWGQGTVTVS 116  
Db 80 APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDEGYWGQGTVTVS 135

RESULT 11  
AAE25961  
ID AAE25961 standard; Protein; 238 AA.  
XX  
AC AAE25961;  
XX 15-NOV-2002 (first entry)  
DT  
XX KDR binding immunoglobulin related mouse protein #2.  
DE  
XX Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
KW p1C11; scFv antibody.  
XX  
OS Mus sp.  
XX  
XX US2002064528-A1.  
XX  
XX 30-MAY-2002.  
PD  
XX  
XX 12-OCT-2001; 2001US-0976787.  
PF  
XX  
XX 28-JAN-2000; 2000US-0493539.  
PR  
XX  
PA (ZHUZ/) ZHU Z.  
PA (WITT/) WITTE L.  
XX  
PI Zhu Z, Witte L;  
XX  
XX WPI; 2002-589175/63.  
DR  
DR N-PSDB; AAD42825.  
XX  
XX Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR  
XX  
PS Disclosure; Page 17-18; 34pp; English.  
XX  
XX The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is KDR binding immunoglobulin related  
CC mouse protein.  
XX  
SQ Sequence 238 AA;

Query Match 99.0%; Score 625; DB 23; Length 238;  
Best Local Similarity 99.1%; Pred. No. 1e-46;  
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHWKQRPQGLEWIGWIDPENGDSY 60  
Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHWKQRPQGLEWIGWIDPENGDSY 60

QY 61 APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDEGYWGQGTVTVS 117  
Db 61 APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDEGYWGQGTVTVS 117

RESULT 12  
AAY97235  
ID AAY97235 standard; Protein; 117 AA.  
XX  
XX AAY97235;  
AC  
XX 19-DEC-2000 (first entry)  
DT  
XX  
XX Variable heavy chain fragment of anti-SI(KDR) antibody.  
DE  
XX Immunoglobulin; antibody; complementary determining region; CDR;  
KW VEGF; vascular endothelial growth factor; KDR;  
KW kinase insert domain containing receptor; multivalent; monovalent;  
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;  
KW glioblastoma multiforme; hemangioblastoma; AIDS;  
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;  
KW acquired immune deficiency syndrome; AIDS; human.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
XX  
XX WO200044777-A1.  
XX  
XX 03-AUG-2000.  
PD  
XX  
XX 28-JAN-2000; 2000WO-US02180.  
PF  
XX  
XX 29-JAN-1999; 99US-0117726.  
PR  
XX 29-JAN-1999; 99US-0240736.  
PR  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
XX  
PI Zhu Z, Witte L;  
XX  
XX WPI; 2000-505966/45.  
DR  
DR N-PSDB; AYA53767.  
XX  
XX Novel immunoglobulin molecules binding kinase insert domain-containing  
PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growth  
XX  
XX  
PS Claim 4; Page 50-51; 55pp; English.  
XX  
XX New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Kaposi's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulins of the invention.  
XX  
SQ Sequence 117 AA;

Query Match 98.9%; Score 624; DB 21; Length 117;  
Best Local Similarity 99.1%; Pred. No. 6e-47;  
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHWKQRPQGLEWIGWIDPENGDSY 60  
Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHWKQRPQGLEWIGWIDPENGDSY 60

Db 1 QVKLQOSGAEIVSGASVKLSTCTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60  
QY 61 APKFOGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGOGTTVTVSS 117  
Db 61 APKFOGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGOGTTVTVSS 117

RESULT 13  
AAE25955  
ID AAE25955 standard; Protein; 117 AA.

XX  
AC AAE25955;

DT 15-NOV-2002 (first entry)

DE Mouse anti-KDR pIC11 scFv antibody VH region #1.

KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
KW pIC11; scFv antibody.

OS Mus musculus.

PN US2002064528-A1.

PD 30-MAY-2002.

PF 12-OCT-2001; 2001US-0976787.

PR 28-JAN-2000; 2000US-0493539.

PA (ZHUZ/) ZHU Z.

PT (WITT/) WITTE L.

PI Zhu Z, Witte L;

DR WPI; 2002-589175/63.

DR N-PSDB; AAD42820.

PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
KDR -

PS Claim 4; Page 11; 34pp; English.

CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR pIC11 scFv antibody  
heavy chain variable region (VH).

SQ Sequence 117 AA;

Query Match 98.9%; Score 624; DB 23; Length 117;  
Best Local Similarity 99.1%; Pred. No. 6e-47;  
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQOSGAEIVSGASVKLSTCTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60  
Db 1 QVKLQOSGAEIVSGASVKLSTCTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60

QY 61 APKFOGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGOGTTVTVSS 117  
Db 61 APKFOGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGOGTTVTVSS 117

RESULT 14  
AAU74412

ID AAU74412 standard; peptide; 117 AA.

AC AAU74412;

DT 26-MAR-2002 (first entry)

DE Antigen-binding protein heavy chain variable domain (VH) #1.

KW Antigen-binding protein; antibody heavy chain variable domain;  
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;  
KW cell proliferation inhibitor.

OS Mus sp.

PN WO200190192-A2.

PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US16924.

PR 24-MAY-2000; 2000US-206749P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

DR WPI; 2002-106189/14.

DR N-PSDB; AAS20283.

PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides -

PS Claim 57; Page 57; 64pp; English.

CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific. Homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This sequence represents a heavy chain variable domain (VH) incorporated  
CC into Fv, an engineered protein containing a heavy chain variable domain  
CC and a light chain variable domain in one polypeptide chain, described in  
CC the method of the invention.

SQ Sequence 117 AA;

Query Match 98.9%; Score 624; DB 23; Length 117;  
Best Local Similarity 99.1%; Pred. No. 6e-47;  
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQOSGAEIVSGASVKLSTCTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60  
Db 1 QVKLQOSGAEIVSGASVKLSTCTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSGY 60

QY 61 APKFOGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGOGTTVTVSS 117  
Db 61 APKFOGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDYEGYWGOGTTVTVSS 117



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RESULT 15
ABJ26724
ID ABJ26724 standard; Protein; 117 AA.
XX
AC ABJ26724;
XX
DT 01-MAY-2003 (first entry)
XX
DE VEGF binding related protein SEQ ID No 7.
XX
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KW leukaemia cell; vascular endothelial growth factor; tumour;
KW bispecific antigen-binding protein; mouse; murine.
XX
OS Mus sp.
XX
PN WO2003002144-A1.
XX
PD 09-JAN-2003.
XX
PF 26-JUN-2002; 2002WO-US20332.
XX
PR 26-JUN-2001; 2001US-301299P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI: 2003-201468/19.
DR N-PSDB; ABT23302.
XX
PT New bispecific antibodies having antigen-binding sites specific for a
PT first vascular endothelial growth factor (VEGF) receptor and for a
PT second VEGF receptor, useful for inhibiting migration of leukemia
PT cells, or for treating tumors -
XX
XX
PS Claim 7; Page 49; 98pp; English.
XX
CC The invention relates to a novel antibody having a first antigen binding
CC site specific for a first vascular endothelial growth factor (VEGF)
CC receptor and a second antigen-binding site specific for a second VEGF
CC receptor. The bispecific antigen-binding proteins block activation of the
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
CC cellular functions such as mitogenesis of vascular endothelial cells
CC and migration of leukaemia cells. The antibodies are useful for treating
CC tumours and for in vivo or in vitro for investigative and diagnostic
CC methods. This sequence represents a mouse protein relating to the
CC bispecific antibodies that bind to the VEGF receptors of the invention.
XX
SQ Sequence 117 AA;

Query Match 98.9%; Score 624; DB 24; Length 117;
Best Local Similarity 99.1%; Pred. No. 6e-47;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSDY 60
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DB 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKQRPQGLEWIGWIDPENGDSDY 60
   |||||||

QY 61 APKFGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYYGDYEGYWGQGTIVTVSS 117
   |||||||
DB 61 APKFGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYYGDYEGYWGQGTIVTVSS 117
   |||||||
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Job time : 118 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:42:53 ; Search time 143.821 Seconds  
(without alignments)  
96.613 Million cell updates/sec

Title: US-09-865-198-22

Perfect score: 631

Sequence: 1 QVKLQSGAELVSGASVKL.....AYYGDYEGYWGQGTIVTSS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	631	100.0	117	9	US-09-976-787-23
2	631	100.0	117	10	US-09-865-198-22
3	631	100.0	117	11	US-09-798-689-7
4	631	100.0	238	9	US-09-976-787-29
5	631	100.0	238	10	US-09-865-198-28
6	631	100.0	238	11	US-09-798-689-21
7	624	98.9	117	9	US-09-976-787-7
8	624	98.9	117	10	US-09-865-198-7
9	624	98.9	240	9	US-09-976-787-28
10	624	98.9	240	10	US-09-865-198-27
11	558.5	88.5	535	10	US-09-968-851-38
12	536.5	85.0	112	14	US-10-032-482-7
13	503.5	79.8	124	10	US-09-974-052-1
14	503.5	79.8	124	10	US-09-974-051-1
15	503.5	79.8	124	11	US-09-974-516-1

	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
	502.5	502.5	488.5	488.5	488.5	488.5	488.5	488.5	488.5	478	476	473	473	467	464	462	454.5	454.5	451.5	448.5	428.5	428	422.5	417.5	417.5	417.5	417.5	417.5	417.5	415.5
	79.6	79.6	77.4	77.4	77.4	77.4	77.4	77.4	77.4	75.8	75.4	75.0	75.0	74.0	73.5	73.2	72.0	72.0	71.6	71.1	67.9	67.8	67.0	66.2	66.2	66.2	66.2	66.2	66.2	65.8
	120	10	255	136	136	136	136	136	136	117	136	117	117	121	121	120	116	116	120	137	139	117	244	124	124	124	124	124	124	242
	10	US-09-910-059-11	US-09-910-059-19	US-09-564-329A-11	US-09-855-153-11	US-09-854-811-11	US-09-934-773-11	US-09-963-620-11	US-09-855-632-11	US-10-225-784-11	US-09-158-120A-18	US-09-749-873-29	US-09-802-083-1	US-10-165-732A-1	US-10-252-978-16	US-10-095-496-1	US-09-910-483-37	US-09-910-483-41	US-10-056-794-15	US-10-283-349-31	US-09-809-739-5	US-09-158-120A-17	US-09-940-391-1	US-09-974-052-9	US-09-974-052-12	US-09-974-051-9	US-09-974-051-12	US-09-974-516-9	US-09-974-516-12	US-10-259-087A-18
	Sequence 11, Appl	Sequence 19, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 18, Appl	Sequence 11, Appl	Sequence 29, Appl	Sequence 1, Appl	Sequence 16, Appl	Sequence 2, Appl	Sequence 37, Appl	Sequence 41, Appl	Sequence 15, Appl	Sequence 31, Appl	Sequence 5, Appl	Sequence 17, Appl	Sequence 1, Appl	Sequence 9, Appl	Sequence 9, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 9, Appl	Sequence 12, Appl	Sequence 18, Appl	

## ALIGNMENTS

RESULT 1  
US-09-976-787-23  
Sequence 23, Application US/09976787  
Patent No. US20020064528A1  
GENERAL INFORMATION:  
APPLICANT: Zhu, Zhenping  
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
FILE REFERENCE: 11245/46505  
CURRENT APPLICATION NUMBER: US/09/976, 787  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 09/493, 539  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/117, 726  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 23  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Mouse  
US-09-976-787-23

Query Match 100.0%; Score 631; DB 9; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.2e-51;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	DB
1 QVKLQSGAELVSGASVKTCTSGFNKDFYHMYKORPEQGLEWIGWIDPENGSDY 60	1 QVKLQSGAELVSGASVKTCTSGFNKDFYHMYKORPEQGLEWIGWIDPENGSDY 60
117	117
61 APRKQKATMTADSSNTAYLQLSLTSEDYAVYYCNAYYGDYEGYWGQGTIVTSS 117	61 APRKQKATMTADSSNTAYLQLSLTSEDYAVYYCNAYYGDYEGYWGQGTIVTSS 117

RESULT 2  
US-09-865-198-22

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; Sequence 22, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-22
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Query Match          100.0%; Score 631; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 QVKLQOSGAELVSGASVKLSCTTSGFNKDFYMHWKORPEQGLEWIGWIDPENGSDSY 60
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Db      1 QVKLQOSGAELVSGASVKLSCTTSGFNKDFYMHWKORPEQGLEWIGWIDPENGSDSY 60
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OY      61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYCNAYYGDEYEGWGQTTVTVSS 117
      |||
Db      61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYCNAYYGDEYEGWGQTTVTVSS 117
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RESULT 3

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US-09-798-689-7
; Sequence 7, Application US/09798689
; Publication No. US20030103973A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; TITLE OF INVENTION: Combined With Radiation and Chemotherapy
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-7
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Query Match          100.0%; Score 631; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 QVKLQOSGAELVSGASVKLSCTTSGFNKDFYMHWKORPEQGLEWIGWIDPENGSDSY 60
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Db      1 QVKLQOSGAELVSGASVKLSCTTSGFNKDFYMHWKORPEQGLEWIGWIDPENGSDSY 60
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```
OY      61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYCNAYYGDEYEGWGQTTVTVSS 117
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Db      61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYCNAYYGDEYEGWGQTTVTVSS 117
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RESULT 4

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US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29
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Query Match          100.0%; Score 631; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6e-51;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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      |||
Db      1 QVKLQOSGAELVSGASVKLSCTTSGFNKDFYMHWKORPEQGLEWIGWIDPENGSDSY 60
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OY      61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYCNAYYGDEYEGWGQTTVTVSS 117
      |||
Db      61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYCNAYYGDEYEGWGQTTVTVSS 117
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RESULT 5

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US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28
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Query Match          100.0%; Score 631; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6e-51;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 QVKLQOSGAELVSGASVKLSCTTSGFNKDFYMHWKORPEQGLEWIGWIDPENGSDSY 60
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OY      61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYCNAYYGDEYEGWGQTTVTVSS 117
      |||
Db      61 APKFOGKATMTADSSSNTAYLQLSLTSEDTAVYYCNAYYGDEYEGWGQTTVTVSS 117
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RESULT 6  
US-09-798-669-21

; Sequence 21, Application US/09798689  
; Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; TITLE OF INVENTION: Combined with Radiation and Chemotherapy  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/326,552  
; PRIOR FILING DATE: 1994-10-20  
; PRIOR APPLICATION NUMBER: 08/196,041  
; PRIOR FILING DATE: 1994-02-10  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-798-689-21

Query Match 100.0%; Score 631; DB 11; Length 238;  
Best Local Similarity 100.0%; Pred. No. 2.6e-51;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60  
QY 61 APKFGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDEYGGGTTVTSS 117  
Db 61 APKFGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDEYGGGTTVTSS 117

RESULT 7

US-09-976-787-7  
; Sequence 7, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 7  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-976-787-7

Query Match 98.9%; Score 624; DB 9; Length 117;  
Best Local Similarity 99.1%; Pred. No. 5.4e-51;  
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60  
Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60  
QY 61 APKFGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDEYGGGTTVTSS 117  
Db 61 APKFGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDEYGGGTTVTSS 117

RESULT 8

US-09-865-198-7  
; Sequence 7, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methc  
; TITLE OF INVENTION: Production  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; PRIOR FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 7  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-7

Query Match 98.9%; Score 624; DB 10; Length 117;  
Best Local Similarity 99.1%; Pred. No. 5.4e-51;  
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60  
Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60  
QY 61 APKFGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDEYGGGTTVTSS 117  
Db 61 APKFGKATMTADSSSNTAYLQLSSLTSEDYAVYYCNAYYGDEYGGGTTVTSS 117

RESULT 9

US-09-976-787-28  
; Sequence 28, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 28  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-976-787-28

Query Match 98.9%; Score 624; DB 9; Length 240;  
Best Local Similarity 99.1%; Pred. No. 1.2e-50;  
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60  
Db 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60

OY 61 APKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYGYDEGYWGQGTTVTVSS 117  
Db 61 APKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYGYDEGYWGQGTTVTVSS 117

RESULT 10

US-09-865-198-27  
; Sequence 27, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-like Antigen Binding Proteins and Metho  
; TITLE OF INVENTION: Production  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; PRIOR FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Wordperfect 8.0 for Windows  
; SEQ ID NO 27  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-27

Query Match 98.9%; Score 624; DB 10; Length 240;  
Best Local Similarity 99.1%; Pred. No. 1.2e-50;  
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QVKLQSGAELVSGASVYKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
Db 1 QVKLQSGAELVSGASVYKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
OY 61 APKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYGYDEGYWGQGTTVTVSS 117  
Db 61 APKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYGYDEGYWGQGTTVTVSS 117

RESULT 11

US-09-968-851-38  
; Sequence 38, Application US/09968851  
; Publication No. US20020193561A1  
; GENERAL INFORMATION:  
; APPLICANT: CONSEILLER, EMMANUEL  
; BRACCO, LAURENT  
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL  
; USES THEREOF  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
; DUNNER, LLP  
; STREET: 1300 I Street, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/968,851  
; FILING DATE: 03-Oct-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/983,035  
; FILING DATE: 20-Feb-1998  
; APPLICATION NUMBER: PCT/FR96/01111  
; FILING DATE: 17-JUL-1996  
; APPLICATION NUMBER: FR 95/08729

; FILING DATE: 19-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Strauss, William L.  
; REGISTRATION NUMBER: 47,114  
; REFERENCE/DOCKET NUMBER: 03804.0142  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4400  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 535 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-968-851-38

Query Match 88.5%; Score 558.5; DB 10; Length 535;  
Best Local Similarity 88.9%; Pred. No. 3.4e-44;  
Matches 104; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

OY 1 QVKLQSGAELVSGASVYKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGSDSY 60  
Db 3 QVKLQSGAELVSGASVYKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGSDSY 62  
OY 61 APKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYGYDEGYWGQGTTVTVSS 117  
Db 63 APKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYGYDEGYWGQGTTVTVSS 118

RESULT 12

US-10-032-482-7  
; Sequence 7, Application US/10032482  
; Publication No. US20020197270A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Itun  
; APPLICANT: ROTTER, Varda  
; APPLICANT: Wolkowicz, Roland  
; APPLICANT: RUIZ, Pedro  
; APPLICANT: EREZ-ALON, Neta  
; APPLICANT: HERKEL, Johannes  
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR  
; TITLE OF INVENTION: IMMUNITY  
; FILE REFERENCE: COHEN42  
; CURRENT APPLICATION NUMBER: US/10/032,482  
; PRIOR FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: US/09/445,602  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: PCT/IL98/00266  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: IL 121041  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-032-482-7

Query Match 85.0%; Score 536.5; DB 14; Length 112;  
Best Local Similarity 88.5%; Pred. No. 7.1e-43;  
Matches 100; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

OY 4 LQSGAELVSGASVYKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGSDSYAPK 63  
Db 1 LQSGAELVSGASVYKLSCTTSGFNKIDFYMHVWKORPEQGLEWIGWIDPENGSDSYAPK 60  
OY 64 FQKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYGYDEGYWGQGTTVTVSS 116  
Db 61 FQKATMTADSSSNTAYLQLSLTSEDYAVYYCNAYGYDEGYWGQGTTVTVSS 112



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RESULT 13
US-09-974-052-1
; Sequence 1, Application US/09974052
; Patent No. US20020165387A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,052
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-974-052-1

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	Query Match	79.8%;	Score 503.5;	DB 10;	Length 124;	
	Best Local Similarity	76.4%;	Pred. No. 9.4e-40;			
	Matches	97;	Conservative	8;	Mismatches	9; Indels 13; Gaps 2.
QY	1	QVKLQQSGAELVSGASVKLSCTTSGFNKIDFYMHMWKORPEOGLEWIGIDPENGSDSY	60			
	:	: :       :     :     :     :     :     :     :     :     :     :				
Db	1	EVQLQQSGAELVRSGASVKMSCTASGFNIKDYHMHWKQRPEQGLEWIGIDPENGDTEY	60			
QY	61	APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA-----YYGDEGYWGQG	110			
		:				
Db	61	APKFQGKATMTTDYSSNTAYLQLSSLTSEDYAVYYCNTRGSLSTMITTRWFDD---VMGAG	117			
QY	111	TTTVVSS	117			
Db	118	TTVAVSS	124			

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RESULT 14
US-09-974-051-1
; Sequence 1, Application US/09974051
; Publication No. US20020183495A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,051
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus

```

```

; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-974-051-1

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Query Match	79.8%;	Score 503.5;	DB 10;	Length 124;
Best Local Similarity	76.4%;	Pred. No. 9.4e-40;		
Matches 97; Conservative	8;	Mismatches 9;	Indels 13;	Gaps 2;

```

QY      1 QVKLQOOGAELVSGASVKLSCTTSGFNKIDFYMHMVWKORPEOGLEWIGWIDPENGDS DY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 EVOLQOOGAELVRS GASVKRMSCTASGFNIKDYMHMVWKORPEOGLEWIGWIDPENGDT EY 60

QY      61 APKFQKGATMTADSSSNTAYIQLSSLTSEDYAVYYCNA-----YYGDYEGYWGOG 110
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 APKFQKGATMTTDDYSSNTAYIQLSSLTSEDYAVYYC NTRGLSTMITTRWFED---VMGAG 117

QY      111 TTVTVSS 117
      ||| |||
Db      118 TTVAVSS 124

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RESULT 15
US-09-974-516-1
; Sequence 1, Application US/09974516
; Publication No. US20030027994A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,516
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-974-516-1

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[illegible]

Search completed: July 30, 2003, 10:20:30  
Job time : 144.821 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 37.7043 Seconds  
(without alignments)  
131.295 Million cell updates/sec

Title: US-09-865-198-22

Perfect score: 631

Sequence: 1 QVKLQSGAELVSGASVKL.....AYYGDYEGYWGQGTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued Patents\_AA:\*
- 2: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558.5	88.5	535	4 US-08-983-035A-38	Sequence 38, Appl
2	536.5	85.0	118	3 US-08-767-128-22	Sequence 22, Appl
3	517.5	82.0	270	2 US-08-652-507-2	Sequence 2, Appl
4	511.5	81.1	124	1 US-08-017-570-6	Sequence 6, Appl
5	511.5	81.1	124	1 US-08-471-426-6	Sequence 6, Appl
6	511.5	81.1	124	5 PCT-US94-01709-6	Sequence 6, Appl
7	511.5	81.1	553	2 US-08-661-052-16	Sequence 16, Appl
8	511.5	81.1	553	3 US-09-188-082-16	Sequence 16, Appl
9	511.5	81.1	553	4 US-09-364-088-16	Sequence 16, Appl
10	511.5	81.1	553	4 US-09-102-716-16	Sequence 16, Appl
11	506.5	80.3	124	1 US-08-017-570-4	Sequence 4, Appl
12	506.5	80.3	124	1 US-08-471-426-4	Sequence 4, Appl
13	506.5	80.3	124	5 PCT-US94-01709-4	Sequence 4, Appl
14	503.5	79.8	124	4 US-09-672-609-1	Sequence 1, Appl
15	503.5	79.8	124	4 US-09-025-403A-1	Sequence 1, Appl
16	502.5	79.6	281	4 US-09-423-439-44	Sequence 44, Appl
17	502.5	79.6	642	4 US-09-423-439-26	Sequence 26, Appl
18	502.5	79.6	666	4 US-09-423-439-51	Sequence 51, Appl
19	499.5	79.2	255	3 US-09-171-945-19	Sequence 19, Appl
20	488.5	77.4	136	4 US-09-564-329A-11	Sequence 11, Appl
21	484.5	76.8	120	3 US-09-171-945-11	Sequence 11, Appl
22	481.5	76.3	136	5 US-08-348-548-8	Sequence 8, Appl
23	481.5	76.3	136	5 PCT-US95-15716-8	Sequence 8, Appl
24	481	76.2	125	2 US-08-561-521-44	Sequence 44, Appl
25	481	76.2	125	5 PCT-US95-01219-44	Sequence 44, Appl
26	478	75.8	117	2 US-08-290-592E-18	Sequence 18, Appl
27	478	75.8	117	5 PCT-US95-10053-15	Sequence 15, Appl

28	478	75.8	117	5 PCT-US96-09448-18	Sequence 18, Appl
29	476	75.4	136	3 US-08-646-265A-29	Sequence 29, Appl
30	471.5	74.7	118	2 US-08-232-081B-38	Sequence 38, Appl
31	469	74.3	123	2 US-08-561-521-9	Sequence 9, Appl
32	469	74.3	123	5 PCT-US95-01219-9	Sequence 9, Appl
33	467	74.0	121	2 US-08-822-830B-13	Sequence 13, Appl
34	467	74.0	121	4 US-09-157-452B-16	Sequence 16, Appl
35	464	73.5	121	2 US-08-822-830B-2	Sequence 2, Appl
36	464	73.5	121	4 US-09-157-452B-2	Sequence 2, Appl
37	462	73.2	120	2 US-08-950-660-2	Sequence 2, Appl
38	462	73.2	120	5 PCT-US93-00030-2	Sequence 2, Appl
39	462	73.2	120	5 PCT-US93-00924-2	Sequence 2, Appl
40	461	73.1	140	2 US-08-561-521-4	Sequence 4, Appl
41	461	73.1	140	5 PCT-US95-01219-4	Sequence 4, Appl
42	459	72.7	136	1 US-08-024-253-2	Sequence 2, Appl
43	456	72.3	254	2 US-08-792-824-4	Sequence 4, Appl
44	456	72.3	254	2 US-08-792-824-7	Sequence 7, Appl
45	456	72.3	254	2 US-08-792-824-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-08-983-035A-38  
Sequence 38, Application US/08983035A  
Patent No. 6326464  
GENERAL INFORMATION:  
APPLICANT: CONSELLER, EMMANUEL  
BRACCO, LAURENT  
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP  
STREET: 1300 I Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983, 035A  
FILING DATE: 20-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/01111  
FILING DATE: 17-JUL-1996  
APPLICATION NUMBER: FR 95/08729  
FILING DATE: 19-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Straus, William L.  
REGISTRATION NUMBER: 47,114  
REFERENCE/DOCKET NUMBER: 03804.0142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-08-983-035A-38  
Query Match 88.5%; Score 558.5; DB 4; Length 535;  
Best Local Similarity 88.9%; Pred. No. 8.2e-49;

Matches	104;	Conservative	7;	Mismatches	5;	Indels	1;	Gaps	1;
QY	1	QVKLQOOSGAELVGSASVYKLSCTTSGFNIKD	FYMHMWKQRP	EOGLEWIGWIDPENGDS	SDY	60			
Db	3	QVQLQESGAELVGSASVYKLSCTASGFNIKDY	MMHWKQRP	EOGLEWIGWIDPEN	GDT	62			
QY	61	APKFQGGKATMTADSSSNAYVLQLSLTSEDT	AVYYCNAYGDE	GYWGQGT	TVTSS	117			
Db	63	APKFQGGKATMTADTSSSNAYVLQLSLTSEDT	AVYYCN	FYGDALDYWGQGT	TVTSS	118			

## RESULT 2

Sequence 22, Application US/08767128  
Patent No. 611079  
GENERAL INFORMATION:  
APPLICANT: WYLIE, DWANE E.  
APPLICANT: LOPEZ, OSVALDO  
APPLICANT: MURRAY, PETER JOSEPH  
APPLICANT: GOEBEL, PETER  
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
STREET: 3100 No. 6111079west Center, 90 South Seventh St  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/767,128  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE: 04-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09258  
FILING DATE: 05-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/541,373  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/462,798  
FILING DATE: 05-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.49USF1  
TELEPHONE: 612/371-5278  
TELEFAX: 612/332-9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-767-128-22

Query Match	85.0%;	Score 536.5;	DB 3;	Length 118;
Best Local Similarity	85.6%;	Pred. NO. 2.3e-47;		
Matches 101; Conservative	7;	Mismatches 9;	Indels 1;	Gaps 1;

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Qy      1 QVKLQSGABLVSGASVKLSCTTSGFNKDPFYMHWKORPEQGLEWIGWIBENGSDSY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 EVQLQQSGAEIVRSGASVKLSCTASGFNIKDYMHMWKORPEQGLEWIGWIBENGDT 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      61 APKFQGKATMTADSSSNTAYLQLSLTSEDPAVYYCNAY-YGDYEGYWGQGTAYTVSS 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 DPKFQGKATMTADTSSNIAYLQLSLTSEDPAVYYCNPYGYDDAMDYWGQGTAYTVSS 118

```

## RESULT 3

US-08-652-507-2  
Sequence 2, Application US/08652507  
Patent No. 5876691  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye, P.C.  
STREET: 1100 No. 5876691th Glebe Road, 8th Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,507  
FILING DATE: 02-Jul-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Arthur R. Crawford  
REGISTRATION NUMBER: 25,327  
REFERENCE/DOCKET NUMBER: 117-211  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-652-507-2

Query Match	82.0%;	Score 517.5;	DB 2;	Length 270;
Best Local Similarity	81.3%;	Pred. No. 5.3e-45;		
Matches 100; Conservative	5;	Mismatches 9;	Indels 9;	Gaps 2;

QY	I QVXLQOSGAELVGSGASVKLSCTTSGFNIKDFYMHMVKQRPEOGLWIGMIDPENGDSDY	60
	:       :       :       :	
Dd	27 QVXLQOSGAELVRSGTSVKLSTAGSFNIKDSYMHMLRQGPEGLEWIGMIDPENGDTEY	86
QY	61 APRKGAKATMTADSSSNTAYIQLSSLTSEDYAVYYCN-----AYYGDEGYMGOGTTVT	114
	:       :       :       :	
Dd	87 APRKGAKATFTTDTSNSTAYIQLSSLTSEDTAVYYCNEGTPTGPYYFD---YMGGQTIVT	143
QY	115 VSS 117.	
Dd	144 VSS 146	

## RESULT 4

US-08-017-570-6  
; Sequence 6, Application US/08017570

```
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-017-570-6

Query Match      81.1%; Score 511.5; DB 1; Length 124;
Best Local Similarity 77.2%; Pred. No. 8.4e-45;
Matches 98; Conservative 9; Mismatches 7; Indels 13; Gaps 2;

QY      1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
      :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVQLQSGAELVRSASVKMSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENGDT 60
QY      61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYYCNA-----YGDYEGYWGQG 110
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 APKFGKATMTDTSSNTAYLQLSLTSEDYAVYYCNRGLSTMTTRWFPD---VWGAG 117
QY      111 TTVTVSS 117
      |||:|||||
Db      118 TTVTVSS 124

RESULT 5
US-08-471-426-6
; Sequence 6, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
```

```
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-426-6
```

```
Query Match      81.1%; Score 511.5; DB 1; Length 124;
Best Local Similarity 77.2%; Pred. No. 8.4e-45;
Matches 98; Conservative 9; Mismatches 7; Indels 13; Gaps 2;
```

```
QY      1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENGDSY 60
      :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVQLQSGAELVRSASVKMSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENGDT 60
QY      61 APKFGKATMTADSSNTAYLQLSLTSEDYAVYYCNA-----YGDYEGYWGQG 110
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 APKFGKATMTDTSSNTAYLQLSLTSEDYAVYYCNRGLSTMTTRWFPD---VWGAG 117
QY      111 TTVTVSS 117
      |||:|||||
Db      118 TTVTVSS 124
```

```
RESULT 6
PCT-US94-01709-6
; Sequence 6, Application PC/TUS9401709
; GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01709
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```





Db 338 PKFOGKATFTTDSNTAYLQLSLTSEDYAVYYCNEGTPGTYFD---YWGQGTIVTV 394  
QY 116 SS 117  
Db 395 SS 396

RESULT 9

US-09-364-088-16  
; Sequence 16, Application US/09364088  
; Patent No. 6365161  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo, et al.  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
; OF ANTI-FC RECEPTOR ANTIBODIES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street, 24th floor  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/364,088  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/188,082  
; FILING DATE: 07-JUNE-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/484,172  
; FILING DATE: 07-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Remillard, Jane E.  
; REGISTRATION NUMBER: 38,872  
; REFERENCE/DOCKET NUMBER: MXI-043CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-7414  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-364-088-16

Query Match 81.1%; Score 511.5; DB 4; Length 553;  
Best Local Similarity 80.3%; Pred. No. 5.1e-44;  
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGSDSYA 61  
Db 278 IKLQSGAELVRSSTSVKLSCTASGFNIKDSYMHVLRQPEQGLEWIGWIDPENGDTTEYA 337  
QY 62 PKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYC-----AYYGDYEGYWGQGTIVTV 115  
Db 338 PKFOGKATFTTDSNTAYLQLSLTSEDYAVYYCNEGTPGTYFD---YWGQGTIVTV 394  
QY 116 SS 117  
Db 395 SS 396

RESULT 10  
US-09-102-716-16  
; Sequence 16, Application US/09102716

; Patent No. 6395272  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; Robert Graziانو  
; Joel Goldstein  
; Chezian Somasundaram  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
; OF ANTI-FC RECEPTOR ANTIBODIES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/102,716  
; FILING DATE: 22-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/661,052  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MXI-043CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
; US-09-102-716-16

Query Match 81.1%; Score 511.5; DB 4; Length 553;  
Best Local Similarity 80.3%; Pred. No. 5.1e-44;  
Matches 98; Conservative 6; Mismatches 9; Indels 9; Gaps 2;

QY 2 VKLQSGAELVSGASVKLSCTTSGFNKDFYMHVVKORPEQGLEWIGWIDPENGSDSYA 61  
Db 278 IKLQSGAELVRSSTSVKLSCTASGFNIKDSYMHVLRQPEQGLEWIGWIDPENGDTTEYA 337  
QY 62 PKFOGKATMTADSSSNTAYLQLSLTSEDYAVYYC-----AYYGDYEGYWGQGTIVTV 115  
Db 338 PKFOGKATFTTDSNTAYLQLSLTSEDYAVYYCNEGTPGTYFD---YWGQGTIVTV 394  
QY 116 SS 117  
Db 395 SS 396

RESULT 11  
US-08-017-570-4  
; Sequence 4, Application US/08017570  
; Patent No. 5472693  
; GENERAL INFORMATION:  
; APPLICANT: GOURLIE, BRIAN B  
; APPLICANT: RIXON, MARK W  
; APPLICANT: MEZES, PETER S  
; APPLICANT: KAPLAN, DONALD A  
; APPLICANT: SCHLOW, JEFFREY  
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC  
; ANTIGEN CHIMERIC ANTIBODIES  
; NUMBER OF SEQUENCES: 24

```

CORRESPONDENCE ADDRESS:
ADDRESS: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,570
FILING DATE: 19930216
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-017-570-4

```

Query Match	80.3%;	Score 506.5;	DB 1;	Length 124;
Best Local Similarity	76.4%;	Pred. No. 2.7e-44;		
Matches 97; Conservative	9;	Mismatches 8;	Indels 13;	Gaps 2;

```
QY      1 QVKLQSGAELVSGSGAVKLSCTTSGFNKDFYMHMWKORPEQGLEWIGMIDPENGS DY 600
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      1 EVQLQQSGAELVRSGLVSMSTASGFNIKDYIMHWKORPEQGLEWIGMIDPENGDTEY 600
```

```

QY      61 APKFGKATMTADSSNTAYLQLSSLTSEPTAVYYCNA-----YYGDYEGYWGOG 110
      ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 APKFGKATMTTDTSSNTAYLQLSSLTSEPTAVYYCNRGLSTMITTRWFFD---VWGAG 117

```

Qy	111	TTVTVSS	117
Db	118	TTTAVSS	124

## RESULT 12

US-08-471-426-4  
; Sequence 4, Application US/08471426  
; Patent No. 5808033

```

; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Duane C. Ulmer  
STREET: P.O. Box 1967

CITY: Midland  
STATE: MI

COUNTRY: US  
ZIP: 48641-1967

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

;
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;

```

```

; SOFTWARE Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-4

```

Query Match	80.3%;	Score 506.5;	DB 1;	Length 124;
Best Local Similarity	76.4%;	Pred. No. 2.7e-44;		
Matches 97;	Conservative	9;	Mismatches 8;	Indels 13;
				Gaps 2;

```
QY      1 QVKTQQSGAEIVGSGASVKLSCTTSGFNKDFYMHVVKQRPQQGLEWIGWIDPENGDS DY 600
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      1 EVQLQQSGAEIVRSGASVKMSCTASGFNFKDYMHVVKQRPQQGLEWIGWIDPENGDT EY 600
```

```

QY      61 APKFGKATMTADSSNSTAYLQLSSLTSEDTAVYYCNA-----YYGDYEGYWGQG 110
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 APKFGKATMTTDTSSNSTAYLQLSSLTSEDTAVYYCNRGLSTMTTRWFFD--VMGAG 117

```

Qy	111	TTVTSS	117
Db	118	TTTAVSS	124

## RESULT 13

PCT-US94-01709-4  
; Sequence 4, Application PC/TUS9401709  
; GENERAL INFORMATION:

APPLICANT: THE DOW CHEMICAL COMPANY  
APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES  
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC  
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Duane C. Ulmer  
STREET: P.O. Box 1967  
CITY: Midland

STATE: MI  
COUNTRY: US  
ZIP: 48641-

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible

```

```
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: PCT/US94/01703  
FILING DATE:  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: ULMER, DUANE C  
REGISTRATION NUMBER: 34,

REFERENCE/DOCKET NUMBER: 38,777-F  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 636-8104

```

; INFORMATION FOR SEQ ID NO: 4
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids

```

TYPE: amino acid  
TOPOLOGY: linear

```
MOLECULE TYPE: protein
PCT-US94-01/09-4

Query Match      80.3%; Score 506.5; DB 5; Length 124;
Best Local Similarity 76.4%; Pred. No. 2.7e-44;
Matches 97; Conservative 9; Mismatches 8; Indels 13; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENDSDY 60
   :|:||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EVQLQSGAELVRSASVKMSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENDTEY 60

QY 61 APKFQKATMTADSSNTAYLQLSLTSEDYAVYYCNA-----YYGDYEGYWGQG 110
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 APKFQKATMTDTSSNTAYLQLSLTSEDYAVYYCNRGLSTMTTRWFFD--VMGAG 117

QY 111 TTVTVSS 117
   ||| | | |
Db 118 TTVAVSS 124

RESULT 14
US-09-672-609-1
; Sequence 1, Application US/09672609
; Patent No. 6333405
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/672,609
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/025,403
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-672-609-1

Query Match      79.8%; Score 503.5; DB 4; Length 124;
Best Local Similarity 76.4%; Pred. No. 5.4e-44;
Matches 97; Conservative 8; Mismatches 9; Indels 13; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENDSDY 60
   :|:||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EVQLQSGAELVRSASVKMSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENDTEY 60

QY 61 APKFQKATMTADSSNTAYLQLSLTSEDYAVYYCNA-----YYGDYEGYWGQG 110
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 APKFQKATMTDTSSNTAYLQLSLTSEDYAVYYCNRGLSTMTTRWFFD--VMGAG 117

QY 111 TTVTVSS 117
   ||| | | |
Db 118 TTVAVSS 124

RESULT 15
US-09-025-403A-1
; Sequence 1, Application US/09025403A
; Patent No. 6417337
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
```

```
APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/025,403A
; CURRENT FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19642
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,694
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-025-403A-1
```

```
Query Match      79.8%; Score 503.5; DB 4; Length 124;
Best Local Similarity 76.4%; Pred. No. 5.4e-44;
Matches 97; Conservative 8; Mismatches 9; Indels 13; Gaps 2;

QY 1 QVKLQSGAELVSGASVKLSCTTSGFNKDFYMHVWKORPEQGLEWIGWIDPENDSDY 60
   :|:||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EVQLQSGAELVRSASVKMSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENDTEY 60

QY 61 APKFQKATMTADSSNTAYLQLSLTSEDYAVYYCNA-----YYGDYEGYWGQG 110
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 APKFQKATMTDTSSNTAYLQLSLTSEDYAVYYCNRGLSTMTTRWFFD--VMGAG 117

QY 111 TTVTVSS 117
   ||| | | |
Db 118 TTVAVSS 124
```

Search completed: July 30, 2003, 09:38:31  
Job time : 38.7043 secs

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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 31.3422 Seconds  
(without alignments)  
325.245 Million cell updates/sec

Title: US-09-865-198-23

Perfect score: 549

Sequence: 1 DIHLTQSPAIMSASPGKVT.....CQQRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:\*

1: pirl:\*

2: pirl2:\*

3: pirl3:\*

4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	93.4	106	2 B54378	Ig light chain V r
2	508	92.5	140	2 PL0013	Ig kappa chain pre
3	483	88.0	130	2 A32513	Ig kappa chain pre
4	483	88.0	132	2 S05268	Ig kappa chain pre
5	482	87.8	107	2 PC4405	Ig kappa chain V r
6	481	87.6	99	2 D38601	Ig kappa chain V r
7	476	86.7	107	2 A30562	Ig kappa chain V r
8	474	86.3	106	2 G27887	Ig kappa chain V r
9	472	86.0	106	2 PS0070	Ig kappa chain V r
10	471	85.8	107	2 B30562	Ig kappa chain V r
11	470	85.6	105	2 S26338	Ig kappa chain V r
12	465	84.7	103	2 S29591	Ig kappa chain V r
13	465	84.7	108	2 PL0278	Ig kappa chain V r
14	464	84.5	130	1 JL0079	Ig kappa chain pre
15	463	84.3	106	2 PS0071	Ig kappa chain V r
16	461	84.0	104	2 B49049	Ig kappa chain V r
17	461	84.0	108	2 PL0276	Ig kappa chain V r
18	461	84.0	108	2 PL0277	Ig kappa chain V r
19	461	84.0	120	2 S66536	Ig kappa chain V r
20	460	83.8	107	2 PD0011	Ig light chain V r
21	459.5	83.7	108	2 G30560	Ig kappa chain V r
22	458	83.4	91	2 S17626	Ig kappa chain V r
23	455	82.9	130	2 B32456	Ig kappa chain pre
24	453	82.5	108	2 PS0069	Ig kappa chain V r
25	451	82.1	235	2 S25058	Ig kappa chain - m
26	450	82.0	91	2 S17630	Ig kappa chain V r
27	450	82.0	104	2 JC6076	anti-D-dimer monoc
28	450	82.0	107	2 A42848	Ig light chain V r
29	450	82.0	107	2 PT0406	Ig kappa chain V r

30	448	81.6	107	2 S11119	Ig kappa chain V r
31	448	81.6	120	2 A34871	Ig kappa chain V r
32	447	81.4	107	2 S11118	Ig kappa chain V r
33	446.5	81.3	108	2 S38720	Ig light chain V r
34	446	81.2	100	2 S29590	Ig kappa chain V r
35	446	81.2	108	2 S29581	Ig kappa chain V r
36	446	81.2	130	2 S04573	Ig kappa chain pre
37	444	80.9	123	2 S05269	Ig kappa chain pre
38	443	80.7	107	2 PT0401	Ig light chain V r
39	441	80.3	106	2 PL0082	Ig kappa chain V r
40	441	80.3	107	2 PT0398	Ig light chain V r
41	440	80.1	97	2 S26341	Ig light chain V r
42	440	80.1	107	2 S11121	Ig light chain V r
43	437	79.6	107	2 PT0402	Ig kappa chain V r
44	436	79.4	97	2 PH1085	Ig light chain V r
45	436	79.4	99	2 S29585	Ig kappa chain V r

ALIGNMENTS

RESULT 1

B54378

Ig light chain V region anti-triplex DNA - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000

C:Accession: B54378

R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.

J. Biol. Chem. 269, 7019-7023, 1994

A:Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluoresc

A:Reference number: A54378; MUID:94165109; PMID:7509814

A:Accession: B54378

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-106 <AGA>

A:Cross-references: GB:S68985; NID:G545746; PIDN:AAB30096.1; PID:G545747

A:Experimental source: spleen and myeloma cell line MOPC 315.43

A>Note: sequence inconsistent with nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIPI:144175)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 513; DB 2; Length 106;

Best Local Similarity 94.3%; Pred. No. 6.5e-35;

Matches 99; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy

2 IEHTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLWIYSTSNLASGVPARF 61

Db 2 IVLTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLWIYSTSKLASGVPARF 61

Oy

62 SGSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106

Db 62 SGSGSGTSYSLISRMEADATYYCQQRSSYPFTFGAGTKLEIK 106

RESULT 2

PL0013

Ig kappa chain precursor V region (4C11) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000

C:Accession: PL0013

R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.

Mol. Immunol. 25, 33-40, 1988

A:Title: Structural basis of stimulatory anti-idiotypic antibodies.

A:Reference number: PL0011; MUID:88142863; PMID:3125424

A:Accession: PL0013

A:Molecule type: mRNA

A:Residues: 1-140 <CHE>

A:Experimental source: cell line 4C11

C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin





A:Accession: S26338  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-105 <STA>  
A:Cross-references: EMBL:X59197; NID:gs2328; PIDN:CAA41907.1; PID:gl334069  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F,16-89/Domain: immunoglobulin homology <IMM>

Query Match	85.6%	Score 470;	DB 2;	Length 105;
Best Local Similarity	88.5%	Pred. No. 1.9e-31;		
Matches 92;	Conservative 4;	Mismatches 8;	Indels 0;	Gaps 0;

```
QY      2 IELTQSPAIMSASPGKELYITTCSSASSSVSYMHWFQQPKETGSPKLMIYSTSNLASGVPAKF 61
        ||| ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db       2 IVLTQSPAIMSASPGKELYITSCASSSSVSYMYWYQQKPESPKPWITYRTSNLASGVPAKF 61
```

QY 62 SSGSGTSTLTISMEADATYYCQQRSSYPFTFGSGTKLEI 105  
|||  
Db 62 SSGSGTSTLTISSMEADATYYCQQRHSYPPTFGGSKLEI 105

RESULT 12  
S29591

IG kappa chain V region - mouse  
 C.Species: Mus musculus (house mouse)  
 C.Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C.Accession: S29591  
 R.Kavaler, J.  
 submitted to the EMBL Data Library, April 1991  
 A.Reference number: S26459  
 A.Accession: S29591  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-103 <KAV>  
 A.Cross-references: EMBL:X59094; NID:g52227; PIDN:CAA41820.1; PID:g52228  
 C.Superfamily: immunoglobulin V region; immunoglobulin homology  
 C.Keywords: heterotetramer; immunoglobulin  
 F.15-88/Domain: immunoglobulin homology <IMM>

Query Match	84.7%	Score 465;	DB 2;	Length 103;
Best Local Similarity	88.3%	Pred. No. 4.7e-31;		
Matches 91; Conservative	3;	Mismatches 9;	Indels 0;	Gaps 0;

```

OY      2 IELTQSPAIMSASPEKEVTITCSASSSVSYMHWFQQRKPGTSPKLMITYSTSNLASGVPA RF 61
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 IVLTQSPAIMSASPEKEVTITCSASSSVSYMHWFQQRKPGTSPKRWITYDTSKLASGVPA RF 60

```

QY 62 SGGSGGTSYSLTISRMEADATYYCQQRSSYPPTFGSGTKLE 104  
|||:|||||  
Db 61 SGGSGGTSYSLTISRMEADATYYCQQRSSNPPTFGAGTKLE 103

RESULT 13  
PL0278

Ig kappa chain V region (anti-DNA, 3H9VK) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
 C;Accession: PL0278  
 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J.  
 J. Exp. Med. 171, 265-297, 1990  
 A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A;Reference number: PL0231; MUID:9011618; PMID:2104919  
 A;Accession: PL0278  
 A;Molecule type: mRNA  
 A;Residues: 1-108 <SHL>  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;1-23/Region: framework 1  
 F;16-91/Domain: immunoglobulin homology <IMM>  
 F;24-35/Region: complementarity-determining 1  
 F;36-50/Region: framework 2  
 F;51-57/Region: complementarity-determining 2

F;58-89/Region: framework 3  
F;90-98/Region: complementarity-determining 3  
F;99-108/Region: framework 4

Query Match	84.7%;	Score 465;	DB 2;	Length 108;
Best Local Similarity	86.7%;	Pred. No. 4.9e-31;		
Matches 91; Conservative	4;	Mismatches 8;	Indels 2;	Gaps 1;

```

QY      4 LTQSPAIMSASPEEKVTITCSASSVS--YHNFQOKPGTSPKLWITYSTSNLASGVPARF 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      4 LTQSPAIMASPEEKVTIMTCSADSSVSSGNFHWQOKPGTSPKLWITYRTSNLASGVPARF 63

```

**QY**       62 SGSGSSTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 106  
            |||||  
**Db**       64 SGSGSSTSLTISRMEADATYYCQOWCGYPFTFGTGKLEIK 108  
            |||||

## RESULT 14

Ig kappa chain precursor V region (anti-phenylloxazolone 6F6) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 31-Dec-1991 #sequence\_revision 09-Aug-1996 #text\_change 16-Jul-1999  
 C/Accession: J10079; A49044; B49044  
 R/Kaartinen, M.; Rocca-Serra, J.; Maekela, O.  
 Mol. Immunol. 25, 859-865, 1988  
 A/Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reactive V genes  
 A/Reference number: J10076; MUID:89096973; PMID:3211160  
 A/Accession: J10079  
 A/Molecule type: mRNA  
 A/Residues: 1-130 <KAA>  
 A/Cross-references: GB:M27792; NID:g197159  
 A/Experimental source: mRNA clones for anti-phenylloxazolone antibody 6F6  
 A/Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10 as Arg  
 A/Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation  
 R/Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.  
 Eur. J. Immunol. 22, 1627-1634, 1992  
 A/Title: Non-random features of the repertoire expressed by the members of one V kappa gene  
 A/Reference number: A49044; MUID:92289826; PMID:1601044

A:Accession: A49044  
A:Molecule type: DNA  
A:Residues: 1-25 <MTL>  
A:Cross-references: GB:S37663; NID:g250214; PIDN:AAE2331.1; PID:g250217  
A:Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)

A;Accession: B49044  
A;Molecule type: DNA  
A;Residues: 114-116 <MIL2>  
A;Cross-references: GB:S37664; MID:q250215; P1DN:AAB22332.1; P1D:q250218

A:Experimental source: BALB/c germ-line  
A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 additional sequences extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)  
A:Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)  
C:Genetics:

A: Gene: V(kappa)Ox1  
A: Introns: 17/1  
C: Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <WAT>

F:38-111/Domain: immunoglobulin homology <IMM>  
F:45-109/Disulfide bonds: #status predicted

Query Match	84.5%;	Score 464;	DB 1;	Length 130;	1
Best Local Similarity	86.7%;	Pred. No. 7e-31;			2
Matches 91;	Conservative	3;	Mismatches 11;	Indels 0;	Gaps 0;

```
Oy      2 IELTQSPALMSASPGKEVTITCSASSSVSYNHWFOOKPGETSPKLWITYSTSNLASGVPARF   61
         |||||::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     24 IVLTQSPALMSASPGKEVMTCSASSSVSYNHWYQQKSGTSPKRWTIDTSKLASGVPARF   83
```

```
Qy 62 SGGSGTSTLTSRMEADATYYCQORSSYPFTFGSGTLEIK 106
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 84 SGGSGXSYSLTSSMEADATYYCQOWSNPLTFGAGTLEIK 128
```



RESULT 15 /

PS0071

Ig kappa chain V region (38C13.V8) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000

C;Accession: PS0071

R;Levy, S.; Campbell, M.J.; Levy, R.

J. Exp. Med. 170, 1-13, 1989

A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement

A;Reference number: A92781; MUID:89310348; PMID:2501443

A;Accession: PS0071

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-106 <LEV>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 463; DB 2; Length 106;

Best Local Similarity 86.7%; Pred. No. 7e-31;

Matches 91; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFOQKPGTSPKLIYSTSNLASGVPARF 61

Db 2 IVLTSQSPAIMSASPGKVTMTCSASSSVSYMHWYQOKSGTSPKRWIYDTSKLASGVPARF 61

QY 62 SGSGSGTSTSLTISRMEADAATYVCOQRSSYPFTFGSGTKLEIK 106

Db 62 SGSGSGTSTSLTISRMEADAATYVCOQWSSNPVTFGAPTLEIK 106

Search completed: July 30, 2003, 09:44:11  
Job time : 32.3422 secs



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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:35 ; Search time 16.515 Seconds  
(without alignments)  
301.171 Million cell updates/sec

Title: US-09-865-198-23

Perfect score: 549

Sequence: 1 DIETQSPAIMSASPGKVT.....CQQRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	457	83.2	107	1	KV6F_MOUSE P04940 mus musculu
2	452	82.3	107	1	KV6I_MOUSE P04943 mus musculu
3	452	82.3	107	1	KV6J_MOUSE P04944 mus musculu
4	451	82.1	107	1	KV6H_MOUSE P04942 mus musculu
5	450	82.0	107	1	KV6G_MOUSE P04941 mus musculu
6	450	82.0	108	1	KV6K_MOUSE P04945 mus musculu
7	428	78.0	107	1	KV6B_MOUSE P01676 mus musculu
8	425	77.4	107	1	KV6A_MOUSE P01675 mus musculu
9	424	77.2	107	1	KV6D_MOUSE P01678 mus musculu
10	423	77.0	107	1	KV6C_MOUSE P01677 mus musculu
11	408	74.3	107	1	KV6E_MOUSE P01679 mus musculu
12	405	73.8	129	1	KV4A_MOUSE P01680 mus musculu
13	373.5	68.0	111	1	KV3M_MOUSE P01665 mus musculu
14	368.5	67.1	111	1	KV3O_MOUSE P01667 mus musculu
15	366.5	66.8	111	1	KV3L_MOUSE P01664 mus musculu
16	363.5	66.2	108	1	KV1V_HUMAN P04430 homo sapien
17	363.5	66.2	111	1	KV3H_MOUSE P01662 mus musculu
18	362.5	66.0	111	1	KV3J_MOUSE P01666 mus musculu
19	362.5	66.0	111	1	KV3N_MOUSE P01607 homo sapien
20	361.5	65.8	108	1	KV1O_HUMAN P01669 mus musculu
21	361.5	65.8	111	1	KV3Q_MOUSE P01671 mus musculu
22	361.5	65.8	111	1	KV3S_MOUSE P01661 mus musculu
23	360.5	65.7	131	1	KV3I_MOUSE P01670 mus musculu
24	359.5	65.5	111	1	KV3R_MOUSE P01663 mus musculu
25	358.5	65.3	111	1	KV3K_MOUSE P01594 homo sapien
26	357.5	65.1	108	1	KV1B_HUMAN P04431 homo sapien
27	357.5	65.1	129	1	KV1W_HUMAN P01672 mus musculu
28	354.5	64.6	111	1	KV3T_MOUSE P01668 mus musculu
29	354	64.5	110	1	KV3P_MOUSE P01673 mus musculu
30	351.5	64.0	111	1	KV3U_MOUSE P01643 mus musculu
31	350.5	63.8	108	1	KV5J_MOUSE P01600 homo sapien
32	349.5	63.7	108	1	KV1H_HUMAN P01654 mus musculu
33	349.5	63.7	111	1	KV3A_MOUSE

34	349.5	63.7	111	1	KV3C_MOUSE	P01656 mus musculu
35	349	63.6	129	1	KV3M_HUMAN	P18136 homo sapien
36	348.5	63.5	108	1	KV1L_HUMAN	P01604 homo sapien
37	348.5	63.5	108	1	KV1M_HUMAN	P01605 homo sapien
38	348.5	63.5	108	1	KV1R_HUMAN	P01610 homo sapien
39	348.5	63.5	111	1	KV3D_MOUSE	P03977 mus musculu
40	348	63.4	129	1	KV3L_HUMAN	P18135 homo sapien
41	346.5	63.1	108	1	KV1Y_HUMAN	P80362 homo sapien
42	346.5	63.1	108	1	KV5K_MOUSE	P01644 mus musculu
43	345.5	62.9	108	1	KV1N_HUMAN	P01606 homo sapien
44	345.5	62.9	108	1	KV1P_HUMAN	P01608 homo sapien
45	344.5	62.8	108	1	KV1E_HUMAN	P01597 homo sapien

ALIGNMENTS

RESULT 1					
KV6F_MOUSE					
ID	KV6F_MOUSE	STANDARD;	PRT;	107 AA.	
AC	P04940;				
DT	13-AUG-1987 (Rel. 05, Created)				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-VI region NQ2-17.4.1.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83271467; PubMed=6877353;				
RA	Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;				
RT	"mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone and its early diversification.";				
RT	Nature 304:320-324(1983).				
RL	Nature 304:320-324(1983).				
CC	-I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.				
CC					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC					
DR	EMBL; K00735; AAA38680.1; -.				
DR	HSSP; P01679; 2FBJ.				
DR	InterPro; IPR007110; Ig_Like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Immunoglobulin V region; Hybridoma.				
FT	DOMAIN 1 23 FRAMEWORK-1.				
FT	DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.				
FT	DOMAIN 34 48 FRAMEWORK-2.				
FT	DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.				
FT	DOMAIN 56 87 FRAMEWORK-3.				
FT	DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.				
FT	DOMAIN 97 106 FRAMEWORK-4.				
FT	DISULFID 23 87 BY SIMILARITY.				
FT	NON_TER. 107 107				
SO	SEQUENCE 107 AA; 11561 MW; 6F694284ECFA68E6 CRC64;				
Query Match 83.2%; Score 457; DB 1; Length 107;					
Best Local Similarity 83.8%; Pred. No. 4.9e-40;					
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;					
QY	2 IEITQSPAIMSASPGKVTITCSASSSVSYMHWFQQRGTSPLKMIYSTSNLASGVPAKF 61				
DB	2 IVLTQSPAIMSASPGQKVTITCSASSSVSYMHWFQQRGTSPLKMIYSTSNLASGVPAKF 61				

OY 62 SSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
 DB 62 SSGGSATSYSLTITSMQAEADATYYCQQWSSNPLTFGAGTKLEIK 106

## RESULT 2

KV6I\_MOUSE  
 ID KV6I\_MOUSE STANDARD; PRT; 107 AA.  
 AC P04943;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-VI region NQ6-8.3.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;  
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone and its early diversification.";  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

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 CC -----  
 DR EMBL; K00740; AAA38685.1; -.  
 DR HSSP; P01679; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 2 24 33 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 3 34 48 FRAMEWORK-2.  
 FT DOMAIN 4 49 55 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 5 56 87 FRAMEWORK-3.  
 FT DOMAIN 6 88 96 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 7 97 106 FRAMEWORK-4.  
 FT DISULFID 23 87 BY SIMILARITY.  
 FT NON TER 107 107  
 SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECF0C8E6 CRC64;

Query Match 82.3%; Score 452; DB 1; Length 107;  
 Best Local Similarity 82.9%; Pred. No. 1.6e-39;  
 Matches 87; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTNSLASGVPARF 61  
 DB 2 IVLTPAIMSASPGOKVTMTCSASSSVSYMHWFQOKSGTSPKRWIYDTSKLASGXPARF 61  
 OY 62 SSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
 DB 62 SSGGSATSYSLTITSMQAEADATYYCQQWSSNPLTFGAGTKLEIK 106

## RESULT 3

KV6J\_MOUSE  
 ID KV6J\_MOUSE STANDARD; PRT; 107 AA.  
 AC P04944;  
 DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-VI region NQ5-78.2.6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;  
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone and its early diversification.";  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

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 CC -----  
 DR EMBL; K00744; AAA38689.1; -.  
 DR HSSP; P01679; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 2 24 33 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 3 34 48 FRAMEWORK-2.  
 FT DOMAIN 4 49 55 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 5 56 87 FRAMEWORK-3.  
 FT DOMAIN 6 88 96 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 7 97 106 FRAMEWORK-4.  
 FT DISULFID 23 87 BY SIMILARITY.  
 FT NON TER 107 107  
 SQ SEQUENCE 107 AA; 11611 MW; A38290781F3C30D3 CRC64;

Query Match 82.3%; Score 452; DB 1; Length 107;  
 Best Local Similarity 83.8%; Pred. No. 1.6e-39;  
 Matches 88; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

OY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTNSLASGVPARF 61  
 DB 2 IVLTPAIMSASPGOKVTMTCSASSSVSYMHWFQOKSGTSPKRWIYDTSKLASGXPARF 61  
 OY 62 SSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
 DB 62 XSGSATSYSLTITSMQAEADATYYCQQWSSNPLTFGSGTKLEIK 106

## RESULT 4

KV6H\_MOUSE  
 ID KV6H\_MOUSE STANDARD; PRT; 107 AA.  
 AC P04942;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-VI region NQ5-61.1.2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

```
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K00739; AAA38684.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11605 MW; CA6C4284ECFCB550 CRC64;

Query Match
Best Local Similarity 82.1%; Score 451; DB 1; Length 107;
Matches 87; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 2 IELTSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTSNLASGVPARF 61
DB 2 IVLTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQOKSGTSPKRWIYDTSKLDSGVPARF 61

OY 62 SSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
DB 62 SSGSGATSYSLTITSMQAEADATYYCQQWSSNPLTFGAGTKLEIK 106

RESULT 5
KV6G_MOUSE STANDARD; PRT; 107 AA.
ID _KV6G_MOUSE
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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CC -----
DR EMBL; K00737; AAA38682.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;

Query Match
Best Local Similarity 82.0%; Score 450; DB 1; Length 107;
Matches 87; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 2 IELTSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTSNLASGVPARF 61
DB 2 IVLTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQOKSGTSPKRWIYDTSKLDSGVPARF 61

OY 62 SSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
DB 62 SSGSGATSYSLTITSMQAEADATYYCQQWSSNPLTFGAGTKLXLK 106

RESULT 6
KV6K_MOUSE STANDARD; PRT; 108 AA.
ID _KV6K_MOUSE
AC P04945;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K00746; AAA38691.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
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FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 98 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 99 108 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON TER 108
SQ SEQUENCE 108 AA, 11713 MW, DABF235CD9680AC6 CRC64;

Query Match 82.0%; Score 450; DB 1; Length 108;
Best Local Similarity 82.2%; Pred. No. 2.5e-39;
Matches 88; Conservative 10; Mismatches 7; Indels 2; Gaps 1;

QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPAR 61
DB 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPAR 61

QY 62 SSGSGSTSYSLTISRMEADATYYCQRRSSYP--FTFGSGTKLEIK 106
DB 62 SSGSGSTSYSLTISRMEADATYYCQRRSSYP--FTFGSGTKLEIK 106

RESULT 7
KV6B_MOUSE STANDARD; PRT; 107 AA.
ID KV6B_MOUSE
AC P01676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-VI region XRPC 24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
RT proteins.";
RL Biochemistry 17:5555-5559(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 98 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON TER 107
SQ SEQUENCE 107 AA, 11584 MW, 36E6D022A5EC34D7 CRC64;

Query Match 78.0%; Score 428; DB 1; Length 107;
Best Local Similarity 82.2%; Pred. No. 4.5e-37;
Matches 88; Conservative 5; Mismatches 12; Indels 2; Gaps 2;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPAR 60
DB 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPAR 60

QY 61 FSGSGSTSYSLTISRMEADATYYCQRRSSYP--FTFGSGTKLEIK 106
DB 61 FSGSGSTSYSLTISRMEADATYYCQRRSSYP--FTFGSGTKLEIK 106
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DB 61 FSGSGSTSYSLTISRMEADATYYCQ--WNYPLITFGSGTKLEIK 106

RESULT 8
KV6A_MOUSE STANDARD; PRT; 107 AA.
ID KV6A_MOUSE
AC P01675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-VI region XRPC 44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
RT proteins.";
RL Biochemistry 17:5555-5559(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR PIR; A90420; KYMSX4.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 34 48 FRAMEWORK-2.
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 56 87 FRAMEWORK-3.
FT DOMAIN 88 98 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 97 106 FRAMEWORK-4.
FT DISULFID 23 87 BY SIMILARITY.
FT NON TER 107
SQ SEQUENCE 107 AA, 11627 MW, 27A2D022BC0A34D7 CRC64;

Query Match 77.4%; Score 425; DB 1; Length 107;
Best Local Similarity 81.3%; Pred. No. 9e-37;
Matches 87; Conservative 6; Mismatches 12; Indels 2; Gaps 2;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPAR 60
DB 1 DIELTQSPAITAASLGOKVTITCSASSSVSYMHWFQOKPGTSPKPMIYEISKLASGVPAR 60

QY 61 FSGSGSTSYSLTISRMEADATYYCQRRSSYP--FTFGSGTKLEIK 106
DB 61 FSGSGSTSYSLTISRMEADATYYCQ--WNYPLITFGSGTKLEIK 106

RESULT 9
KV6D_MOUSE STANDARD; PRT; 107 AA.
ID KV6D_MOUSE
AC P01678;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-VI region SAPC 10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
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Life

RT "Kappa Chain joining segments and structural diversity of antibody  
combining sites."  
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BIND GALACTAN.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 34 48 FRAMEWORK-2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 56 87 FRAMEWORK-3.  
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 97 106 FRAMEWORK-4.  
FT DISULFID 23 87 BY SIMILARITY.  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match 77.2%; Score 424; DB 1; Length 107;  
Best Local Similarity 81.3%; Pred. No. 1.1e-36;  
Matches 87; Conservative 5; Mismatches 13; Indels 2; Gaps 2;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTNLASGVPAR 60  
:|||||||:|||||||:|||||||:|||||||:|||||||  
Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVSYMHWYQOKSGTSPKPMWYEISKLASGVPAR 60  
61 FSGSGSGTSYSLTISRMEAEADATYYCQQRSSYP-FTFGSGTKLEIK 106  
|||||||:|||||||:|||||||:|||||||:|||||||  
61 FSGSGSGTSYSLTISRMEAEADATYYCQ-QWNYPLITFGGKTLEIK 106

RESULT 10  
KV6C\_MOUSE STANDARD; PRT; 107 AA.  
ID KV6C\_MOUSE  
AC P01677;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-VI region TEPC 601/TEPC 191.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE (TEPC 601).  
RX MEDLINE=79082830; PubMed=103573;  
RA Rao D.N., Rudikoff S., Potter M.;  
RT "k chain variable regions from three galactan binding myeloma  
RT proteins."  
RL Biochemistry 17:5555-5559(1978).  
RN [2]  
RP SEQUENCE (TEPC 191).  
RX MEDLINE=81054757; PubMed=6776525;  
RA Rudikoff S., Rao D.N., Glandemann C.P.J., Potter M.;  
RT "Kappa Chain joining segments and structural diversity of antibody  
RT combining sites."  
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).  
CC -I- MISCELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.  
CC -I- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS  
CC THAT BIND GALACTAN.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 34 48 FRAMEWORK-2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 56 87 FRAMEWORK-3.  
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 97 106 FRAMEWORK-4.  
FT DISULFID 23 87 BY SIMILARITY.  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11568 MW; 203CD752A5EC34D7 CRC64;

Query Match 77.0%; Score 423; DB 1; Length 107;  
Best Local Similarity 80.4%; Pred. No. 1.4e-36;  
Matches 86; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTNLASGVPAR 60  
:|||||||:|||||||:|||||||:|||||||:|||||||  
Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVSYMHWYQOKSGTSPKPMWYEISKLASGVPAR 60  
61 FSGSGSGTSYSLTISRMEAEADATYYCQQRSSYP-FTFGSGTKLEIK 106  
|||||||:|||||||:|||||||:|||||||:|||||||  
61 FSGSGSGTSYSLTISRMEAEADATYYCQ-QWNYPLITFGGKTLEIK 106

RESULT 11  
KV6E\_MOUSE STANDARD; PRT; 107 AA.  
ID KV6E\_MOUSE  
AC P01679;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ig kappa chain V-VI region J539.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81054757; PubMed=6776525;  
RA Rudikoff S., Rao D.N., Glandemann C.P.J., Potter M.;  
RT "Kappa Chain joining segments and structural diversity of antibody  
RT combining sites."  
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
RX MEDLINE=88217852; PubMed=3449853;  
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,  
RA Davies D.R.;  
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction  
RT study at 2.6-A resolution."  
RL Proteins 1:74-80(1986).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BIND GALACTAN.  
DR PIR; A01942; KVMJS5.  
DR PDB; 2FBJ; 15-OCT-90.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; 3D-structure.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 33 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 34 48 FRAMEWORK-2.  
FT DOMAIN 49 55 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 56 87 FRAMEWORK-3.  
FT DOMAIN 88 96 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 97 106 FRAMEWORK-4.  
FT DISULFID 23 87  
FT STRAND 4 7  
FT STRAND 10 14

FT	TURN	15	16
FT	STRAND	19	25
FT	STRAND	31	37
FT	TURN	39	40
FT	STRAND	44	48
FT	TURN	49	51
FT	STRAND	52	53
FT	TURN	55	56
FT	TURN	59	60
FT	STRAND	61	66
FT	TURN	67	68
FT	STRAND	69	74
FT	HELIX	79	81
FT	STRAND	83	91
FT	TURN	92	93
FT	STRAND	94	97
FT	STRAND	101	107
FT	NON TER	107	107
SQ	SEQUENCE	107 AA;	11502 MW; EA30C9A3E903979C CRC64;

Query Match	74.38;	Score 408;	DB 1;	Length 107;
Best Local Similarity	77.68;	Pred. No. 4.9e-35;		
Matches 83; Conservative		9; Mismatches 13;	Indels 2;	Gaps 2;

```
Oy      1 DIELTSPAIMSASPEKTYITTCSSASSVSVMHWFQOKGTS PKLWIYSTSNLASCVPAR 600
      : ||||| : ||| : ||||| ||||| : ||| ||||| ||||| |||||
Db      1 EIVLTSPAITAALGQKTYITTCSSASSVSSLHWYQQXGTS PKPWIEISKLASCVPAR 600
```

```

Oy      61 FSGSGSGTSYSLTISRMEADATYYCQQRSSYP-FTEGSGTKLEIK 106
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 FSGSGSGTSYSLTINTMEADDAIYYCQ-QWTYPLITFGAGTKLEIK 106

```

```

RESULT 12
KV4A_MOUSE
ID KV4A_MOUSE STANDARD; PRT; 129 AA.
AC P01680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

RP SEQUENCE FROM N.A.  
RX MEDLINE=82115300; Pubmed=6799208;  
RA Kwan S.-P., Max E.E., Seldman J.G., Leder P., Scharff M.D.;  
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107.";  
RL Cell 26:57-66(1981).  
CC -I- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO  
CC AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS  
CC SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE  
CC NORMAL KAPPA CHAIN S107.

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```
DR EMBL; J005577; AAA38780.1; -.
DR EMBL; V00780; CAA24157.1; -.
DR PIR; A01943; KVM57B.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00477; Ig; 1.
DR SMART; SMO0406; IGV; 1.
```

DR	PROSITE; PS50835; IG_LIKE; 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL 1 22
FT	CHAIN 23 129 IG KAPPA CHAIN V-IV REGION S107B.
FT	DOMAIN 23 45 FRAMEWORK-1.
FT	DOMAIN 46 57 COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 58 72 FRAMEWORK-2.
FT	DOMAIN 73 79 COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 80 111 FRAMEWORK-3.
FT	DOMAIN 112 118 COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 119 128 FRAMEWORK-4.
FT	DISULFID 45 111 BY SIMILARITY.
FT	NON TER 129 129
SQ	SEQUENCE 129 AA; 13833 MW; E4BBB73072DC6FB6E4 CRC64;

Query Match	73.8%;	Score 405;	DB 1;	Length 129;
Best Local Similarity	80.0%;	Pred. No. 1.2e-34;		
Matches	84;	Conservative	7;	Mismatches 10;
			Indels	4;
			Gaps	2;

```
Oy      4 LTQSPAIMSASPGKVTITTCSSASSV-SYHWEIFQQKPGETSPKLWITYSTSNLASCVPARF 61
          |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      26 LTQSPAIMAASLGQKVMTTCSASSSVSSSLYHMYQQKSGASPPLIHRTSNLASCVPARF 85
```

```
Oy      62 SGSGSGTYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
        ||||| :|||| | | | | | | | | |  
Db      86 SGSGSGTYSLTISVEADDATYYCQQMSGYF--FGSGTKLEIK 128
```

RESULT 13		
KV3M_MOUSE		
ID	KV3M_MOUSE	STANDARD; PRT; 111 AA.
AC	P01665;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	15-JUL-1999 (Rel. 38, Last annotation update)	
DE	1g kappa chain V-III region PC 7043.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus	
OX	NCBI_TaxID=10090;	

RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";   
 RL Nature 276:785-790(1978).  
 DR PIR; A01937; KUMS43.  
 DR HSSP; P80362; 1WTL.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.

FT	DOMAIN	1	23	FRAMEWORK-1.
FT	DOMAIN	24	38	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	39	53	FRAMEWORK-2.
FT	DOMAIN	54	60	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	61	92	FRAMEWORK-3.
FT	DOMAIN	93	101	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	102	111	FRAMEWORK-4.
FT	DISULFID	23	92	BY SIMILARITY.

11	NOV 12 1991	111	AA; 12002 MW; 7A5FCB586C306D29 CRC64;
SQ	SEQUENCE		

Query Match	68.0%;	Score 373.5;	DB 1;	Length 111;
Best Local Similarity	65.8%;	Pred. No. 1.7e-31;		
Matches 73; Conservative	13;	Mismatches 20;	Indels 5;	Gaps 1;

```

QY      1 DIELTQSPAIMSAPGEKVITTCASSSV-----SYMHWFQOKPGTSPKLMWISTNLAAS 55
      |||||:::||:|||||||:::||:|||||||:::||:|||||||

```

Db 1, DIVLTQSPASLAIVSLGQRATISCKASQSVDDGDSINWNYQQKPGQPPKLLIYAASNLES 60

QY 56 GVPARFSGSGSGTSYSLTISRMEADATYYCQQRRESYPFTFGSGTKLEIK 106  
|:|||||::|:|||||:|||||  
61 GIPARFSGSGSGTIDFTLINIHVPEEEDATYYCQSQSNEDPFTFGSGTKLEIK 111

RESULT	14		
KV30_MOUSE			
ID	KV30_MOUSE	STANDARD;	PRT; 111 AA.
AC	P01667;		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	15-JUL-1999	(Rel. 38, Last annotation update)	
DE	IG kappa chain V-III region PC 6308.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		

RX	MEDLINE=79073152; PubMed=103003;		
RA	Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;		
RT	"Rearrangement of genetic information may produce immunoglobulin		
RT	diversity.";		
RL	Nature 276:785-790(1978).		
DR	PIR, C01937; KMS08.		
DR	HSSP, P80362; 1MTL.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IgV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
KW	Immunoglobulin V region.		
FT	DOMAIN	1	23
FT	DOMAIN	24	38
FT	DOMAIN	39	53
FT	DOMAIN	54	60
FT	DOMAIN	61	92
FT	DOMAIN	93	101
FT	DOMAIN	102	111
FT	DISULFID	23	92
FT	NON TER	111	111
SQ	SEQUENCE	111 AA;	12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match	67.1%;	Score 368.5;	DB 1;	Length 111;
Best Local Similarity	64.9%;	Pred. No. 5.6e-31;		
Matches	72;	Conservative	14;	Mismatches 20;
			Indels	5;
			Gaps	1;

```

QY      1 DIELTQSPAIMSASPEKEVTITCSASSV-----SYHWFQOKPGTSPKLMITYSTSNLAS 55
      ||||| ::||::||| ||::||| |||::||| |||::|||
Db      1 DIVLTQSPASLAVSLCQRATISCKASQSDYDPSYNNWYQOKPGQPKLLITYASNLES 60
      ||||| ::||::||| ||::||| |||::||| |||::|||
QY      56 GVPARFSGSGSGTSYLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
      :|||::||| ::||::||| ||::||| |||::||| |||::|||
Db      61 GIPARFSGSGSGTFTLINIHVVEEDATATYYCQSQSNEDPWTFGSGTKLEIK 111

```

```

RESULT 15
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.

```

RX	MEDLINE=79012520; PubMed=99744;
RA	McKean D.J., Bell M., Potter M.;
RT	"Mechanisms of antibody diversity: multiple genes encode structurally
RT	related mouse kappa variable regions.";
RL	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978) .
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR	PIR; A01936; KYMSC1.
DR	HSSP; P80362; 1WTL.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG LIKE; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 23 FRAMEWORK-1.
FT	DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 39 53 FRAMEWORK-2.
FT	DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 61 92 FRAMEWORK-3.
FT	DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 102 111 FRAMEWORK-4.
FT	DISULFID 23 92 BY SIMILARITY.
FT	NON TER 111 111
SO	SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965562 CRC64;

Query Match	66.8%;	Score 366.5;	DB 1;	Length 111;
Best Local Similarity	64.0%;	Pred. No. 8.9e-31;		
Matches 71; Conservative	14;	Mismatches 21;	Indels 5;	Gaps 1;

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OY      1 DIELTQSPALMASEPGEKVTITTCASASSV-----SYMHWFQOKPGTSPKLMIYSTSNLAS 55
        |||||:::||:|||||||:::||:|||||||
Db      1 DIVLTQSPASLAVSLGQRATISCKAQSDVDYTGESYMNWYQQNPQGQPKLLIYAASNLES 60
        |||||:::||:|||||||:::||:|||||||
OY      56 GVPARFSGSGSSTYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
        :|||||:::||:|||||||:::||:|||||||
Db      61 GIPARFSGSGGTIDFTLINIHVEEEDATYYCQGSNEDPYTFGGGTKLEIK 111
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Search completed: July 30, 2003, 09:45:10  
Job time: 16.5515 secs

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AC Q9U410; 7  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain  
DE variable region (Fragment).  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6182;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;  
RT "Amplification, cloning and sequence analysis of the light chain  
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of  
RT Schistosoma japonicum."  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF207620; AAF19434.1; -.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR NON\_TER 1  
FT NON\_TER 106  
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 85.6%; Score 470; DB 5; Length 106;  
Best Local Similarity 87.4%; Pred. No. 1.7e-42;  
Matches 90; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPARFSG 63  
Db 4 LTQSPAIMSASPEKVTITCSASSSVSYVWYLYQKPGSSPRLIYDTSNLAGVPAVRFSG 63  
QY 64 SGSGTSLTISRMEADATYYCOQRSSYPFTFGSGTKLEIK 106  
Db 64 SGSGTSLTISRMEADATYYCOQWTSYPFTFGSGTKLEIK 106

RESULT 6  
Q8K1F0 PRELIMINARY; PRT; 112 AA.  
ID Q8K1F0  
AC Q8K1F0;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Anti-VIPase light chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;  
RA Zhou Y.-X., Taguchi H., Plaque S., Karle S., Nishiyama Y., Paul S.;  
RT "Innate proteolytic antibodies: Failed D-VIPase response to the D-  
RT entantioner of VIP and identification of L-VIPase VL domains."  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF516285; AAM64203.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR NON\_TER 1  
FT NON\_TER 112  
SQ SEQUENCE 112 AA; 11901 MW; F6644663201AA239 CRC64;

Query Match 82.3%; Score 452; DB 11; Length 112;  
Best Local Similarity 86.4%; Pred. No. 1.5e-40;  
Matches 89; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPARFSG 63  
Db 4 LTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPARFSG 63  
QY 64 SGSGTSLTISRMEADATYYCOQRSSYPFTFGSGTKLEIK 106  
Db 64 SGSGTSLTISRMEADATYYCOQWSSNPFTFGSGTKLEIK 106

## RESULT 7

Q9JL76 PRELIMINARY; PRT; 97 AA.  
ID Q9JL76  
AC Q9JL76;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Anti-myosin immunoglobulin light chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DBA/2;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of  
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
RT with cardiac myosin."  
RL Infect. Immun. 68:5803-5808 (2000).  
DR EMBL; AF206030; AAF69328.1; -.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR NON\_TER 1  
FT NON\_TER 97  
SQ SEQUENCE 97 AA; 10542 MW; C9BE1FFE1F49DA1C CRC64;

Query Match 79.1%; Score 434.5; DB 11; Length 97;  
Best Local Similarity 86.6%; Pred. No. 9.2e-39;  
Matches 84; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 11 MSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPARFSGSGSTSY 70  
Db 1 LSASPEKVTITCRASSSVSYMHWFQOKPGSSPKPMIYATSNLASGVPARFSGSGSTSY 60  
QY 71 SLTISRMEADATYYCOQRSS-YPTFGSGTKLEIK 106  
Db 61 SLTISRVEADATYYCOQWSSKMYTFFGGTKLEIK 97

## RESULT 8

Q91W12 PRELIMINARY; PRT; 235 AA.  
ID Q91W12  
AC Q91W12;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Unknown (Protein for MGC:6582).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;



```
Query Match          66.6%; Score 365.5; DB 11; Length 111;
Best Local Similarity 64.9%; Pred. No. 2.4e-31;
Matches 72; Conservative 10; Mismatches 24; Indels 5; Gaps 1;

QY 1 DIELTQSPAIMSASPGKVTITCSASSV----SYMHWFOQKPGTSPKLMWYSTSNLAS 55
DB 1 DIQLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMWYQOKPGQPPKLLIYLASNL 60

QY 56 GVPARFSGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
DB 61 GVPARFSGSGSGTDFLTINIHPEEEDATATYYCQHSRELPHYFGGCTKLEIK 111

RESULT 12
Q9RLA5 PRELIMINARY; PRT; 214 AA.
AC Q9RLA5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match          66.0%; Score 362.5; DB 11; Length 214;
Best Local Similarity 66.4%; Pred. No. 1.1e-30;
Matches 71; Conservative 9; Mismatches 26; Indels 1; Gaps 1;

QY 1 DIELTQSPAIMSASPGKVTITCSASSV-SYMWFOQKPGTSPKLMWYSTSNLASG 59
DB 1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQOKPGKSPKLLIYRANRLVDG 60

QY 60 RFGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
DB 61 RFGSGSGQDYSLTISLSEYEDMGTYCLQYDEFPFTFGSGTKLEIK 107

RESULT 13
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match          65.7%; Score 360.5; DB 4; Length 108;
Best Local Similarity 63.6%; Pred. No. 8e-31;
Matches 68; Conservative 20; Mismatches 18; Indels 1; Gaps 1;

QY 1 DIELTQSPAIMSASPGKVTITCSASSV-SYMWFOQKPGTSPKLMWYSTSNLASG 59
DB 1 DIQMTQSPSSLASAVGDRVTITCRASQSISSYLNWYQOKPGKAPNLLIYAASSLQSG 60

QY 60 RFGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
DB 61 RFGSGSGTDFLTITSLQPEDFATYYCQQSYSTSWTFEGGTKEIK 107

RESULT 14
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyelective monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match          64.8%; Score 356; DB 4; Length 107;
Best Local Similarity 64.5%; Pred. No. 2.4e-30;
Matches 69; Conservative 19; Mismatches 17; Indels 2; Gaps 2;

QY 1 DIELTQSPAIMSASPGKVTITCSASSV-SYMWFOQKPGTSPKLMWYSTSNLASG 59
DB 1 DIQMTQSPSSLASAVGDRVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLQSG 60

QY 60 RFGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
DB 61 RFGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
```

Db 61 RFSGSGSGTDFLTITSLQPEDPATYCCQSSYS-TLTFGGGKVEIK 106

RESULT 15

Q9UL78

ID Q9UL78 PRELIMINARY; PRT; 109 AA.

AC Q9UL78;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Myosin-reactive immunoglobulin light chain variable region

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035036; AAD56272.1; -.

DR HSSP; P80362; IWTL.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1

FT NON\_TER 109

SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7E197 CRC64;

Query Match 64.8%; Score 356; DB 4; Length 109;

Best Local Similarity 62.0%; Pred. No. 2.4e-30;

Matches 67; Conservative 16; Mismatches 23; Indels 2; Gaps 1;

QY 1 DIELTQSPAIMSASPEKVTITCSASSV--SYMHWFQOKPGTSPKLTWYSTSNLASGVP 58

Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLITYGASSRATGIP 60

QY 59 ARFSGSGSGTYSYSLTISRMEADATYYCCQRSSYPFTFGSGTKLEIK 106

Db 61 DRFSGSGSGTDFLTITSLRLEPEDCAVYYCCQYGSPLTFGGGKVEIK 108

Search completed: July 30, 2003, 09:42:49  
Job time : 84.1643 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 106 Seconds  
(without alignments)  
158.727 Million cell updates/sec

Title: US-09-865-198-23  
Perfect score: 549  
Sequence: 1 DIELTQSPAIMASPGKVT.....CQQRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*  
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10: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*  
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21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	100.0	106	22	AAE13144 Humanised antibody
2	549	100.0	106	23	AAU74418 Antigen-binding pr
3	549	100.0	106	24	ABJ26730 VEGF binding relat
4	549	100.0	108	21	AAV97236 Variable light cha
5	549	100.0	108	22	AAE25960 VEGF antagonist an
6	549	100.0	108	23	AAE25956 Mouse anti-KDR p1c
7	549	100.0	108	23	AAU74413 Antigen-binding pr
8	549	100.0	108	24	ABJ26725 VEGF binding relat
9	549	100.0	125	22	AAE13146 Chimeric p1c11 lig

10	549	100.0	125	22	AAE25960
11	549	100.0	125	23	AAE25961
12	549	100.0	238	23	AAE25963
13	549	100.0	238	23	AAU74420
14	549	100.0	238	23	AAU74420
15	549	100.0	238	24	AAE25960
16	549	100.0	240	23	AAU74419
17	549	100.0	240	23	ABJ26731
18	549	100.0	240	24	AAE25960
19	549	100.0	330	22	AAE25960
20	539	98.2	125	23	AAE28917
21	534	97.3	108	16	AAE28917
22	534	97.3	235	18	AAE28917
23	532	96.9	108	13	AAE21290
24	532	96.9	108	18	AAE21290
25	529	96.4	107	22	AAE21290
26	529	96.4	129	15	AAE21290
27	529	96.4	129	20	AAE21290
28	529	96.4	129	20	AAE21290
29	527	96.0	256	22	AAE21290
30	527	96.0	256	22	AAE21290
31	526	95.8	107	22	AAE21290
32	524	95.4	108	13	AAE21290
33	523	95.3	236	20	AAE21290
34	523	95.3	270	16	AAE21290
35	523	95.3	553	18	AAE21290
36	523	95.3	553	20	AAE21290
37	523	95.3	553	22	AAE21290
38	523	95.3	553	22	AAE21290
39	521	94.9	281	20	AAE21290
40	521	94.9	666	20	AAE21290
41	520	94.7	106	23	AAE21290
42	519	94.5	109	23	AAE21290
43	519	94.5	556	22	AAE21290
44	519	94.5	556	22	AAE21290
45	518	94.4	105	17	AAE21290

ALIGNMENTS

RESULT 1	
AAE13144	
ID	AAE13144 standard; Protein; 106 AA.
AC	AAE13144;
DT	28-JAN-2002 (first entry)
XX	
DE	Humanised antibody light chain fragment.
XX	
KW	Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
KW	cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
KW	monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
KW	human; chimeric.
XX	
OS	Chimeric - Homo sapiens.
OS	Chimeric - Mus sp.
XX	
PN	WO200174296-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US10504.
XX	
PR	31-MAR-2000; 2000US-0540770.
XX	
PA	(IMCL-) IMCLONE SYSTEMS INC.
XX	(CORR ) CORNELL RES FOUND INC.
PI	Witte L, Rafil S;
XX	
DR	WPI; 2001-662942/76.

DR N-PSDB; AAD21670.

XX  
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with  
PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
XX Claim 8; Page 16; 68pp; English.

XX  
CC The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains mouse complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised  
CC antibody light chain fragment used in the exemplification of the  
CC invention.

XX  
SQ Sequence 106 AA;

Query Match 100.0%; Score 549; DB 22; Length 106;  
Best Local Similarity 100.0%; Pred. No. 6.4e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIELTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60  
Db 1 DIELTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60

OY 61 FSGSGSGTSTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
Db 61 FSGSGSGTSTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106

RESULT 2  
AAU74418  
ID AAU74418 standard; peptide; 106 AA.

XX  
AC AAU74418;

DT 26-MAR-2002 (first entry)

XX  
DE Antigen-binding protein light chain variable domain (VH) #2.

XX  
KW Antigen-binding protein; antibody light chain variable domain;  
KW cytosstatic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;  
KW cell proliferation inhibitor.

XX  
OS Mus sp.

XX  
PN WO200190192-A2.

XX  
PD 29-NOV-2001.

XX  
PF 24-MAY-2001; 2001WO-US16924.

XX  
PR 24-MAY-2000; 2000US-206749P.

XX  
PA (IMCL-) IMCLONE SYSTEMS INC.

XX  
PI Zhu Z;

XX  
DR WPI; 2002-106189/14.

XX  
DR N-PSDB; AAU20289.

PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides

XX  
PS Claim 61; Page 61; 64pp; English.

XX  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (CL domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This sequence represents a light chain variable domain (VH) incorporated  
CC into Fv, an engineered protein containing a heavy chain variable domain  
CC and a light chain variable domain in one polypeptide chain, described in  
CC the method of the invention.

XX  
SQ Sequence 106 AA;

Query Match 100.0%; Score 549; DB 23; Length 106;  
Best Local Similarity 100.0%; Pred. No. 6.4e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIELTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60  
Db 1 DIELTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLIWYSTSNLASGVPAR 60

OY 61 FSGSGSGTSTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
Db 61 FSGSGSGTSTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106

RESULT 3  
ABJ26730  
ID ABJ26730 standard; Protein; 106 AA.

XX  
AC ABJ26730;

DT 01-MAY-2003 (first entry)

XX  
DE VEGF binding related protein SEQ ID No 23.

XX  
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.

XX  
OS Mus sp.

XX  
PN WO2003002144-A1.

XX  
PD 09-JAN-2003.

XX  
PF 26-JUN-2002; 2002WO-US20332.

XX  
PR 26-JUN-2001; 2001US-301299P.

XX  
PA (IMCL-) IMCLONE SYSTEMS INC.

XX  
PI Zhu Z;

XX  
DR WPI; 2003-201468/19.

XX  
DR N-PSDB; ABT23308.

PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -  
XX  
PS Disclosure; Page 54; 98pp; English.  
XX  
CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse protein relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX  
SQ Sequence 106 AA;  
  
Query Match 100.0%; Score 549; DB 24; Length 106;  
Best Local Similarity 100.0%; Pred. No. 6.4e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DIELTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTSNLASGVPAR 60  
Db 1 DIELTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTSNLASGVPAR 60  
Oy 61 FSGSGSGTSTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
Db 61 FSGSGSGTSTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
  
RESULT 4  
AA97236  
ID AAY97236 standard; Protein; 108 AA.  
XX  
AC AAY97236;  
XX  
DT 19-DEC-2000 (first entry)  
XX  
DE Variable light chain fragment of anti-SI(KDR) antibody.  
XX  
KW Immunoglobulin; antibody; complementary determining region; CDR;  
KW VEGF; vascular endothelial growth factor; KDR;  
KW kinase insert domain containing receptor; multivalent; monovalent;  
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;  
KW glioblastoma multiforme; hemangioblastoma; AIDS;  
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;  
KW acquired immune deficiency syndrome; AIDS; human.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200044777-A1.  
XX  
PD 03-AUG-2000.  
XX  
PF 28-JAN-2000; 2000WO-US02180.  
XX  
PR 29-JAN-1999; 99US-0117726.  
PR 29-JAN-1999; 99US-0240736.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z, Witte L;  
XX  
DR WPI; 2000-505966/45.  
DR N-PSDB; AAA53768.  
XX  
PT Novel immunoglobulin molecules binding kinase insert domain-containing  
PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growth

XX  
PS Claim 4; Page 51; 55pp; English.  
XX  
CC New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Kaposi's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulins of the invention.  
XX  
SQ Sequence 108 AA;  
  
Query Match 100.0%; Score 549; DB 21; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.5e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DIELTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTSNLASGVPAR 60  
Db 1 DIELTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTSNLASGVPAR 60  
Oy 61 FSGSGSGTSTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
Db 61 FSGSGSGTSTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
  
RESULT 5  
AAB82710  
ID AAB82710 standard; Protein; 108 AA.  
XX  
AC AAB82710;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE VEGF antagonist antibody IMC-1C11 light chain variable region.  
XX  
KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; light chain.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
FH Key Location/Qualifiers  
XX  
FT Region 24..33  
FT /label= CDR-L1  
FT /note= "complementarity determining region 1"  
FT 49..55  
FT /label= CDR-L2  
FT /note= "complementarity determining region 2"  
FT 88..96  
FT /label= CDR-L3  
FT /note= "complementarity determining region 3"  
XX  
PN WO200154723-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 29-JAN-2001; 2001WO-US02839.  
XX  
PR 28-JAN-2000; 2000US-0178791.  
PR 31-MAR-2000; 2000US-0539692.

XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX Kerbel R;  
XX WPI; 2001-514531/56.  
DR N-PSDB; AAH26406.  
XX  
PT Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX  
XX Disclosure; Page 38-39; 42pp; English.  
XX  
CC The present sequence is that of the light chain variable region of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
SQ Sequence 108 AA;  
  
Query Match 100.0%; Score 549; DB 22; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.5e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
DB 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
QY 61 FSGSGSGTSTLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 61 FSGSGSGTSTLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
  
RESULT 6  
AAE25956  
ID AAE25956 standard; Protein; 108 AA.  
XX  
AC AAE25956;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Mouse anti-KDR p1C11 scFv antibody VL region #1.  
XX  
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; light chain variable region; VL; angiogenesis;  
KW p1C11; scFv antibody.  
XX  
OS Mus musculus.  
XX  
PN US20002064528-A1.  
XX  
PD 30-MAY-2002.  
XX  
PF 12-OCT-2001; 2001US-0976787.

XX 28-JAN-2000; 2000US-0493539.  
XX (ZHUZ/) ZHU Z.  
PA (WITT/) WITTE L.  
XX  
PI Zhu Z, Witte L;  
XX  
DR WPI; 2002-589175/63.  
DR N-PSDB; AAD42821.  
XX  
PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR -  
XX  
XX Claim 4; Page 11; 34pp; English.  
XX  
CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody  
CC light chain variable region (VL).  
XX  
SQ Sequence 108 AA;  
  
Query Match 100.0%; Score 549; DB 23; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.5e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
DB 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
QY 61 FSGSGSGTSTLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 61 FSGSGSGTSTLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
  
RESULT 7  
AAU74413  
ID AAU74413 standard; peptide; 108 AA.  
XX  
AC AAU74413;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Antigen-binding protein light chain variable domain (VH) #1.  
XX  
KW Antigen-binding protein; antibody light chain variable domain;  
KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KW vascular endothelial growth factor receptor; VEGF;  
KW cell proliferation inhibitor.  
XX  
OS Mus sp.  
XX  
PN WO200190192-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US16924.  
XX  
PR 24-MAY-2000; 2000US-206749P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2002-106189/14.  
DR N-PSDB; AAS20284.



XX New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides  
XX  
PS Claim 57; Page 57; 64pp; English.  
XX  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (C1 domain), and P2 has an antigen-binding  
CC site located to the N terminus of the C1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogenous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This sequence represents a light chain variable domain (VH) incorporated  
CC into Fv, an engineered protein containing a heavy chain variable domain  
CC and a light chain variable domain in one polypeptide chain, described in  
CC the method of the invention.  
XX  
SQ Sequence 108 AA;

Query Match 100.0%; Score 549; DB 23; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.5e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASASPEKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTSNLASGVPAR 60  
|||  
Db 1 DIELTQSPAIMASASPEKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTSNLASGVPAR 60  
61 FSGSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
|||  
61 FSGSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106

RESULT 8  
ABJ26725  
ID ABJ26725 standard; Protein; 108 AA.  
XX  
AC ABJ26725;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE VEGF binding related protein SEQ ID No 8:  
XX  
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.  
XX  
OS Mus sp.  
XX  
PN WO2003002144-A1.  
XX  
PD 09-JAN-2003.  
XX  
PF 26-JUN-2002; 2002WO-US20332.  
XX  
PR 26-JUN-2001; 2001US-301299P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;

XX WPI; 2003-201468/19.  
DR N-PSDB; ABT23303.  
XX  
PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -  
XX  
PS Claim 7; Page 49-50; 98pp; English.  
XX  
CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse protein relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX  
SQ Sequence 108 AA;

Query Match 100.0%; Score 549; DB 24; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.5e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASASPEKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTSNLASGVPAR 60  
|||  
Db 1 DIELTQSPAIMASASPEKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTSNLASGVPAR 60  
61 FSGSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
|||  
61 FSGSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106

RESULT 9  
AAE13146  
ID AAE13146 standard; Protein; 125 AA.  
XX  
AC AAE13146;  
XX  
DT 28-JAN-2002 (first entry)  
XX  
DE Chimeric p1C11 light chain fragment.  
XX  
KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
KW cytosstatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;  
KW monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;  
KW human; p1C11 vector.  
XX  
OS Chimeric - Homo sapiens.  
OS Chimeric - Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT Protein /label= Leader\_peptide  
FT 20..125  
FT /note= "Mature chimeric p1C11 light chain fragment"  
FT Region 43..52  
FT /label= CDR\_L1  
FT Region 68..74  
FT /label= CDR\_L2  
FT Region 107..115  
FT /label= CDR\_L3  
XX  
PN WO200174296-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US10504.  
XX



PR 31-MAR-2000; 2000US-0540770.  
XX  
XX (IMCL-) IMCLONE SYSTEMS INC.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
XX Witte L, Rafii S;  
PI  
XX WPI; 2001-662942/76.  
DR N-PSDB; AAD21683.  
XX  
PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
PT tumors such as leukemias or multiple myeloma comprises treatment with  
PT an antagonist of a vascular endothelial growth factor receptor -  
XX  
XX Example 3; Fig 11; 68pp; English.  
PS  
XX The invention relates to a method for inhibiting the growth of non-solid  
CC tumour cells that are stimulated by a ligand of vascular endothelial  
CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
CC variable region joined to human constant region, where the humanised  
CC mouse variable region contains mouse complementarity determining region  
CC (CDR) grafted into human variable region. The method is useful for  
CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
CC multiple myelomas and lymphoid cells, particularly those related to  
CC non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric  
CC pIC11 light chain fragment which is used for the construction of chimeric  
CC pIC11 IgG expression vector. Chimeric pIC11 light chain contains cloned  
CC variable light chain (VL) and human kappa light chain constant region  
CC (CL).  
XX  
XX Sequence 125 AA;  
SQ  
Query Match 100.0%; Score 549; DB 22; Length 125;  
Best Local Similarity 100.0%; Pred. No. 7.4e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 DIETQSPAIMSASPGKVTITCSASSSVSYMWFQOKPGTSPKLTWYSTSNLASGVPAR 60  
DB 20 DIETQSPAIMSASPGKVTITCSASSSVSYMWFQOKPGTSPKLTWYSTSNLASGVPAR 79  
OY 61 FSGSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 80 FSGSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 125  
RESULT 10  
AAB82702  
ID AAB82702 standard; Protein; 125 AA.  
XX  
AC AAB82702;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE VEGF antagonist antibody IMC-1C11 light chain variable region.  
XX  
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;  
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;  
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;  
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;  
KW colon carcinoma; ovarian carcinoma; neuroblastoma;  
KW glioblastoma multiforme; melanoma; therapy; light chain.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
FH Key 1 Location/Qualifiers  
FT Peptide 1..19  
FT Protein /label= Signal\_peptide  
FT 20..125  
FT /label= Mature\_protein  
XX

FT Region 43..52  
FT /label= CDR-L1  
FT /note= "complementarity determining region 1"  
FT Region 68..74  
FT /label= CDR-L2  
FT /note= "complementarity determining region 2"  
FT Region 107..115  
FT /label= CDR-L3  
FT /note= "complementarity determining region 3"  
XX  
XX WO200154723-A1.  
XX  
XX 02-AUG-2001.  
XX  
XX 29-JAN-2001; 2001WO-US02839.  
XX  
XX 28-JAN-2000; 2000US-0178791.  
PR 31-MAR-2000; 2000US-0539692.  
XX  
XX (SUNN-) SUNNYBROOK HEALTH SCI CENT.  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
XX Kerbel R;  
PI  
XX WPI; 2001-514531/56.  
DR N-PSDB; AAH26414.  
XX  
XX Treating or controlling an angiogenic dependent condition (e.g. a  
PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
PT administering a combination of an antiangiogenic molecule and a  
PT chemotherapeutic agent -  
XX  
XX Disclosure; Fig 1; 42pp; English.  
PS  
XX The present sequence is that of the light chain variable region of  
CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
CC or a fragment of it, can be used as an anti-angiogenic molecule,  
CC together with a chemotherapeutic acid, for the treatment of an  
CC angiogenic dependent condition in a mammal, especially a human.  
CC The invention relates generally to a method of treating or  
CC controlling an angiogenic dependent condition by administering an  
CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
CC regression or arrest of the condition while minimising or  
CC preventing significant toxicity of the chemotherapeutic agent.  
CC The anti-angiogenic molecule inhibits or blocks the action of a  
CC vascular endothelium survival factor such as VEGF or its receptor,  
CC and is especially IMC-1C11. Conditions that can be treated include,  
CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
CC especially a solid tumour, including breast carcinoma, lung  
CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
XX  
SQ Sequence 125 AA;  
Query Match 100.0%; Score 549; DB 22; Length 125;  
Best Local Similarity 100.0%; Pred. No. 7.4e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 DIETQSPAIMSASPGKVTITCSASSSVSYMWFQOKPGTSPKLTWYSTSNLASGVPAR 60  
DB 20 DIETQSPAIMSASPGKVTITCSASSSVSYMWFQOKPGTSPKLTWYSTSNLASGVPAR 79  
OY 61 FSGSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 80 FSGSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 125  
RESULT 11  
AAE25966  
ID AAE25966 standard; Protein; 125 AA.  
XX

AC AAE23p66;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Mouse anti-KDR pIC11 scFv antibody VL region #2.  
XX  
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; light chain variable region; VL; angiogenesis;  
KW pIC11; scFv antibody.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Signal-peptide  
FT Protein 20..125  
FT /note= "Mouse pIC11 scFv antibody mature VL region"  
FT Region 43..52  
FT /note= "Light chain complementarity  
FT determining region 1 (CDR-L1)"  
FT Region 68..74  
FT /note= "Light chain complementarity  
FT determining region 2 (CDR-L2)"  
FT Region 107..115  
FT /note= "Light chain complementarity  
FT determining region 3 (CDR-L3)"  
XX  
XX US2002064528-A1.  
XX  
XX 30-MAY-2002.  
XX  
XX 12-OCT-2001; 2001US-0976787.  
XX  
XX 28-JAN-2000; 2000US-0493539.  
XX  
XX (ZHUZ/) ZHU Z.  
XX PA (WITT/) WITTE L.  
XX PI Zhu Z, Witte L;  
XX  
XX WPI; 2002-589175/63.  
XX DR N-PSDB; AAD42833.  
XX  
XX Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR -  
XX  
XX Disclosure; Fig 4; 34pp; English.  
XX  
XX The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is mouse anti-KDR pIC11 scFv antibody  
CC light chain variable region (VL).  
XX  
SQ Sequence 125 AA;  
  
Query Match 100.0%; Score 549; DB 23; Length 125;  
Best Local Similarity 100.0%; Pred. No. 7.4e-32;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
DB 20 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 79  
OY 61 FSGSGSGTISLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 80 FSGSGSGTISLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 125

RESULT 12  
AAE25961  
ID AAE25961 standard; Protein; 238 AA.  
XX  
XX AAE25961;  
AC  
XX 15-NOV-2002 (first entry)  
DT  
XX  
DE KDR binding immunoglobulin related mouse protein #2.  
XX  
XX Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
KW pIC11; scFv antibody.  
XX  
XX Mus sp.  
OS  
XX  
XX US2002064528-A1.  
XX  
XX 30-MAY-2002.  
XX  
XX 12-OCT-2001; 2001US-0976787.  
XX  
XX 28-JAN-2000; 2000US-0493539.  
XX  
XX (ZHUZ/) ZHU Z.  
XX PA (WITT/) WITTE L.  
XX PI Zhu Z, Witte L;  
XX  
XX WPI; 2002-589175/63.  
XX DR N-PSDB; AAD42825.  
XX  
XX Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR -  
XX  
XX Disclosure; Page 17-18; 34pp; English.  
XX  
XX The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is KDR binding immunoglobulin related  
CC mouse protein.  
XX  
SQ Sequence 238 AA;  
  
Query Match 100.0%; Score 549; DB 23; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.3e-31;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
DB 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 192  
OY 61 FSGSGSGTISLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 193 FSGSGSGTISLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 238  
  
RESULT 13  
AAE25963  
ID AAE25963 standard; Protein; 238 AA.  
XX  
XX AAE25963;  
AC  
XX 15-NOV-2002 (first entry)  
DT

XX DE KDR binding immunoglobulin related mouse protein #3.  
XX XX  
KM Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
KM foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
KM VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
KM PIC1; scFv antibody.  
XX XX  
OS Mus sp.  
XX PN US2002064528-A1.  
XX PD 30-MAY-2002.  
XX PF 12-OCT-2001; 2001US-0976787.  
XX PR 28-JAN-2000; 2000US-0493539.  
XX PA (ZHUZ/) ZHU Z.  
XX PA (WITT/) WITTE L.  
XX PI Zhu Z, Witte L;  
XX DR WPI; 2002-589175/63.  
XX XX  
PT Novel immunoglobulin molecule for reducing tumor growth, binds to  
PT kinase insert domain-containing receptor with an affinity comparable to  
PT human vascular endothelial growth factor, and neutralizes activation of  
PT KDR -  
XX XX  
PS Disclosure; Page 17-18; 34pp; English.  
XX XX  
CC The present invention relates to novel immunoglobulin molecules that bind  
CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
CC to human vascular endothelial growth factor (VEGF) and that neutralises  
CC activation of KDR. Sequences of the invention are useful for neutralising  
CC the activation of KDR, for reducing tumour growth and for inhibiting  
CC angiogenesis. The present sequence is KDR binding immunoglobulin related  
CC mouse protein.  
XX XX  
SQ Sequence 238 AA;  
  
Query Match 100.0%; Score 549; DB 23; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.3e-31;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLWYSTSNLASGVPAR 60  
Db 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLWYSTSNLASGVPAR 192  
  
QY 61 FSGSGSGTSTSLTISRMEADATYCCQORSSYPFTFGSGTKLEIK 106  
Db 193 FSGSGSGTSTSLTISRMEADATYCCQORSSYPFTFGSGTKLEIK 238  
  
RESULT 14  
AAU74420  
ID AAU74420 standard; Protein; 238 AA.  
XX XX  
AC AAU74420;  
XX XX  
DT 26-MAR-2002 (first entry)  
XX XX  
DE Antigen-binding protein, single chain variable fragment version #2.  
XX XX  
KM Antigen-binding protein; single chain variable fragment; scFv; antigen;  
KM cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
KM vascular endothelial growth factor receptor; VEGF;  
KM cell proliferation inhibitor.  
XX XX  
OS Mus sp.  
OS Synthetic.

XX XX Key Location/Qualifiers  
FH 1..117  
FT Region /label= VH  
FT /note= "Heavy chain variable domain. Specifically  
FT claimed in claim 61"  
FT Region 118..132  
FT /label= Linker  
FT /note= "15 amino acid linker joins the VH and VL  
FT regions of the single chain variable fragment  
FT protein. Encoded by AAS20285"  
FT 133..238  
FT /label= VL  
FT /note= "Light chain variable domain. Specifically  
FT claimed in claim 61"  
XX PN WO200190192-A2.  
XX XX  
XX PD 29-NOV-2001.  
XX XX  
XX PF 24-MAY-2001; 2001WO-US16924.  
XX PR 24-MAY-2000; 2000US-206749P.  
XX PA (IMCL-) IMCLONE SYSTEMS INC.  
XX PI Zhu Z;  
XX DR WPI; 2002-106189/14.  
XX XX  
PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
PT tumour growth and for inhibiting angiogenesis, comprises a complex of  
PT two polypeptides and two second polypeptides  
XX XX  
PS Claim 63; Page 62-63; 64pp; English.  
XX XX  
CC The invention describes an antigen-binding protein (I) comprising a  
CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
CC are stably associated in an immunoglobulin like complex. P1 has an  
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
CC light chain constant domain (CL domain), and P2 has an antigen-binding  
CC site located to the N terminus of the CH1 domain. (I) is useful for:  
CC neutralising the activation of a vascular endothelial growth factor  
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
CC reducing endothelial cell proliferation; inhibiting VEGF induced  
CC migration of human leukaemia cells; blocking interaction of a protein and  
CC its ligand; promoting interactions between immune cells and target cells;  
CC and in vivo and in vitro for investigative, diagnostic or treatment  
CC methods. The design of (I) provides for efficient production so that  
CC substantially all of the antigen-binding proteins produced are assembled  
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
CC and in tetrameric form. The heavy chain constant domains which constitute  
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
CC antibody and which provide other antibody functions can be present. There  
CC is no requirement for processing in vitro to obtain the complete product.  
CC This is the amino acid sequence of a single chain variable fragment  
CC (scFv), an engineered protein containing a variable light and variable  
CC heavy domain on one polypeptide, described in the method of the  
CC invention.  
XX XX  
SQ Sequence 238 AA;  
  
Query Match 100.0%; Score 549; DB 23; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.3e-31;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLWYSTSNLASGVPAR 60  
Db 133 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLWYSTSNLASGVPAR 192  
  
QY 61 FSGSGSGTSTSLTISRMEADATYCCQORSSYPFTFGSGTKLEIK 106  
Db 193 FSGSGSGTSTSLTISRMEADATYCCQORSSYPFTFGSGTKLEIK 238

RESULT 15  
ABJ26732  
ID ABJ26732 standard; Protein; 238 AA.  
XX  
AC ABJ26732;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE VEGF binding related protein SEQ ID No 28.  
XX  
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
KW leukaemia cell; vascular endothelial growth factor; tumour;  
KW bispecific antigen-binding protein; mouse; murine.  
XX  
OS Mus sp.  
XX  
PN WO2003002144-A1.  
XX  
PD 09-JAN-2003.  
XX  
PF 26-JUN-2002; 2002WO-US20332.  
XX  
PR 26-JUN-2001; 2001US-301299P.  
XX  
PA (IMCL-) IMCLONE SYSTEMS INC.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2003-201468/19.  
XX  
PT New bispecific antibodies having antigen-binding sites specific for a  
PT first vascular endothelial growth factor (VEGF) receptor and for a  
PT second VEGF receptor, useful for inhibiting migration of leukemia  
PT cells, or for treating tumors -  
XX  
XX  
PS Disclosure; Page 56-57; 98pp; English.  
XX  
CC The invention relates to a novel antibody having a first antigen binding  
CC site specific for a first vascular endothelial growth factor (VEGF)  
CC receptor and a second antigen-binding site specific for a second VEGF  
CC receptor. The bispecific antigen-binding proteins block activation of the  
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
CC cellular functions such as mitogenesis of vascular endothelial cells  
CC and migration of leukaemia cells. The antibodies are useful for treating  
CC tumours and for in vivo or in vitro for investigative and diagnostic  
CC methods. This sequence represents a mouse protein relating to the  
CC bispecific antibodies that bind to the VEGF receptors of the invention.  
XX  
SQ Sequence 238 AA;  
  
Query Match 100.0%; Score 549; DB 24; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.3e-31;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DIELTQSPAIMSASPEKVTITCSASSSVSMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
DB 133 DIELTQSPAIMSASPEKVTITCSASSSVSMHWFQOKPGTSPKLMWYSTSNLASGVPAR 192  
  
QY 61 FSGSGSGTSTSLTISRMEADATYYCCQRSSYPPTFGSGTKLEIK 106  
DB 193 FSGSGSGTSTSLTISRMEADATYYCCQRSSYPPTFGSGTKLEIK 238

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2003, 09:42:53 ; Search time 130.299 Seconds  
(without alignments)  
96.613 Million cell updates/sec

Title: US-09-865-198-23  
Perfect score: 549  
Sequence: 1 DIETQSPAIMSASPGKVT.....CQQRSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues  
Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	549	100.0	106	9	US-09-976-787-24
2	549	100.0	106	10	US-09-865-198-23
3	549	100.0	106	11	US-09-798-689-8
4	549	100.0	108	9	US-09-976-787-8
5	549	100.0	108	10	US-09-865-198-8
6	549	100.0	238	9	US-09-976-787-29
7	549	100.0	238	10	US-09-865-198-28
8	549	100.0	238	11	US-09-798-689-21
9	549	100.0	240	9	US-09-976-787-28
10	549	100.0	240	10	US-09-865-198-27
11	534	97.3	235	10	US-09-910-059-17
12	532	96.9	108	10	US-09-910-059-9
13	527	96.0	256	15	US-10-247-488-2
14	527	96.0	258	15	US-10-247-488-4
15	526	95.8	107	15	US-10-232-187-4

16	518	94.4	105	10	US-09-982-107-12	Sequence 12, Appl
17	518	94.4	669	10	US-09-807-721-2	Sequence 2, Appli
18	511	93.1	128	11	US-09-967-719C-4	Sequence 4, Appli
19	511	93.1	128	11	US-09-967-719C-6	Sequence 6, Appli
20	509	92.7	107	10	US-09-144-886-88	Sequence 88, Appl
21	506	92.2	119	9	US-09-808-037-28	Sequence 28, Appl
22	506	92.2	119	15	US-10-162-889-28	Sequence 28, Appl
23	506	92.2	239	9	US-09-808-037-6	Sequence 6, Appli
24	506	92.2	239	15	US-10-162-889-6	Sequence 6, Appli
25	506	92.2	242	16	US-10-259-087A-20	Sequence 20, Appl
26	500	91.1	107	10	US-09-144-886-76	Sequence 76, Appl
27	495	90.2	107	10	US-09-144-886-90	Sequence 90, Appl
28	493	89.8	130	15	US-10-195-752-113	Sequence 113, App
29	490	89.3	130	15	US-10-195-752-111	Sequence 111, App
30	484	88.2	107	10	US-09-144-886-75	Sequence 75, Appl
31	484	88.2	107	10	US-09-144-886-78	Sequence 78, Appl
32	482	87.8	242	16	US-10-259-087A-18	Sequence 18, Appl
33	479	87.2	107	10	US-09-144-886-82	Sequence 82, Appl
34	479	87.2	107	10	US-09-144-886-83	Sequence 83, Appl
35	479	87.2	109	10	US-09-144-886-91	Sequence 91, Appl
36	478	87.1	131	9	US-09-881-823-6	Sequence 6, Appli
37	475.5	86.6	112	10	US-09-144-886-89	Sequence 89, Appl
38	468	85.2	412	15	US-10-013-173-6	Sequence 6, Appli
39	468	85.2	412	15	US-10-150-762-6	Sequence 6, Appli
40	468	85.2	423	15	US/10/013	Sequence 8, Appli
41	468	85.2	423	15	US/10/150	Sequence 8, Appli
42	466	84.9	109	10	US-09-144-886-96	Sequence 96, Appl
43	463	84.3	106	10	US-09-158-120A-35	Sequence 35, Appl
44	462.5	84.2	110	15	US-10-283-349-33	Sequence 33, Appl
45	462	84.2	233	15	US-10-071-485-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1  
US-09-976-787-24  
Sequence 24, Application US/09976787  
Patent No. US20020064528A1  
GENERAL INFORMATION:  
APPLICANT: Zhu, Zhenping  
APPLICANT: Walte, Larry  
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
FILE REFERENCE: 11245/46505  
CURRENT APPLICATION NUMBER: US/09/976,787  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 09/493,539  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/117,726  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 24  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Mouse  
US-09-976-787-24

Query Match 100.0%; Score 549; DB 9; Length 106;  
Best Local Similarity 100.0%; Pred. No. 5.8e-40;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKRGTSPLKWIYSTSNLASGVAR 60  
DB 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKRGTSPLKWIYSTSNLASGVAR 60  
QY 61 FSGSGSGTSYSTLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 61 FSGSGSGTSYSTLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106

RESULT 2  
US-09-865-198-23

```
; Sequence 23, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23
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Query Match          100.0%; Score 549; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.8e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60

OY      61 FSGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
Db      61 FSGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
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RESULT 3  
US-09-798-689-8

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; Sequence 8, Application US/09798689
; Publication No. US20030103973A1
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Patricia
; APPLICANT: Rockwell, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; TITLE OF INVENTION: Combined with Radiation and Chemotherapy
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-8
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Query Match          100.0%; Score 549; DB 11; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.8e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60

OY      61 FSGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
```

```
Db      61 FSGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
```

RESULT 4  
US-09-976-787-8

```
; Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-8
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```
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Best Local Similarity 100.0%; Pred. No. 5.9e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
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Db      1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60

OY      61 FSGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
Db      61 FSGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
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RESULT 5  
US-09-865-198-8

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; Sequence 8, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-8
```

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Query Match          100.0%; Score 549; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.9e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60
Db      1 DIELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60

OY      61 FSGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
Db      61 FSGSGSGTSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106
```

```
RESULT 6
US-09-976-787-29
; Sequence 29, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 29
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29
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Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      61 FSGSGSGTSTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 106
         |||||||
DB      193 FSGSGSGTSTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 238
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RESULT 7
US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metho
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28
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Query Match          100.0%; Score 549; DB 10; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      133 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMITYSTSNLASGVPAR 192
         |||||||
OY      61 FSGSGSGTSTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 106
         |||||||
DB      193 FSGSGSGTSTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 238
         |||||||
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RESULT 8
US-09-798-689-21
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; Sequence 21, Application US/09798689
; Publication No. US20030103973A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-21
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Query Match          100.0%; Score 549; DB 11; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      133 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMITYSTSNLASGVPAR 192
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OY      61 FSGSGSGTSTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 106
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DB      193 FSGSGSGTSTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 238
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RESULT 9
US-09-976-787-28
; Sequence 28, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28
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Query Match          100.0%; Score 549; DB 9; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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         |||||||
DB      133 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMITYSTSNLASGVPAR 192
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OY 61 FSGSGSGTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 106  
Db 193 FSGSGSGTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 238

RESULT 10

US-09-865-198-27  
; Sequence 27, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-like Antigen Binding Proteins and Metho  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; PRIOR FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Wordperfect 8.0 for windows  
; SEQ ID NO 27  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-865-198-27

Query Match 100.0%; Score 549; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIETQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
Db 133 DIETQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 192  
OY 61 FSGSGSGTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 106  
Db 193 FSGSGSGTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 238

RESULT 11

US-09-910-059-17  
; Sequence 17, Application US/09910059  
; Patent No. US20020142359A1  
; GENERAL INFORMATION:  
; APPLICANT: Copley, Clive G  
; APPLICANT: Edge, Michael Derek  
; APPLICANT: Emery, Stephen Charles  
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,  
; FILE REFERENCE: 1991-209  
; CURRENT APPLICATION NUMBER: US/09/910,059  
; PRIOR FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 09/171,945  
; PRIOR FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: PCT/GB97/01165  
; PRIOR FILING DATE: 1997-04-29  
; PRIOR APPLICATION NUMBER: GB 9703103.3  
; PRIOR FILING DATE: 1997-02-14  
; PRIOR APPLICATION NUMBER: GB9609405.7  
; PRIOR FILING DATE: 1996-05-04  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chimaeric light chain sequence  
US-09-910-059-17

Query Match 97.3%; Score 534; DB 10; Length 235;  
Best Local Similarity 96.2%; Pred. No. 2.4e-38;

Matches 102; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 23 DIETQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 82  
OY 61 FSGSGSGTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 106  
Db 83 FSGSGSGTSLTISRMEADATYYCQORSTYPLTFGAGTKLEIK 128

RESULT 12

US-09-910-059-9  
; Sequence 9, Application US/09910059  
; Patent No. US20020142359A1  
; GENERAL INFORMATION:  
; APPLICANT: Copley, Clive G  
; APPLICANT: Edge, Michael Derek  
; APPLICANT: Emery, Stephen Charles  
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,  
; FILE REFERENCE: 1991-209  
; CURRENT APPLICATION NUMBER: US/09/910,059  
; PRIOR FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 09/171,945  
; PRIOR FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: PCT/GB97/01165  
; PRIOR FILING DATE: 1997-04-29  
; PRIOR APPLICATION NUMBER: GB 9703103.3  
; PRIOR FILING DATE: 1997-02-14  
; PRIOR APPLICATION NUMBER: GB9609405.7  
; PRIOR FILING DATE: 1996-05-04  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-910-059-9

Query Match 96.9%; Score 532; DB 10; Length 108;  
Best Local Similarity 95.3%; Pred. No. 1.7e-38;  
Matches 101; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 DIETQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
Db 1 DIETQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
OY 61 FSGSGSGTSLTISRMEADATYYCQORSSYPFTFGSGTKLEIK 106  
Db 61 FSGSGSGTSLTISRMEADATYYCQORSTYPLTFGAGTKLEIK 106

RESULT 13

US-10-247-488-2  
; Sequence 2, Application US/10247488  
; Publication No. US20030022244A1  
; GENERAL INFORMATION:  
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &  
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53  
; FILE REFERENCE: 1196336-RAMOT  
; CURRENT APPLICATION NUMBER: US/10/247,488  
; PRIOR FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: US/09/526,738  
; PRIOR FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Humanus  
US-10-247-488-2



Query Match 96.0%; Score 527; DB 15; Length 256;  
Best Local Similarity 95.3%; Pred. No. 1e-37;  
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
Db 132 DIETQSPAIMSASPGKVTITCSASSSVNYMHWFQOKPGTSPKLMWISTSNLASGVPAR 191

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIK 106  
Db 192 FSGSGSGTSYSLTISRMEADAATYYCQRRSSYPFTFGSGTKLQIK 237

RESULT 14

US-10-247-488-4  
; Sequence 4, Application US/10247488  
; Publication No. US20030022244A1  
; GENERAL INFORMATION:  
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &  
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53  
; FILE REFERENCE: 1196336-RAMOT  
; CURRENT APPLICATION NUMBER: US/10/247,488  
; PRIOR FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: US/09/526,738  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Humanus  
US-10-247-488-4

Query Match 96.0%; Score 527; DB 15; Length 258;  
Best Local Similarity 95.3%; Pred. No. 1.1e-37;  
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
Db 134 DIETQSPAIMSASPGKVTITCSASSSVNYMHWFQOKPGTSPKLMWISTSNLASGVPAR 193

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIK 106  
Db 194 FSGSGSGTSYSLTISRMEADAATYYCQRRSSYPFTFGSGTKLQIK 239

RESULT 15

US-10-232-187-4  
; Sequence 4, Application US/10232187  
; Publication No. US20030092091A1  
; GENERAL INFORMATION:  
; APPLICANT: Abrahamson, Julie A.  
; APPLICANT: Bochner, Bruce  
; APPLICANT: Erickson-Miller, Connie L.  
; APPLICANT: Kikly, Kristine K.  
; APPLICANT: Schleimer, Robert  
; APPLICANT: Nulku, Turkan E.  
; TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies  
; FILE REFERENCE: GH50042-1  
; CURRENT APPLICATION NUMBER: US/10/232,187  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/187,595  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: PCT/US01/07193  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/315,943  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/349,830  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: 60/394,741  
; PRIOR FILING DATE: 2002-07-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-232-187-4

Query Match 95.8%; Score 526; DB 15; Length 107;  
Best Local Similarity 95.3%; Pred. No. 5.3e-38;  
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60  
Db 1 EILITQSPAIMSASPGKVSITCSATSSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPAR 60

QY 61 FSGSGSGTSYSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIK 106  
Db 61 FSGSGSGTSYSLTISRMEADAATYYCQRRSSYPFTFGSGTKLEIK 106

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2003, 09:31:34 ; Search time 34.1595 Seconds  
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Perfect score: 549

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	534	97.3	235	3 US-09-171-945-17	Sequence 17, Appl
2	532	96.9	108	3 US-09-171-945-9	Sequence 9, Appl
3	529	96.4	129	2 US-08-116-778E-2	Sequence 2, Appl
4	529	96.4	129	2 US-08-438-562-2	Sequence 2, Appl
5	529	96.4	129	2 US-08-483-528B-92	Sequence 92, Appl
6	523	95.3	270	2 US-08-652-507-2	Sequence 2, Appl
7	523	95.3	553	3 US-08-661-052-16	Sequence 16, Appl
8	523	95.3	553	2 US-09-188-082-16	Sequence 16, Appl
9	523	95.3	553	4 US-09-364-088-16	Sequence 16, Appl
10	523	95.3	553	4 US-09-102-716-16	Sequence 16, Appl
11	521	94.9	281	4 US-09-423-439-44	Sequence 44, Appl
12	521	94.9	666	4 US-09-423-439-51	Sequence 51, Appl
13	518	94.4	105	3 US-08-434-000A-12	Sequence 12, Appl
14	518	94.4	105	4 US-09-312-157-12	Sequence 12, Appl
15	516	94.0	106	1 US-07-634-278-1	Sequence 1, Appl
16	516	94.0	106	1 US-07-634-278-16	Sequence 16, Appl
17	516	94.0	106	1 US-08-477-728-1	Sequence 1, Appl
18	516	94.0	106	1 US-08-477-728-16	Sequence 16, Appl
19	516	94.0	106	1 US-08-474-040-1	Sequence 1, Appl
20	516	94.0	106	1 US-08-474-040-16	Sequence 16, Appl
21	516	94.0	106	1 US-08-487-200-1	Sequence 1, Appl
22	516	94.0	106	1 US-08-487-200-16	Sequence 16, Appl
23	516	94.0	106	1 US-08-488-113B-163	Sequence 163, App
24	516	94.0	106	1 US-08-477-484B-163	Sequence 163, App
25	516	94.0	106	1 US-08-107-669D-49	Sequence 49, Appl
26	516	94.0	106	1 US-08-472-788A-83	Sequence 83, Appl
27	516	94.0	106	2 US-08-477-531B-49	Sequence 49, Appl

28	516	94.0	106	2 US-08-646-360-163	Sequence 163, App
29	516	94.0	106	2 US-08-082-842A-83	Sequence 83, Appl
30	516	94.0	106	3 US-08-839-765-163	Sequence 163, App
31	516	94.0	106	3 US-09-136-389-163	Sequence 163, App
32	516	94.0	106	3 US-08-484-537-1	Sequence 1, Appl
33	516	94.0	106	3 US-08-484-537-16	Sequence 16, Appl
34	516	94.0	106	4 US-09-610-838-163	Sequence 163, App
35	516	94.0	239	3 US-08-279-772A-8	Sequence 8, Appl
36	516	94.0	239	3 US-08-902-486-11	Sequence 11, Appl
37	516	94.0	599	1 US-08-463-163-3	Sequence 3, Appl
38	498	90.7	144	4 US-09-318-786-29	Sequence 29, Appl
39	493	89.8	130	4 US-09-393-385B-113	Sequence 113, App
40	490	89.3	130	4 US-09-393-385B-111	Sequence 111, App
41	489	89.1	128	3 US-08-619-491-2	Sequence 2, Appl
42	489	89.1	128	5 PCT-US95-07302-2	Sequence 2, Appl
43	483	88.0	244	2 US-08-553-497A-20	Sequence 20, Appl
44	481	87.6	107	1 US-08-211-202-3	Sequence 3, Appl
45	481	87.6	246	1 US-08-469-486-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1  
US-09-171-945-17  
; Sequence 17, Application US/09171945  
; Patent No. 6277599  
; GENERAL INFORMATION:  
; APPLICANT: Emery, Stephen  
; APPLICANT: Copley, Clive Graham  
; APPLICANT: Edge, Michael Derek  
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said  
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System  
; FILE REFERENCE: Monoclonal Antibody to CEA  
; CURRENT APPLICATION NUMBER: US/09/171,945  
; CURRENT FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: GB9703103.3  
; PRIOR FILING DATE: 1997-02-14  
; PRIOR APPLICATION NUMBER: GB9609405.7  
; PRIOR FILING DATE: 1996-05-04  
; PRIOR APPLICATION NUMBER: PCT/GB97/01165  
; PRIOR FILING DATE: 1997-04-29  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: humanized  
US-09-171-945-17  
  
Query Match 97.3%; Score 534; DB 3; Length 235;  
Best Local Similarity 96.2%; Pred. No. 2.2e-40;  
Matches 102; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLMWYSTSNLASCVPAR 60  
DB 23 DIELTQSPAIMSASPGKVTITCSASSSVYMHWFQKPGTSPKLMWYSTSNLASCVPAR 82  
QY 61 FSGSGSGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 83 FSGSGSGTSYSLTISRMEADATYYCQQRSTYPLTFGAGTKLEIK 128  
  
RESULT 2  
US-09-171-945-9  
; Sequence 9, Application US/09171945  
; Patent No. 6277599  
; GENERAL INFORMATION:  
; APPLICANT: Emery, Stephen  
; APPLICANT: Copley, Clive Graham  
; APPLICANT: Edge, Michael Derek

;; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said  
;; FILE REFERENCE: Antibody, and Their Therapeutic Use in an Adept System  
;; CURRENT APPLICATION NUMBER: US/09/171,945  
;; CURRENT FILING DATE: 1998-10-29  
;; PRIOR APPLICATION NUMBER: GB9703103.3  
;; PRIOR FILING DATE: 1997-02-14  
;; PRIOR APPLICATION NUMBER: GB9609405.7  
;; PRIOR FILING DATE: 1996-05-04  
;; PRIOR APPLICATION NUMBER: PCT/GB97/01165  
;; PRIOR FILING DATE: 1997-04-29  
;; NUMBER OF SEQ ID NOS: 131  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 9  
;; LENGTH: 108  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; OTHER INFORMATION: Description of Artificial Sequence: humanized  
US-09-171-945-9

Query Match 96.4%; Score 532; DB 3; Length 108;  
Best Local Similarity 95.3%; Pred. No. 1.4e-40;  
Matches 101; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db 1 DIETQSPAIMSASPGKVTITCSASSSVTYMHWFQOKPGTSPKLTWYSTNLSGVPAR 60

QY 61 FSGSGSTSYSLTISRMEADATYYCQRRSSYPFTGSGTKLEIK 106  
Db 61 FSGSGSTSYSLTISRMEADATYYCQRRSTYPLTFGAGTKLEIK 106

## RESULT 3

US-08-116-778E-2

;; Sequence 2, Application US/08116778E  
;; Patent No. 5830470  
;; GENERAL INFORMATION:

;; APPLICANT: NAKAMURA, KAZUYASU  
;; APPLICANT: KOIKE, MASAMICHI  
;; APPLICANT: SHITARA, KENYA  
;; APPLICANT: HANAI, NOBUO  
;; APPLICANT: KUMANA, YOSHIHISA  
;; APPLICANT: HASEGAWA, MAMORU  
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
;; NUMBER OF SEQUENCES: 49  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: NIXON & VANDERHAYE P.C.  
;; STREET: 1100 NORTH GLEBE ROAD  
;; CITY: ARLINGTON  
;; STATE: VIRGINIA  
;; COUNTRY: U.S.A.  
;; ZIP: 22201-4714

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/116,778E  
;; FILING DATE: 07-SEP-93

;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:

;; NAME: WILSON, MARY J.  
;; REGISTRATION NUMBER: 32,955  
;; REFERENCE/DOCKET NUMBER: 249-59  
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (703)816-4000  
;; TELEFAX: (703)816-4100  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 129 amino acids

;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FEATURE:  
;; NAME/KEY: sig\_peptide  
;; LOCATION: -22..-1  
;; IDENTIFICATION METHOD: BY SIMILARITY  
;; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED  
;; IDENTIFICATION METHOD: CONSENSUS  
;; FEATURE:  
;; NAME/KEY: domain  
;; LOCATION: 24..33  
;; IDENTIFICATION METHOD: BY SIMILARITY  
;; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED  
;; IDENTIFICATION METHOD: CONSENSUS  
;; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"

;; FEATURE:  
;; NAME/KEY: domain  
;; LOCATION: 49..55  
;; IDENTIFICATION METHOD: BY SIMILARITY  
;; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED  
;; IDENTIFICATION METHOD: CONSENSUS  
;; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"

;; FEATURE:  
;; NAME/KEY: domain  
;; LOCATION: 88..96  
;; IDENTIFICATION METHOD: BY SIMILARITY  
;; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED  
;; IDENTIFICATION METHOD: CONSENSUS  
;; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"

US-08-116-778E-2

Query Match 96.4%; Score 529; DB 2; Length 129;  
Best Local Similarity 97.1%; Pred. No. 3.2e-40;  
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTNLSGVPAR 61  
Db 24 IELTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLTWYSTNLSGVPAR 83

QY 62 SGGSGSTSYSLTISRMEADATYYCQRRSSYPFTGSGTKLEIK 106  
Db 84 SGGSGSTSYSLTISRMEADATYYCQRRSSYPFTGGGTKLEIK 128

## RESULT 4

US-08-438-562-2

;; Sequence 2, Application US/08438562  
;; Patent No. 5874255  
;; GENERAL INFORMATION:

;; APPLICANT: NAKAMURA, KAZUYASU  
;; APPLICANT: KOIKE, MASAMICHI  
;; APPLICANT: SHITARA, KENYA  
;; APPLICANT: HANAI, NOBUO  
;; APPLICANT: KUMANA, YOSHIHISA  
;; APPLICANT: HASEGAWA, MAMORU  
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
;; NUMBER OF SEQUENCES: 49  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: NIXON & VANDERHAYE P.C.  
;; STREET: 1100 NORTH GLEBE ROAD  
;; CITY: ARLINGTON  
;; STATE: VIRGINIA  
;; COUNTRY: U.S.A.  
;; ZIP: 22201-4714

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/438,562  
;; FILING DATE: 10-MAY-95

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22..-1
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; FEATURE:
; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
;
US-08-438-562-2

Query Match          96.4%; Score 529; DB 2; Length 129;
Best Local Similarity 97.1%; Pred. No. 3.2e-40;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IELTSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPARF 61
Db 24 IVLTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPARF 83

QY 62 SSGSGSTSYSLTISRMEADATYYCCQRRSSYPFTFGSGTKLEIK 106
Db 84 SSGSGSTSYSLTISRMEADATYYCCQRRSSYPFTFGSGTKLEIK 128

RESULT 5
US-08-483-528B-92
; Sequence 92, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,528B
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22..-1
; IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN
; IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
; FEATURE:
; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
;
US-08-483-528B-92

Query Match          96.4%; Score 529; DB 2; Length 129;
Best Local Similarity 97.1%; Pred. No. 3.2e-40;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IELTSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPARF 61
Db 24 IVLTQSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPARF 83

QY 62 SSGSGSTSYSLTISRMEADATYYCCQRRSSYPFTFGSGTKLEIK 106
Db 84 SSGSGSTSYSLTISRMEADATYYCCQRRSSYPFTFGSGTKLEIK 128

RESULT 6
US-08-652-507-2
; Sequence 2, Application US/08652507
; Patent No. 5876691
; GENERAL INFORMATION:
; APPLICANT:
```

TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderye, P.C.  
; STREET: 1100 No. 5876691th Glebe Road, 8th Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,507  
; FILING DATE: 02-Jul-1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arthur R. Crawford  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 117-211  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 270 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-03-652-507-2

Query Match 95.3%; Score 523; DB 2; Length 270;  
Best Local Similarity 97.1%; Pred. No. 2.4e-39;  
Matches 100; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 4 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPARFSG 63  
DB 165 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPARFSG 224  
QY 64 SSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 225 SSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGAGTKLEIK 267

RESULT 7  
US-08-661-052-16  
; Sequence 16, Application US/08661052  
; Patent No. 5837243  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano  
; APPLICANT: Chezian Somasundaram  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,052

FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/484,172  
; FILING DATE: 07-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MXI-043CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-661-052-16

Query Match 95.3%; Score 523; DB 2; Length 553;  
Best Local Similarity 97.1%; Pred. No. 5.2e-39;  
Matches 100; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 4 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPARFSG 63  
DB 415 LTQSPAIMSASPGKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPARFSG 474  
QY 64 SSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 475 SSGSTSYSLTISRMEADAATYYCQQRSSYPFTFGAGTKLEIK 517

RESULT 8  
US-09-188-082-16  
; Sequence 16, Application US/09188082  
; Patent No. 6270765  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano  
; APPLICANT: Chezian Somasundaram  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/188,082  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/661,052  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MXI-043CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid



TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-188-082-16

Query Match 95.3%; Score 523; DB 3; Length 553;  
Best Local Similarity 97.1%; Pred. No. 5.2e-39;  
Matches 100; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPEKEVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPARFSG 63  
DB 415 LTQSPAIMSASPEKEVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPARFSG 474  
QY 64 SSGGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 475 SSGGTSYSLTISRMEADATYYCQQRSSYPFTFGAGTKLEIK 517

## RESULT 9

US-09-364-088-16  
Sequence 16, Application US/09364088  
Patent No. 6365161  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo, et al.  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street, 24th floor  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/364,088  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/188,082  
FILING DATE: 07-JUNE-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remillard, Jane E.  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: MXI-043CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-7414  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-364-088-16

Query Match 95.3%; Score 523; DB 4; Length 553;  
Best Local Similarity 97.1%; Pred. No. 5.2e-39;  
Matches 100; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPEKEVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPARFSG 63  
DB 415 LTQSPAIMSASPEKEVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPARFSG 474  
QY 64 SSGGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 475 SSGGTSYSLTISRMEADATYYCQQRSSYPFTFGAGTKLEIK 517

## RESULT 10

US-09-102-716-16  
Sequence 16, Application US/09102716  
Patent No. 6395272  
GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo  
Joel Goldstein  
Robert Graziano  
Chezian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/102,716  
FILING DATE: 22-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-102-716-16

Query Match 95.3%; Score 523; DB 4; Length 553;  
Best Local Similarity 97.1%; Pred. No. 5.2e-39;  
Matches 100; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPEKEVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPARFSG 63  
DB 415 LTQSPAIMSASPEKEVTITCSASSSVSYMHWFQOKPGTSPKLMWYSTSNLASGVPARFSG 474  
QY 64 SSGGTSYSLTISRMEADATYYCQQRSSYPFTFGSGTKLEIK 106  
DB 475 SSGGTSYSLTISRMEADATYYCQQRSSYPFTFGAGTKLEIK 517

## RESULT 11

US-09-423-439-44  
Sequence 44, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.

CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
US-09-423-439-44

Query Match 94.9%; Score 521; DB 4; Length 281;  
Best Local Similarity 95.2%; Pred. No. 3.8e-39;  
Matches 100; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IELTSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPARF 61  
DB 159 IVLTSIPAISASPEKVTITCSASSSVTYMHWFQOKPGTSPKLMYSTSNLASGVPARF 218  
QY 62 SSGSGTSLTISRMEADATYCCQRRSYPFTFGSGTKLEIK 106  
DB 219 SSGSGTSLTISRMEADATYCCQRRSTYPLTFGAGTKLEIK 263

RESULT 12  
US-09-423-439-51  
Sequence 51, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:

LENGTH: 666 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-423-439-51

Query Match 94.9%; Score 521; DB 4; Length 666;  
Best Local Similarity 95.2%; Pred. No. 9.5e-39;  
Matches 100; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IELTSPAIMSASPEKVTITCSASSSVSYMHWFQOKPGTSPKLMYSTSNLASGVPARF 61  
DB 156 IVLTSIPAISASPEKVTITCSASSSVTYMHWFQOKPGTSPKLMYSTSNLASGVPARF 215  
QY 62 SSGSGTSLTISRMEADATYCCQRRSYPFTFGSGTKLEIK 106  
DB 216 SSGSGTSLTISRMEADATYCCQRRSTYPLTFGAGTKLEIK 260

RESULT 13  
US-08-434-000A-12  
Sequence 12, Application US/08434000A  
Patent No. 6046037  
GENERAL INFORMATION:  
APPLICANT: ANDREW C. HIATT, JULIAN  
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,000A  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: 1

APPLICATION NUMBER: 08/367,395  
FILING DATE: 12/30/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 212/127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 552-8400  
TELEFAX: (619) 552-0159  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: Guy's 13 Kappa  
US-08-434-000A-12

Query Match 94.4%; Score 518; DB 3; Length 105;



Wed Jul 30 10:26:15 2003

us-09-865-198-23.ra1

Search completed: July 30, 2003, 09:38:32  
Job time : 35.1595 secs